

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 13, 2005, 18:34:54 ; Search time 246 Seconds
(without alignments)
3595.614 Million cell updates/sec

Title: US-09-611-257A-24

Perfect score: 12028

Sequence: 1 MLPHRVPCVTPPLRGSR.....KDTILSLSLSDPTDMDPZ 2287

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A. Geneseq 16Dec04:*

1: geneseqp1980s:*

2: geneseqp1990s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003as:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	12028	100.0	2287	4	AAB66475	Rat alpha
2	11657	96.9	2254	2	AA114590	Rat T-typ
3	11626	96.7	2272	2	AA114592	Rat T-typ
4	11610.5	96.5	2265	2	AA114591	Rat T-typ
5	11606.5	96.5	2247	2	AA114593	Rat T-typ
6	11542.5	96.0	2428	3	AA170720	Rat pancer
7	10857	90.3	2250	2	AA114586	Rat T-t
8	10833	90.1	2268	2	AA114588	Rat T-t
9	10820.5	90.0	2273	4	AAE01019	Human T-t
10	10810.5	89.9	2261	2	AA114587	Human T-t
11	10806.5	89.8	2243	2	AA114589	Human T-t
12	10806.5	89.8	2243	7	ADJ68819	Human T-t
13	10732.5	89.2	2377	8	ADQ89064	Human T-t
14	10533	87.6	2266	4	AAB66481	Human T-t
15	10265.5	85.8	2359	4	AAB66476	Human T-t
16	10222	85.7	2353	6	ABP72254	Human T-t
17	10222	85.7	2353	6	ABP72254	Human T-t
18	10222	85.7	2353	7	ADJ69322	Human T-t
19	10222	85.7	2353	7	ADJ69322	Human T-t
20	10222	85.7	2353	7	ADJ69322	Human T-t
21	10222	85.7	2353	7	ADJ69322	Human T-t
22	10222	85.7	2353	7	ADJ69322	Human T-t
23	10222	85.7	2353	7	ADJ69322	Human T-t
24	10222	85.7	2353	7	ADJ69322	Human T-t
25	10222	85.7	2353	7	ADJ69322	Human T-t
26	10222	85.7	2353	7	ADJ69322	Human T-t
27	10222	85.7	2353	7	ADJ69322	Human T-t
28	10222	85.7	2353	7	ADJ69322	Human T-t
29	10222	85.7	2353	7	ADJ69322	Human T-t
30	10222	85.7	2353	7	ADJ69322	Human T-t
31	10222	85.7	2353	7	ADJ69322	Human T-t
32	10222	85.7	2353	7	ADJ69322	Human T-t
33	10222	85.7	2353	7	ADJ69322	Human T-t
34	10222	85.7	2353	7	ADJ69322	Human T-t
35	10222	85.7	2353	7	ADJ69322	Human T-t
36	10222	85.7	2353	7	ADJ69322	Human T-t
37	10222	85.7	2353	7	ADJ69322	Human T-t
38	10222	85.7	2353	7	ADJ69322	Human T-t
39	10222	85.7	2353	7	ADJ69322	Human T-t
40	10222	85.7	2353	7	ADJ69322	Human T-t
41	10222	85.7	2353	7	ADJ69322	Human T-t
42	10222	85.7	2353	7	ADJ69322	Human T-t
43	10222	85.7	2353	7	ADJ69322	Human T-t
44	10222	85.7	2353	7	ADJ69322	Human T-t
45	10222	85.7	2353	7	ADJ69322	Human T-t

Mon Apr 18 12:41

26	5409	45.0	2175	6	ABU08511	Human T-t
27	5409	45.0	2175	8	ADH69265	Human TCC
28	5405.5	44.9	2188	5	AAU10536	Human T-t
29	5405.5	44.9	2188	6	ABU08512	Human T-t
30	5405.5	44.9	2188	8	ADH69267	Human TCC
31	5345	44.4	1835	2	AA114597	Rat T-typ
32	5345	44.4	1835	8	ADH69268	Rat T-typ
33	5342.5	44.4	1823	2	AA114596	Human T-t
34	5179.5	43.1	1792	4	AAB66477	Rat Brain
35	4807	40.0	982	4	AAU23743	Human EST
36	3950	32.8	1854	2	AAW79161	Human cal
37	3950	32.8	1854	2	AAW79161	Human cal
38	3553	29.5	1657	8	ADN24183	Bacterial
39	3397	28.2	2435	4	ABB60448	Drosophila
40	3125	26.0	644	4	AAB66478	Human alp
41	2975	24.7	1859	4	ABG10954	Novel hum
42	1911.5	15.9	853	8	AAU93437	Human pol
43	1911.5	15.9	853	8	ADL31041	Human pro
44	1686.5	14.0	518	4	AAB66479	Human alp
45	1682	14.0	2339	2	AAU33549	Sequence

ALIGNMENTS

RESULT 1
AAB66475
ID AAB66475 standard; protein; 2287 AA.
XX
AC AAB66475;
XX
DT 09-APR-2001 (first entry)
XX
DE Rat alpha-IG calcium channel protein.
XX
KW Rat; expressed sequence tag; EST; antiarrhythmic; anticonvulsant;
KW hypotensive; cardiant; nootropic; T-type calcium channel subunit;
KW cardiac hypertrophy; cardiac arrhythmia; hypertension; sleep disorder;
KW epilepsy; alpha-IG calcium channel.
XX
OS Rattus sp.
XX
PN WO200102561-A2.
XX
PD 11-JAN-2001.
XX
PF 04-JUL-2000; 2000WO-CA000794.
XX
PR 02-JUL-1999; 99US-00346794.
XX
(NEUR-) NEUROMED TECHNOLOGIES INC.
XX
PI Snutch TP, Baillie DL;
XX
DR WPI; 2001-123111/13.
XX
DR N-PSDB; AAF31677.
XX
PT Novel T-type calcium channel alpha-1 subunit gene useful for treating
PT cardiac hypertrophy, cardiac arrhythmia, hypertension, sleep disorder and
PT epilepsy.
XX
PS Disclosure; Page 63-72; 103pp; English.
XX
CC The present sequence is given in a specification providing sequences and
CC partial sequences for three types of mammalian (human and rat) T-type
CC calcium channel subunits. An expression cassette has been generated which
CC comprises a nucleotide sequence encoding a T-type calcium channel alpha_1
CC subunit operably linked to control sequences to effect its expression.
CC The novel calcium channel nucleic acids and proteins are useful for
CC treating conditions characterised by undesirable levels of T-type calcium
CC channel activity such as cardiac hypertrophy, cardiac arrhythmia,
CC hypertension, sleep disorder and epilepsy
XX

[illegible]

QY 2101 IRLPAPCGLEPSWAKDPETESSLELDTLSWISGDLPLSSQERPLPRDLKKCYSVET 2160
 Db 2101 IRLPAPCGLEPSWAKDPETESSLELDTLSWISGDLPLSSQERPLPRDLKKCYSVET 2160
 QY 2161 QSCRPRPGFWLDEQRRHSIAVSCLSGSGQPRLCPSGSSILGGQPLGGPGSRPKKLSPPSI 2220
 Db 2161 QSCRPRPGFWLDEQRRHSIAVSCLSGSGQPRLCPSGSSILGGQPLGGPGSRPKKLSPPSI 2220
 QY 2221 SIDPPESQSRPPCPGVCLRRAPASDSDKPSVSPPLDSTAASPSPKKDTLSLSGLSSD 2280
 Db 2221 SIDPPESQSRPPCPGVCLRRAPASDSDKPSVSPPLDSTAASPSPKKDTLSLSGLSSD 2280
 QY 2281 PTMDPZ 2287
 Db 2281 PTMDPZ 2287

RESULT 2
 AAY14590
 ID AAY14590 standard; protein; 2254 AA.
 AC AAY14590;
 XX
 DT 07-DEC-1999 (first entry)
 XX
 DE Rat T-type voltage-gated Ca channel alpha-1-G (rCav1a).
 XX
 KW Human; T-type voltage-gated calcium channel; membrane; pore; ion;
 KW activation; current; rat; screen; drug; cardiomyopathy; epilepsy.
 OS Rattus sp.
 XX
 PN WO929847-A1.
 XX
 PD 17-JUN-1999.
 XX
 PF 30-OCT-1998; 98WO-US023161.
 XX
 PR 05-DEC-1997; 97US-00985809.
 XX
 PA (LOYO) UNIV LOYOLA CHICAGO.
 XX
 PI Perez-Reyes E, Cribbs LL;
 XX
 DR WPI; 1999-394972/33.
 DR N-PSDB; AAX83485.
 XX
 PT New T-type voltage-gated calcium channels.
 XX
 PS Disclosure; Page 67-76; 138pp; English.

This sequence represents a rat T-type voltage-gated calcium (Ca) channel alpha-1-G designated rCav1a. Voltage gated channels are membrane bound glycosylated proteins formed of several subunits. The large alpha subunits form a pore in the membrane that is selective for a given ionic species. Each alpha subunit contains 4 domains (I, II, III and IV) and each domain contains 6 putative transmembrane helical segments (S1-S6). T-type Ca channels are activated at a lower voltage than L- or N-type channels. Characteristics of T-type channels include short current time, slow activation kinetics near threshold, fast inactivation kinetics and slow tail current. The sequences AAX83481-X83492 represent novel T-type voltage-gated Ca channel genes from humans and rats. Each of the novel Ca channels contains a putative IVS4 region comprising the amino acid sequence AAY14598. Cells expressing the T-type voltage-gated calcium channel proteins can be used to screen for drugs which affect calcium channels. Methods are also disclosed for treating a disease or disorder associated with a deficiency in a native T-type calcium channel nucleic acid, e.g. to treat cardiomyopathy, epilepsy, etc

Sequence 2254 AA;

Query Match 96.9%; Score 11657; DB 2; Length 2254;
 Best Local Similarity 99.7%; Pred. No. 0;

	Matches	2219;	Conservative	0;	Mismatches	6;	Indels	0;	Gaps	0;
QY	62	GAAGAGSTGKPGSADSEAGLPPALAPVFFYLSQDSRPSWCLRTVCNPFWRVSM	121							
Db	30	GRQPGSTGKPGSADSEAGLPPALAPVFFYLSQDSRPSWCLRTVCNPFWRVSM	89							
QY	122	VLLNCVTLGMRPCEDTACDSORCIILOAFDDFIPAFPAVEMVVMKVALGIFGKKCYLG	181							
Db	90	VLLNCVTLGMRPCEDTACDSORCIILOAFDDFIPAFPAVEMVVMKVALGIFGKKCYLG	149							
QY	182	DTWNRDLDFIIVAGMLKSLQNVSFSAVRVRLRPLRANRVPMSRILVTLTLLDTLP	241							
Db	150	DTWNRDLDFIIVAGMLKSLQNVSFSAVRVRLRPLRANRVPMSRILVTLTLLDTLP	209							
QY	242	MLGNVLLCFFVFFIFGIVGQVLMAGLLNRCFLPENFSLDPLSDVLEPIYQTEDESPF	301							
Db	210	MLGNVLLCFFVFFIFGIVGQVLMAGLLNRCFLPENFSLDPLSDVLEPIYQTEDESPF	269							
QY	302	ICSPRENGMRSCSVPTLRGGGGPPCSDLYETVNSSNTTCVNMNOYVYTNCSAGEHN	361							
Db	270	ICSPRENGMRSCSVPTLRGGGGPPCSDLYETVNSSNTTCVNMNOYVYTNCSAGEHN	329							
QY	362	PFKGINFDNIGYAMIAIFQVITLGGVNDIMYFVMDAHSFYFIYFILLIIVGSPFMINL	421							
Db	330	PFKGINFDNIGYAMIAIFQVITLGGVNDIMYFVMDAHSFYFIYFILLIIVGSPFMINL	389							
QY	422	CLVVIATPSETKQRESQLMRQVRFLSNASTLASFPSPGSCYBELLKYVLILKAAR	481							
Db	390	CLVVIATPSETKQRESQLMRQVRFLSNASTLASFPSPGSCYBELLKYVLILKAAR	449							
QY	482	RLAQSRAIGVRAGLLSPPVARSQGPSPGSCSTRHRLSVHHLVHHHHHHHHVHLGN	541							
Db	450	RLAQSRAIGVRAGLLSPPVARSQGPSPGSCSTRHRLSVHHLVHHHHHHHHVHLGN	509							
QY	542	GTLRVPRASPEIQDRDANGSRRLMLPPPSTPSPGPPRGAESVHSFYHADCHLEPVRQ	601							
Db	510	GTLRVPRASPEIQDRDANGSRRLMLPPPSTPSPGPPRGAESVHSFYHADCHLEPVRQ	569							
QY	602	APPPRCPSEASGRTVSGKYPTVHTSPPEILKOKALVEVAPSPGPPTLTSTNIPGPF	661							
Db	570	APPPRCPSEASGRTVSGKYPTVHTSPPEILKOKALVEVAPSPGPPTLTSTNIPGPF	629							
QY	662	SSMHKLETSQSTGACHSSCKISSPCSKADSGAGDPCPCYARTGAGEPESADHVPDSD	721							
Db	630	SSMHKLETSQSTGACHSSCKISSPCSKADSGAGDPCPCYARTGAGEPESADHVPDSD	689							
QY	722	SEAVYEFTQDAQHSDLRDPHSRRORSGLGDAEPSSVLAFWRLICDTFRKIVDSKYFGRG	781							
Db	690	SEAVYEFTQDAQHSDLRDPHSRRORSGLGDAEPSSVLAFWRLICDTFRKIVDSKYFGRG	749							
QY	782	IMAILVNTLSMGIYHEQPEELTNALEISNIVFTSLFALEMLLKLVLVGPFGYIKNPYN	841							
Db	750	IMAILVNTLSMGIYHEQPEELTNALEISNIVFTSLFALEMLLKLVLVGPFGYIKNPYN	809							
QY	842	IFDGVIVISWWEIVGQGGGLSVLRTFELMVLKLVRLPALQROLVLMKTMNDVATP	901							
Db	810	IFDGVIVISWWEIVGQGGGLSVLRTFELMVLKLVRLPALQROLVLMKTMNDVATP	869							
QY	902	CMLLMFIFISILGWHLPFGCKFASBERDGTLPDRKNFDSLWAIIVTFQILTQEDWNV	961							
Db	870	CMLLMFIFISILGWHLPFGCKFASBERDGTLPDRKNFDSLWAIIVTFQILTQEDWNV	929							
QY	962	LYNGMASTSSWAALFYIALMTFGNYVLFNLVAILVEGFOAGDATKSESSEDPFSPSVD	1021							
Db	930	LYNGMASTSSWAALFYIALMTFGNYVLFNLVAILVEGFOAGDATKSESSEDPFSPSVD	989							
QY	1022	GGDKRKRLLVALGHAELRSLPLPLIHTAATPMSPKSSSTGVGEALGSGSRTSS	1081							
Db	990	GGDKRKRLLVALGHAELRSLPLPLIHTAATPMSPKSSSTGVGEALGSGSRTSS	1049							
QY	1082	SGSAEPGAHHEMKCPPSARSPHSPWSAASWTSRRSRNSLGRAPSLKRRSPSGERRS	1141							
Db	1050	SGSAEPGAHHEMKCPPSARSPHSPWSAASWTSRRSRNSLGRAPSLKRRSPSGERRS	1109							

Qy	1142	LLSGEQSDESSBEDRASPAGSDHRRHGSLEAKSFDLPDTLQVPGHRTASGR	1201	Qy	2222	IDPESQSRPPSPGVCLRRRAPASDKDPSVSPDLSTAAASPSPKOTLSLGLSDP	2281
Db	1110	LLSGEQSDESSBEDRASPAGSDHRRHGSLEAKSFDLPDTLQVPGHRTASGR	1169	Db	2190	IDPESQSRPPSPGVCLRRRAPASDKDPSVSPDLSTAAASPSPKOTLSLGLSDP	2249
Qy	1202	SSASEHQCNGKSGASRLARTLRTDDPOLGDDDDNDGNLSKGERIQAWVRSRLPACCRE	1261	Qy	2282	TDMDP 2286	
Db	1170	SSASEHQCNGKSGASRLARTLRTDDPOLGDDDDNDGNLSKGERIQAWVRSRLPACCRE	1229	Db	2250	TDMDP 2254	
Qy	1262	RDSWSAYIPPOSREFLLCHRIITHKMFHDVVLVIFLNCITTIAMERPKIDPHSAERIFL	1321				
Db	1230	RDSWSAYIPPOSREFLLCHRIITHKMFHDVVLVIFLNCITTIAMERPKIDPHSAERIFL	1289				
Qy	1322	TLSNYIFTAVFLAEMTVKVALGWCFCGEQAYLRSSWVLDGLLVLSVIDILVMSVSDSG	1381				
Db	1290	TLSNYIFTAVFLAEMTVKVALGWCFCGEQAYLRSSWVLDGLLVLSVIDILVMSVSDSG	1349				
Qy	1382	TKILGMLRVLRARTLRPLRVISRAOGLKLVVETILMSSLPKIGNIVVICCAFFIIFGLG	1441				
Db	1350	TKILGMLRVLRARTLRPLRVISRAOGLKLVVETILMSSLPKIGNIVVICCAFFIIFGLG	1409				
Qy	1442	VOLFKGFFVFCQGEDTRNINKSDCAEASRWVRHKNYFNDLGOALMSLFLVLSKDGWVD	1501				
Db	1410	VOLFKGFFVFCQGEDTRNINKSDCAEASRWVRHKNYFNDLGOALMSLFLVLSKDGWVD	1469				
Qy	1502	IMYDGLDVGVDQOPIWNNPMLLYFISPLLIYAFVFLNMFVGVVFNHFKROHOREE	1561				
Db	1470	IMYDGLDVGVDQOPIWNNPMLLYFISPLLIYAFVFLNMFVGVVFNHFKROHOREE	1529				
Qy	1562	EARREERLRLEKRSKEKQMAEACQKPYSDYSRPELLVHLLCTSHYLDLFTIGVI	1621				
Db	1530	EARREERLRLEKRSKEKQMAEACQKPYSDYSRPELLVHLLCTSHYLDLFTIGVI	1589				
Qy	1622	GLNVVTMAEHVQOQILDEALKICNYIFTIVFVFSVFKLVAFAPRRFPQDRWNLDLA	1681				
Db	1590	GLNVVTMAEHVQOQILDEALKICNYIFTIVFVFSVFKLVAFAPRRFPQDRWNLDLA	1649				
Qy	1682	IVLLSIMGITLBEIEVNSLPINPTIIRIMEVLRARVLLKLVAVGMRLHLLTVMOALP	1741				
Db	1650	IVLLSIMGITLBEIEVNSLPINPTIIRIMEVLRARVLLKLVAVGMRLHLLTVMOALP	1709				
Qy	1742	QVNLGLLFWLLFFFAALGVLEFGLDECEHPCEGLGRHATFRNFGMAFLTLFRVSTG	1801				
Db	1710	QVNLGLLFWLLFFFAALGVLEFGLDECEHPCEGLGRHATFRNFGMAFLTLFRVSTG	1769				
Qy	1802	DNWNGIMKDPDRCDQESTCINTYIPYFVSFVLTQAFVLNVVIAVLMKHLSESKEA	1861				
Db	1770	DNWNGIMKDLRCDQESTCINTYIPYFVSFVLTQAFVLNVVIAVLMKHLSESKEA	1829				
Qy	1862	KEEAELAELELEMKTLSPHSPGLSPFLWPGVGVNSTDPKPGAPHTTAHIGASGF	1921				
Db	1830	KEEAELAELELEMKTLSPHSPGLSPFLWPGVGVNSTDPKPGAPHTTAHIGASGF	1889				
Qy	1922	SLEHPTWVPHPEEVPVPLGPDLLTVKSGVSRTHSLPNDSCYRNGSTAEKSLGRHWGL	1981				
Db	1890	SLEHPTWVPHPEEVPVPLGPDLLTVKSGVSRTHSLPNDSCYRNGSTAEKSLGRHWGL	1949				
Qy	1982	PKAQSGSLSVHSOPADTSCILQPKDVHYLLQPHGAPTWGAIPLKLPPOGRPLAORPLR	2041				
Db	1950	PKAQSGSLSVHSOPADTSCILQPKDVHYLLQPHGAPTWGAIPLKLPPOGRPLAORPLR	2009				
Qy	2042	ROAAIRTDLDVQGLGSRDILLSEVSGPSCPLTSSSFWGSGSIQVQORSIGQSKVSKHI	2101				
Db	2010	ROAAIRTDLDVQGLGSRDILLSEVSGPSCPLTSSSFWGSGSIQVQORSIGQSKVSKHI	2069				
Qy	2102	RLPAPCPGLEPWSAKDPETRSLSLELDTLSWISGDLPLPSSQEPPLPRDLKCYVETO	2161				
Db	2070	RLPAPCPGLEPWSAKDPETRSLSLELDTLSWISGDLPLPSSQEPPLPRDLKCYVETO	2129				
Qy	2162	SCRRPFGWLDDEORRHUSIAVCLDSGQPLCPSPSSIGGQPLGGPGRSPKPKLSPSPIS	2221				
Db	2130	SCRRPFGWLDDEORRHUSIAVCLDSGQPLCPSPSSIGGQPLGGPGRSPKPKLSPSPIS	2189				

RESULT 3
AAV14592
ID AAV14592 standard; protein; 2272 AA.
XX
AC AAV14592;
XX
07-DEC-1999 (first entry)
DT
DE Rat T-type voltage-gated Ca channel alpha-1-G (rCav1c).
XX
XX Human; T-type voltage-gated calcium channel; membrane; pore; ion;
KW activation; current; rat; screen; drug; cardiomyopathy; epilepsy.
KW
XX Rattus sp.
OS
XX WO9929847-A1.
PN
XX
PD 17-JUN-1999.
XX
XX 30-OCT-1998; 98WO-US023161.
PF
XX
XX 05-DEC-1997; 97US-00985809.
PR
XX (LOYO) UNIV LOYOLA CHICAGO.
FA
XX
XX Perez-Reyes E, Cribbs LL;
PI
XX WPI; 1999-394972/33.
DR
XX N-PSDB; AAX83487.
XX
XX New T-type voltage-gated calcium channels.
PT
XX
XX Disclosure; Page 85-94; 138pp; English.
PS
XX This sequence represents a rat T-type voltage-gated calcium (Ca) channel
CC alpha-1-G designated rCav1c. Voltage gated channels are membrane bound
CC glycosylated proteins formed of several subunits. The large alpha
CC subunits form a pore in the membrane that is selective for a given ionic
CC species. Each alpha subunit contains 4 domains (I, II, III and IV) and
CC each domain contains 6 putative transmembrane helical segments (S1-S6). T
CC -type Ca channels are activated at a lower voltage than L- or N-type
CC channels. Characteristics of T-type channels include short current time,
CC slow activation kinetics near threshold, fast inactivation kinetics and
CC slow tail current. The sequences AAX83481-X83492 represent novel T-type
CC voltage-gated Ca channel genes from humans and rats. Each of the novel Ca
CC channels contains a putative IVS4 region comprising the amino acid
CC sequence AAV14598. Cells expressing the T-type voltage-gated calcium
CC channel proteins can be used to screen for drugs which affect or disorder
CC channels. Methods are also disclosed for treating a disease or disorder
CC associated with a deficiency in a native T-type calcium channel, nucleic
CC acid, e.g. to treat cardiomyopathy, epilepsy, etc
XX
SQ Sequence 2272 AA;

Query Match 96.7%; Score 11626; DB 2; Length 2272;
Best Local Similarity 98.8%; Pred. No. 0;
Matches 2217; Conservative 0; Mismatches 8; Indels 18; Gaps 1;
Qy 62 GAAGAGSTEDPGSADSEAGLPALAPVWFFYLSQDSRPSWCLRTVCNPFERVSNL 121
Db 30 GRCGPGSTEDPGSADSEAGLPALAPVWFFYLSQDSRPSWCLRTVCNPFERVSNL 89
Qy 122 VLLNCVTLGNFRCEPDICDSORCRLQAFDDFIAPFAVEMVVMVWALGIFGKKCYLG 181

Db 90 VILLNCVTLGMPCCEDIAQDSQRCRILQAFDDPIFAFPAVENVVRVWALGIFGKKCYLG 149
Qy 182 DTWNRLDFFIVTAGMLEYSLDQNSFSVAVTVVRVLRPLRAINRVPMSRILVTLTLDTP 241
Db 150 DTWNRLDFFIVTAGMLEYSLDQNSFSVAVTVVRVLRPLRAINRVPMSRILVTLTLDTP 209
Qy 242 MLGNVLLCFFVFFIFIGVGVOLWAGLLNRNCFLENFSLPLSVDLEPYQTENEDESP 301
Db 210 MLGNVLLCFFVFFIFIGVGVOLWAGLLNRNCFLENFSLPLSVDLEPYQTENEDESP 269
Qy 302 ICSPRENGMRSCRSYPTLRGEGGGPPCSLDYETYNSSNTTCVNNQYNTCSAGEHN 361
Db 270 ICSPRENGMRSCRSYPTLRGEGGGPPCSLDYETYNSSNTTCVNNQYNTCSAGEHN 329
Qy 362 PPKGAINFONIGVAMTAIFQVITLQWVDIMTFVMDAHSFYNFIPIYFILLIIVGSPFMNL 421
Db 330 PPKGAINFONIGVAMTAIFQVITLQWVDIMTFVMDAHSFYNFIPIYFILLIIVGSPFMNL 389
Qy 422 CLVVIATQSETKORESQLMRQVRFLSNASTLASFSFGSCYBELLKYLVIILRKAAR 481
Db 390 CLVVIATQSETKORESQLMRQVRFLSNASTLASFSFGSCYBELLKYLVIILRKAAR 449
Qy 482 RLAQVSRALIGVRAGLLSSPVARSQBPQSPGSCSTRSHRRLSVHHLVHHHHHHHHYHLGN 541
Db 450 RLAQVSRALIGVRAGLLSSPVARSQBPQSPGSCSTRSHRRLSVHHLVHHHHHHHHYHLGN 509
Qy 542 GTLRVPASPEIQDRDANGSRRLMLPPSTPTPSGPPRGASVHSFYHADCHLEPVRQ 601
Db 510 GTLRVPASPEIQDRDANGSRRLMLPPSTPTPSGPPRGASVHSFYHADCHLEPVRQ 569
Qy 602 APPPCPSASGRVGVSGKVPVHTSPPEILKOKALVEVAPSPGPTLTSTFNIPPGPF 661
Db 570 APPPCPSASGRVGVSGKVPVHTSPPEILKOKALVEVAPSPGPTLTSTFNIPPGPF 629
Qy 662 SSMHKLLETQSTGACHSSCKISSPCSKADSGAGCPDSCPYCARTGAGEPESADHVMPSD 721
Db 630 SSMHKLLETQSTGACHSSCKISSPCSKADSGAGCPDSCPYCARTGAGEPESADHVMPSD 689
Qy 722 SEAVYEFTQDAQHSDLRDPHSRRRQSLGPDAPSSVLAFWRLICDTFRKI VDSKYFGRG 781
Db 690 SEAVYEFTQDAQHSDLRDPHSRRRQSLGPDAPSSVLAFWRLICDTFRKI VDSKYFGRG 749
Qy 782 IMAILVNTLSGIEVHEQPEELTNALEISNIVFTSLFALEMLKLVVGPYIKNPYN 841
Db 750 IMAILVNTLSGIEVHEQPEELTNALEISNIVFTSLFALEMLKLVVGPYIKNPYN 809
Qy 842 IFDGVIVTISVWEIVGQCGGLSVLRTFRLMRVLKLVRLPALQRLVLMKTMNDNVATF 901
Db 810 IFDGVIVTISVWEIVGQCGGLSVLRTFRLMRVLKLVRLPALQRLVLMKTMNDNVATF 869
Qy 902 CMLLMFIFIFSLGMHLFGCKPASPBRDGTLPDRKNFDSLWAIIVTVFOILTQEDWNKV 961
Db 870 CMLLMFIFIFSLGMHLFGCKPASPBRDGTLPDRKNFDSLWAIIVTVFOILTQEDWNKV 929
Qy 962 LYNGMASTSSWAALYFIALMTGNYVLFWLVAIVVEGFAQSGDATKSESEDFPSVD 1021
Db 930 LYNGMASTSSWAALYFIALMTGNYVLFWLVAIVVEGFAQSGDATKSESEDFPSVD 989
Qy 1022 GDGDKRRLALVALGEHAELRKSLLPPLIHTAATPMSPHKSSSTGVGEALGSGSRRTSS 1081
Db 990 GDGDKRRLALVALGEHAELRKSLLPPLIHTAATPMSPHKSSSTGVGEALGSGSRRTSS 1049
Qy 1082 SGSAEPGAHMKCPSPASRSPHSWASASWTSRRSRNSLGRAPSLKRRSPSGERRS 1141
Db 1050 SGSAEPGAHMKCPSPASRSPHSWASASWTSRRSRNSLGRAPSLKRRSPSGERRS 1109
Qy 1142 LLSGEGQESQDEEESSEEDRASPAGSDHHRGSLEREAKSSFDLPVLQVGLHRTASGR 1201
Db 1110 LLSGEGQESQDEEESSEEDRASPAGSDHHRGSLEREAKSSFDLPVLQVGLHRTASGR 1169
Qy 1202 SSASEHODCNKGSASGLARTLTDDPQLDGDNDNDEGNLSKGERIQAWVRSLPACCBE 1261
Db 1170 SSASEHODCNKGSASGLARTLTDDPQLDGDNDNDEGNLSKGERIQAWVRSLPACCBE 1229

Qy 1262 RDSWSAYIPPPQSRFRLLCHRIITHKMPDHVVLVIIFLNCITTIAMERPKIDPHSABRIPL 1321
Db 1230 RDSWSAYIPPPQSRFRLLCHRIITHKMPDHVVLVIIFLNCITTIAMERPKIDPHSABRIPL 1289
Qy 1322 TILSNYIFTAVFLAEMTVKVVVALGWCFCGEQAYLRSSWNVDLGLLVLSVIDILVSMVSDSG 1381
Db 1290 TILSNYIFTAVFLAEMTVKVVVALGWCFCGEQAYLRSSWNVDLGLLVLSVIDILVSMVSDSG 1349
Qy 1382 TKILGMLRVLRLRLTLRPLRVISRAQGLKLVVETLMSLKPIGNIVIVICAPFIIFGILG 1441
Db 1350 TKILGMLRVLRLRLTLRPLRVISRAQGLKLVVETLMSLKPIGNIVIVICAPFIIFGILG 1409
Qy 1442 VOLFKGKFPVCCOEDTRNITNKSDCAEASRYRVRHKNYFNDLGOALMSLFLVASKOGWVD 1501
Db 1410 VOLFKGKFPVCCOEDTRNITNKSDCAEASRYRVRHKNYFNDLGOALMSLFLVASKOGWVD 1469
Qy 1502 IMYDGLDAVGVDQOQPMHNPWMLLYFISFLIIVAFVFLNMFVGVVFNPHKCRQHQEEE 1561
Db 1470 IMYDGLDAVGVDQOQPMHNPWMLLYFISFLIIVAFVFLNMFVGVVFNPHKCRQHQEEE 1529
Qy 1562 EARRBEKRLRELEKKRRSEKOMA-----EAOCKPYYSYDSRFRLL 1603
Db 1530 EARRBEKRLRELEKKRRSEKOMA-----EAOCKPYYSYDSRFRLL 1589
Qy 1604 VHHLCTSHVLDLFIITGVIGLVNVTWAMEHYQOQILDEALKICNYIFTVIFVPSYFKLV 1663
Db 1590 VHHLCTSHVLDLFIITGVIGLVNVTWAMEHYQOQILDEALKICNYIFTVIFVPSYFKLV 1649
Qy 1664 AFAPRRFFODRWQOLDLAILLSIMGITLEETEVNLSLNPNTIIRIMVRLRIARVLKUL 1723
Db 1650 ARGFRFRFODRWQOLDLAILLSIMGITLEETEVNLSLNPNTIIRIMVRLRIARVLKUL 1709
Qy 1724 KMAVGMRALLHTVMQALPOVGNLGLLFMLLFFIFAALGVVELFGDLECDETHPCEGLGRHA 1783
Db 1710 KMAVGMRALLHTVMQALPOVGNLGLLFMLLFFIFAALGVVELFGDLECDETHPCEGLGRHA 1769
Qy 1784 TFRNFGMAFLTIFRVTSTGDNWNGIMKDPSPDCDOESTCYNVTISPFIYFVSFVLTAQFVLV 1843
Db 1770 TFRNFGMAFLTIFRVTSTGDNWNGIMKDPSPDCDOESTCYNVTISPFIYFVSFVLTAQFVLV 1829
Qy 1844 NVVIAVLMKHLBESKEAKEAELEMKTILSPQSPHPLSGSPFLPWPGEVGNSTDS 1903
Db 1830 NVVIAVLMKHLBESKEAKEAELEMKTILSPQSPHPLSGSPFLPWPGEVGNSTDS 1889
Qy 1904 PKPGAPHTTAAHGAASGFSLEHTVMVPHPEEVVPLGPDLITVRKSGVSRTHSLPNDSYM 1963
Db 1890 PKPGAPHTTAAHGAASGFSLEHTVMVPHPEEVVPLGPDLITVRKSGVSRTHSLPNDSYM 1949
Qy 1964 CRNGSTAERSLGHGWLKPAQSGSILSVHSOPADTSCILQPKDVHYLLLOPHGAPTGA 2023
Db 1950 CRNGSTAERSLGHGWLKPAQSGSILSVHSOPADTSCILQPKDVHYLLLOPHGAPTGA 2009
Qy 2024 IPKLPPPGRSPLAQRPLRQAARITDSDLVQGLSGREDLLSEVSGPSCPLTRSSSSFWGGS 2083
Db 2010 IPKLPPPGRSPLAQRPLRQAARITDSDLVQGLSGREDLLSEVSGPSCPLTRSSSSFWGGS 2069
Qy 2084 SIQVQORSGIQSKVSKHRLPAPCPGLEPSPWAKDPPETRSSLELDTLWISGDLPLSSQ 2143
Db 2070 SIQVQORSGIQSKVSKHRLPAPCPGLEPSPWAKDPPETRSSLELDTLWISGDLPLSSQ 2129
Qy 2144 BEPLPRDLKKCYSVETQSCRRRPGFWLDEORRHSTAVCLDSGSPRLCPSSSILGGQP 2203
Db 2130 BEPLPRDLKKCYSVETQSCRRRPGFWLDEORRHSTAVCLDSGSPRLCPSSSILGGQP 2189
Qy 2204 LGGPGSRPKKLSPPSISIDPPESQGRPPCPGVCLRRRAPASDSDKPSVSSPLDSTAA 2263
Db 2190 LGGPGSRPKKLSPPSISIDPPESQGRPPCPGVCLRRRAPASDSDKPSVSSPLDSTAA 2249
Qy 2264 SPSPKXDTLSLGLSSDPTDMDP 2286
Db 2250 SPSPKXDTLSLGLSSDPTDMDP 2272

330 PFKGAINFNDIGNAMIAI FQVITLEGVNDIMYFVMDAHSFYNIPIYFILLIIVGSEFFMINL 389
Db
422 CLVVIATQFSETKQESQLMREORVRFLSNASTLASFSEPGSCYBELLKXVYLIRKAAR 481
Qy
390 CLVVIATQFSETKQESQLMREORVRFLSNASTLASFSEPGSCYBELLKXVYLIRKAAR 449
Db
482 RLQVSRAGVRAIGLSSPVARSQOEQPGSGCTRSRRRLSVHLVHHHHHHHHVHLGN 541
Qy
450 RLQVSRAGVRAIGLSSPVARSQOEQPGSGCTRSRRRLSVHLVHHHHHHHHVHLGN 509
Db
542 GTLRVPASPEIQDRDANGSRRLMLPPSTPTSGGPPRGASVHSFYHADCHLEPVRCQ 601
Qy
510 GTLRVPASPEIQDRDANGSRRLMLPPSTPTSGGPPRGASVHSFYHADCHLEPVRCQ 569
Db
602 APPRCPSEASGTVGSGKYVTVHTSPPEILKDKALVEVAPSGPPTLTSTFNIPGPF 661
Qy
570 APPRCPSEASGTVGSGKYVTVHTSPPEILKDKALVEVAPSGPPTLTSTFNIPGPF 629
Db
662 SSMHKLLETQSTGACHSSCKISSPCSKADSGAGCPDSCPYCARTGAGPESADHVMPDSD 721
Qy
630 SSMHKLLETQSTGACHSSCKISSPCSKADSGAGCPDSCPYCARTGAGPESADHVMPDSD 689
Db
722 SEAVYETQAOHSDLRDHSRRRQSLGPDAPSSVLAFWRLICDTFRKIVDSKYFGRG 781
Qy
690 SEAVYETQAOHSDLRDHSRRRQSLGPDAPSSVLAFWRLICDTFRKIVDSKYFGRG 749
Db
782 IMIAILVNTLSMGTEYHQEPEELTNALEISNIIVFTSLFALEMLLKLIVGPGFYKPNYN 841
Qy
750 IMIAILVNTLSMGTEYHQEPEELTNALEISNIIVFTSLFALEMLLKLIVGPGFYKPNYN 809
Db
842 IPDGVIVISWEIVGQGGSLVLRTRFLMRVLKVRFLPALORQIVLMTKMDNVATF 901
Qy
810 IPDGVIVISWEIVGQGGSLVLRTRFLMRVLKVRFLPALORQIVLMTKMDNVATF 869
Db
902 CMLLMFIFISILGMHIFGCKFASERDGTLPDRKNFDSLLWAIIVTVFQILTQEDMNKV 961
Qy
870 CMLLMFIFISILGMHIFGCKFASERDGTLPDRKNFDSLLWAIIVTVFQILTQEDMNKV 929
Db
962 LYNMGASTSSWAALFIALMTFGNVVLFNLLVAILVGFQAGDATKSESEPOFFSPVD 1021
Qy
930 LYNMGASTSSWAALFIALMTFGNVVLFNLLVAILVGFQAGDATKSESEPOFFSPVD 989
Db
1022 GDGRKRLALVALGHAELRSLAPPLIHTAATPMHSPKSSSTGVGEALGSGSRRTSS 1081
Qy
990 GDGRKRLALVALGHAELRSLAPPLIHTAATPMHSPKSSSTGVGEALGSGSRRTSS 1049
Db
1082 SGSAPCAAHMKCPSPASRSPHSPWSAASWTGRRSRNLSLGEAPSLKRRSPSGERRS 1141
Qy
1050 SGSAPCAAHMKCPSPASRSPHSPWSAASWTGRRSRNLSLGEAPSLKRRSPSGERRS 1109
Db
1142 LLSGEGQESQDEEESSEEDASAGSDHRRHSGSLEREAKSSFDLPDTLQVPLHRTASGR 1201
Qy
1110 LLSGEGQESQDEEESSEEDASAGSDHRRHSGSLEREAKSSFDLPDTLQVPLHRTASGR 1169
Db
1202 SSASEHQCNGKASGLARTLRTDDPQLDGDNDNDGNLSKGERIQAWVRSLPACCCE 1261
Qy
1170 SSASEHQCNGKASGLARTLRTDDPQLDGDNDNDGNLSKGERIQAWVRSLPACCCE 1229
Db
1262 RDSWSAYIFPQOSRFLCHRIIHTKMFHDVHLVIFLNCITTIAMERPKIDPHSAERIFL 1321
Qy
1230 RDSWSAYIFPQOSRFLCHRIIHTKMFHDVHLVIFLNCITTIAMERPKIDPHSAERIFL 1289
Db
1322 TLSNYIFTAVFLAEMTVKVALGWCFCGQAYLRSSWNVLDGLVILSVIDILVSMVSDSG 1381
Qy
1290 TLSNYIFTAVFLAEMTVKVALGWCFCGQAYLRSSWNVLDGLVILSVIDILVSMVSDSG 1349
Db
1382 TKILGMLRVLRLLRTPRLVRSRAGQLKLVETILMSLKEPIGNIVVICCAFFIIFILG 1441
Qy
1350 TKILGMLRVLRLLRTPRLVRSRAGQLKLVETILMSLKEPIGNIVVICCAFFIIFILG 1409
Db
1442 VOLFKGKFFVCCQEDTRNITNKSDCAEASYRWRHRYKFNFDNLGQALMSLFLVASKDGWD 1501
Qy
1410 VOLFKGKFFVCCQEDTRNITNKSDCAEASYRWRHRYKFNFDNLGQALMSLFLVASKDGWD 1469
Db

1502 IMYDGLDVGVDQOQIMHNPMLLIYFISLLIYVAFVLMNFVGVVVENFHKCKHQEHEE 1561
Qy
1470 IMYDGLDVGVDQOQIMHNPMLLIYFISLLIYVAFVLMNFVGVVVENFHKCKHQEHEE 1529
Db
1562 EARRREKRLRLLEKKRRSKERQMAEAOCKPYSDYSRFRLLVHHLCTSHYLDLPIITGVI 1621
Qy
1530 EARRREKRLRLLEKKER-----KAQCKPYSDYSRFRLLVHHLCTSHYLDLPIITGVI 1582
Db
1622 GLNVVTMAMEHYQOQIOLDEALKICNYIETVIFVSESVFKLVAFAFRFPFODRNOLDLA 1681
Qy
1583 GLNVVTMAMEHYQOQIOLDEALKICNYIETVIFVSESVFKLVAFAFRFPFODRNOLDLA 1642
Db
1682 IVLTSIMGITLEELEVNLSLPINPTIIRIMRVLRIRARVLKILKMAVGMREALLHTVMQALP 1741
Qy
1643 IVLTSIMGITLEELEVNLSLPINPTIIRIMRVLRIRARVLKILKMAVGMREALLHTVMQALP 1702
Db
1742 QVGNLGLLMLLFFIIFAALGVELFGDLECDETHPCBGLGRHATFRNFGMAFLTLPFRVSTG 1801
Qy
1703 QVGNLGLLMLLFFIIFAALGVELFGDLECDETHPCBGLGRHATFRNFGMAFLTLPFRVSTG 1762
Db
1802 DNWNGIMKDPSPRDCDQBSTCYNTVISPIYFVSFVLTAFVLMNVVIAVLMKHEESNKEA 1861
Qy
1763 DNWNGIMKDPSPRDCDQBSTCYNTVISPIYFVSFVLTAFVLMNVVIAVLMKHEESNKEA 1822
Db
1862 KEAELEAELEEMKTLSPQHSPLGSPFLWPGVEGVNSTDSPKPGAPHTTAHIGAASGF 1921
Qy
1823 KEAELEAELEEMKTLSPQHSPLGSPFLWPGVEGVNSTDSPKPGAPHTTAHIGAASGF 1882
Db
1922 SLEHPTMVPHPEEVVPLGPDLLTVRKSGVSRTHSLPNDSPNDSTACRSLSGHRGWL 1981
Qy
1883 SLEHPTMVPHPEEVVPLGPDLLTVRKSGVSRTHSLPNDSPNDSTACRSLSGHRGWL 1942
Db
1982 PKAQSGSILSVISOPADTSCIIQLPKDVHYLIQPHGAPTGAIPKLPPLPPGSRPLAQRPLR 2041
Qy
1943 PKAQSGSILSVISOPADTSCIIQLPKDVHYLIQPHGAPTGAIPKLPPLPPGSRPLAQRPLR 2002
Db
2042 RQAIRTSDLDVQGLSGREDLLSEVSGPCPLTRSSFWGSSIOVQORSQGIQSKVSKHI 2101
Qy
2003 RQAIRTSDLDVQGLSGREDLLSEVSGPCPLTRSSFWGSSIOVQORSQGIQSKVSKHI 2062
Db
2102 RLAPACGLEPESWAKOPPETRSLELDTLSMTISGDLPLSSQEEPLFPDLKKCYSVETQ 2161
Qy
2063 RLAPACGLEPESWAKOPPETRSLELDTLSMTISGDLPLSSQEEPLFPDLKKCYSVETQ 2122
Db
2162 SCRRRPGFWLDEQRRHSIAVSCLDGSOPLCPSLSLGGQPLGGPGRPKKLSPPSIS 2221
Qy
2123 SCRRRPGFWLDEQRRHSIAVSCLDGSOPLCPSLSLGGQPLGGPGRPKKLSPPSIS 2182
Db
2222 IDPPESQGRSPCSPGVCLRRRAPASDSKDPVSSPLDSTAAFPSPKKDTLSLGLSSDP 2281
Qy
2183 IDPPESQGRSPCSPGVCLRRRAPASDSKDPVSSPLDSTAAFPSPKKDTLSLGLSSDP 2242
Db
2282 TDMDP 2286
Qy
2243 TDMDP 2247
Db

RESULT 6
AA70720
ID AA70720 standard; protein; 2428 AA.
XX
AC AA70720;
XX
XX 18-JUL-2000 (first entry)
XX
DE Rat pancreatic T-type calcium channel.
XX
KW Rat; pancreatic T-type calcium channel alpha subunit; insulin;
KW pancreatic beta cell; alpha1g; low voltage activated Ca2+ channel family;
KW antidiabetic; calcium influx; I type calcium channel; NIDDM;
XX type II diabetes; non-insulin dependent diabetes mellitus.
XX

QY	1051	IHTAATPMKSHKSSGTGVEALGSGSRRTSSGSAEPGAAHHEMKCPPSARSPHSPWSA	1110
Db	1094	IHTAATPMKSHKSSGTGVEALGSGSRRTSSGSAEPGAAHHEMKCPPSARSPHSPWSA	1153
QY	1111	ASSWTSRRSRNSLGRAPSLKRRSPGRRRLSGEGQESODEESEEEDRASPGASDHR	1170
Db	1154	ASSWTSRRSRNSLGRAPSLKRRSPGRRRLSGEGQESODEESEEEDRASPGASDHR	1213
QY	1171	HGSLEREAKSFDLPTLTQVPLGRLTASGRSSASEHQDCNGKASGRLARTLTDDPOL	1230
Db	1214	HGSLEREAKSFDLPTLTQVPLGRLTASGRSSASEHQDCNGKASGRLARTLTDDPOL	1273
QY	1231	DGDDDDNDEGNLSKGERIQAWRSRLPACCRDSDSAVIFPQSRFLLCHRIITHKMF	1290
Db	1274	DGDDDDNDEGNLSKGERIQAWRSRLPACCRDSDSAVIFPQSRFLLCHRIITHKMF	1333
QY	1291	HVLVVIIFNCITITAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTVKVALGWC	1350
Db	1334	HVLVVIIFNCITITAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTVKVALGWC	1393
QY	1351	AYLRSSNNVLDGLVLISVIDILVSVSDSGTKILGMLRVLRLLRPLRVISRAQGLK	1410
Db	1394	AYLRSSNNVLDGLVLISVIDILVSVSDSGTKILGMLRVLRLLRPLRVISRAQGLK	1453
QY	1411	LWVETLASSLPKIGNIVVICAPFIIFGILGVQLFKGKPFVCOGEDTRNITNKS	1470
Db	1454	LWVETLASSLPKIGNIVVICAPFIIFGILGVQLFKGKPFVCOGEDTRNITNKS	1513
QY	1471	YRWVRHKYNFNLGOALMSFLVASKOGWVDIMYDGLDVGVDQOQPIMNHNPM	1530
Db	1514	YRWVRHKYNFNLGOALMSFLVASKOGWVDIMYDGLDVGVDQOQPIMNHNPM	1573
QY	1531	FLLIIVAFVLMFVGVVYENFHKQHOEEAREERREKRLRLEKRR-----	1579
Db	1574	FLLIIVAFVLMFVGVVYENFHKQHOEEAREERREKRLRLEKRR-----	1633
QY	1580	SKEQMAEAQCKPYSDYSRFRLLVHHLCTSHYLDLFTIGVIGLVNVTMAEHYQ	1639
Db	1634	SSAASAEQAQCKPYSDYSRFRLLVHHLCTSHYLDLFTIGVIGLVNVTMAEHYQ	1693
QY	1640	DEALKICNIVTIVFVFSVFKLAFVAFRRPFQDRNQLDLAIVLLSIMGITL	1699
Db	1694	DEALKICNIVTIVFVFSVFKLAFVAFRRPFQDRNQLDLAIVLLSIMGITL	1753
QY	1700	SLPINTIIRIMRVLRARVLLKLVAVGMRALLTVMCALPQVGNLGLLFFM	1759
Db	1754	SLPINTIIRIMRVLRARVLLKLVAVGMRALLTVMCALPQVGNLGLLFFM	1813
QY	1760	LGVELFGDLCEDETHPCEGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMK	1819
Db	1814	LGVELFGDLCEDETHPCEGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMK	1873
QY	1820	TCYNTVISPFIYFVSFLVTAQFVLVNVVIAVLMKHEESKEAELELEMK	1879
Db	1874	TCYNTVISPFIYFVSFLVTAQFVLVNVVIAVLMKHEESKEAELELEMK	1933
QY	1880	POHSPILGSPPLWPGVGVNSTDPKCAPHTTAHGAASGFSLEHTVWPHEVP	1939
Db	1934	POHSPILGSPPLWPGVGVNSTDPKCAPHTTAHGAASGFSLEHTVWPHEVP	1993
QY	1940	GPDLITVRKSGVSRTHSLPNDOSYCMRNGSTAESLGRGWGLPKAQS	2053
Db	1994	GPDLITVRKSGVSRTHSLPNDOSYCMRNGSTAESLGRGWGLPKAQS	2053
QY	2000	SCILQPKDVHLLQPHCAPTWGAIPKLPPEGRSFLAQRPLRQAAIRTD	2059
Db	2054	SCILQPKDVHLLQPHCAPTWGAIPKLPPEGRSFLAQRPLRQAAIRTD	2113
QY	2060	EDLLSEVSGSPCLTRSSFWGSSIQVOQRSGIQSKVSHIRLPAPCPGLEP	2119
Db	2114	EDLLSEVSGSPCLTRSSFWGSSIQVOQRSGIQSKVSHIRLPAPCPGLEP	2173
QY	2120	ETRSSLELOTELWSIGDLLPSSQBEPLFRDLKKCYSVETQSCRRRPF	2179

Db	2174	ETRSSLELOTELWSIGDLLPSSQBEPLFRDLKKCYSVETQSCRRRPGSWL	2233
QY	2180	AVSCLDSGSPRLCPSPSSILGGQPLGGPGSRPKKLSPPSISIDPPESOG	2239
Db	2234	AVSCLDSGSPRLCPSPSSILGGQPLGGPGSRPKKLSPPSISIDPPESOG	2293
QY	2240	LRRAPASDSKDPVSSPPLDSTAASPSPKDTLSLGLSSDPTDMDP	2286
Db	2294	LRRAPASDSKDPVSSPPLDSTAASPSPKDTLSLGLSSDPTDMDP	2340
RESULT 7			
AA14586	AA14586 standard; protein; 2250 AA.		
XX	AC	AA14586;	
XX	07-DEC-1999	(first entry)	
XX	Human	T-type voltage-gated Ca channel alpha-1-G (hCav1a).	
XX	Human;	T-type voltage-gated calcium channel; membrane; pore; ion;	
XX	activation;	current; rat; screen; drug; cardiomyopathy; epilepsy.	
XX	Homo sapiens.		
XX	WO9929847-A1.		
XX	17-JUN-1999.		
XX	30-OCT-1998;	98WO-US023161.	
XX	05-DEC-1997;	97US-00985809.	
XX	(LOYO)	UNIV LOYOLA CHICAGO.	
XX	Perez-Reyes E, Cribbs LL;		
XX	WPI; 1999-394972/33.		
XX	N-PSDB; AAX83481.		
XX	New T-type voltage-gated calcium channels.		
XX	Disclosure; Page 31-40; 138pp; English.		
XX	This sequence represents a human T-type voltage-gated calcium (Ca)		
XX	channel alpha-1-G designated hCav1a. Voltage gated channels are membrane		
XX	bound glycosylated proteins formed of several subunits. The large alpha		
XX	subunits form a pore in the membrane that is selective for a given ionic		
XX	species. Each alpha subunit contains 4 domains (I, II, III and IV) and		
XX	each domain contains 6 putative transmembrane helical segments (S1-S6). T		
XX	-type Ca channels are activated at a lower voltage than L- or N-type		
XX	channels. Characteristics of T-type channels include short current time,		
XX	slow activation kinetics near threshold, fast inactivation kinetics and		
XX	slow tail current. The sequences AAX83481-X83492 represent novel T-type		
XX	voltage-gated Ca channel genes from humans and rats. Each of the novel Ca		
XX	channels contains a putative IVS4 region comprising the amino acid		
XX	sequence AA14598. Cells expressing the T-type voltage-gated calcium		
XX	channel proteins can be used to screen for drugs which affect calcium		
XX	channels. Methods are also disclosed for treating a disease or disorder		
XX	associated with a deficiency in a native T-type calcium channel nucleic		
XX	acid, e.g. to treat cardiomyopathy, epilepsy, etc		
XX	Sequence 2250 AA;		
XX	Query Match	90.3%; Score 10857; DB 2; Length 2250;	
XX	Best Local Similarity	93.6%; Pred. No. 0;	
XX	Matches 2084; Conservative	32; Mismatches 104; Indels 6; Gaps 4;	
QY	62	GAAAGAGTEKDPGADSEAGLPPALAPVFFYLSQDRSPRSWCLRTVCNPFVSM	121
Db	30	GRPGGSAEKDPGADSEAGLPPALAPVFFYLSQDRSPRSWCLRTVCNPFVSM	89

Qy	122	VILLNCVTILGNFRCEB	IACDSQRCRILQAFDD	IFAFVAVEMVVKWALGIFGKKCYLG	181				
Db	90	VILLNCVTILGNFRCEB	IACDSQRCRILQAFDD	IFAFVAVEMVVKWALGIFGKKCYLG	149				
Qy	182	DTNRLDFFVIAGMLYS	LDLQNVSPS	AVRTVRVLRLPLRAINRVP	SMRILVTLDDTLP 241				
Db	150	DTNRLDFFVIAGMLYS	LDLQNVSPS	AVRTVRVLRLPLRAINRVP	SMRILVTLDDTLP 209				
Qy	242	MLGNVLLLCFFVFF	IFIGIVGQWAGLLNR	CFLPENFSLPSLDLEPPY	QTEDESPF 301				
Db	210	MLGNVLLLCFFVFF	IFIGIVGQWAGLLNR	CFLPENFSLPSLDLEPPY	QTEDESPF 269				
Qy	302	ICSQPRENGHRS	CB	SVPTILREGGGGPP	CSLDIETYNSSNTTCVNWNQY	TNCSAGEHN 361			
Db	270	ICSQPRENGHRS	CB	SVPTILREGGGGPP	CSLDIETYNSSNTTCVNWNQY	TNCSAGEHN 329			
Qy	362	PFKGAINFDNIG	YAWIAI	FOVITILEGWVD	IMYFMDAHS	FYNFIYFILLIIVGSFFMINL 421			
Db	330	PFKGAINFDNIG	YAWIAI	FOVITILEGWVD	IMYFMDAHS	FYNFIYFILLIIVGSFFMINL 389			
Qy	422	CLVVIATQFSET	KORESOLMREQVR	FLSNASTLAS	SFPCSCYEE	LLKYLVLIRKAAR 481			
Db	390	CLVVIATQFSET	KORESOLMREQVR	FLSNASTLAS	SFPCSCYEE	LLKYLVLIRKAAR 449			
Qy	482	RLAQVSAIGVR	AGLLSSPVARS	QOEPOPGSC	STRSHRRLSVHHLVHHHHHHH	YHLGN 541			
Db	450	RLAQVSAAGVR	GLSSPAPLGGQET	QPSSSCSRSHRRLSVHHLVHHHHHHH	YHLGN 509				
Qy	542	GTLRVP	RASPEI	QDRDANGSRRLML	PPSPPTPSGPP	RGAEVSHSFYHADCHLEPVRCQ 601			
Db	510	GTLR	RASPEI	QDRDANGSRRLML	PPSPPTALSGAP	PGAEVSHSFYHADCHLEPVRCQ 569			
Qy	602	APPRCP	SEASGR	TGVSGKYPTVHT	SPPEI	LKOKALVEVAPSPGPPTIT	SNIPGPFF 661		
Db	570	APPRSP	SEASGR	TGVSGKYPTVHT	SPPETLKE	ALVEVAASSGPPTIT	SLNIPGPY 629		
Qy	662	SSWHKLE	TOSTGACHSSCKI	SSPCS	KADSGACG	PDSCPYCARTGAGEP	SAHDVMPDSD 721		
Db	630	SSWHKLE	TOSTGACQSSCKI	SSPCL	KADSGACG	PDSCPYCAGAGAGEV	ELADREMPDSD 689		
Qy	722	SEAVYE	TQDAQ	HSDLRDP	HSRRRQ	SLGPDAPSSVLA	FWRLICDTFRKIVDSKYPGRG 781		
Db	690	SEAVYE	TQDAQ	HSDLRDP	HS - RRORS	SLGPDAPSSVLA	FWRLICDTFRKIVDSKYPGRG 748		
Qy	782	ITAIL	VNTLSMGIEY	HEQPEET	TNALEI	SNIVP	TSLFALEMLKLIVGPGFYKPNYN 841		
Db	749	ITAIL	VNTLSMGIEY	HEQPEEL	TNALEI	SNIVP	TSLFALEMLKLIVGPGFYKPNYN 808		
Qy	842	IFDGI	VIVISWEI	VGQGGGLSV	LRFLRMLV	KLVRFLPALORQ	LVLMKTMNDVATF 901		
Db	809	IFDGI	VIVISWEI	VGQGGGLSV	LRFLRMLV	KLVRFLPALORQ	LVLMKTMNDVATF 868		
Qy	902	CMLLML	FI	FISILGMEL	FGCK	FASERDGT	LPDRKNFDSILLMAIVTVFOILLTQEDWNKV 961		
Db	869	CMLLML	FI	FISILGMEL	FGCK	FASERDGT	LPDRKNFDSILLMAIVTVFOILLTQEDWNKV 928		
Qy	962	LYNGMA	STSWAAL	LYFTAL	T	FGNYVL	FNLLVAILEVFOAQGDATKSESEPPFFSPSVD 1021		
Db	929	LYNGMA	STSWAAL	LYFTAL	T	FGNYVL	FNLLVAILEVFOAQGDANKSESEPPFFSPSLD 988		
Qy	1022	GDGDR	KKRLAL	VALGEHAEL	RSKLL	PLLI	THTAATPM	SHPKSSSTGVEALGSGSRRTSS 1081	
Db	989	GDGDR	KKCLAL	VSIGHEPE	LURKSL	LLPLI	THTAATP	MSLPKSTSTGUEALGPASRRTSS 1048	
Qy	1082	SGSAEP	GAAH	HEMK	CP	PSARSSPHS	PWSAASSWT	SRSSRNSLGRAPSLKRRSPSGERRS 1141	
Db	1049	SGSAEP	PCAA -	HENK	PS	PSARSSPHS	PWSAASSWT	SRSSRNSLGRA - PS	LKRRSPSGERRS 1107
Qy	1142	LLSGEG	QESQDE	EESS	DEDR	RAS	PAGSDH	RUGSLEREAKS	FDLPDTLPVGLHRTASGR 1201
	1108	LLSGEG	QESQDE	EESS	DEER	RAS	PAGSDH	RUGSLEREAKS	FDLPDTLPVGLHRTASGR 1167

QY	1202	SSASEHQDCKNGKASGRHLARTLTDTDDPQLDGDGDDNDEGNLSKGERIOQAWVRSLPACCBE	1266
DB	1168	GSASEHQDCKNGKASGRGLARALRPDDPPLDGDGDDADDEGNLSKGERVYRATRAELPACCUE	1227
QY	1262	RDSWSAIIYPPQSRFRLLCRIITHKMFHDVLIIVIIPLNCITITAMERPKIDPHSASRIFL	1321
DB	1228	RDSWSAIIYPPQSRFRLLCRIITHKMFHDVLIIVIIPLNCITITAMERPKIDPHSASRIFL	1287
QY	1322	TLSNYIFTAVFLAEMTVKVVVALGWCQEQAYLRSNNVLDGLLVLSIVDILVSMVSDSG	1381
DB	1288	TLSNYIFTAVFLAEMTVKVVVALGWCQEQAYLRSNNVLDGLLVLSIVDILVSMVSDSG	1347
QY	1382	TKILGMLRVLRLLRTRPLRVIISRAOGLKLVVETLMSLSUKPIGNIIVVICAPFIIFGILG	1441
DB	1348	TKILGMLRVLRLLRTRPLRVIISRAOGLKLVVETLMSLSUKPIGNIIVVICAPFIIFGILG	1407
QY	1442	VQLFKGKFFVCOGEDTRNITNKSDCAEASVYRVYRHKYFNFDNLGOALMSLFLVLASKOGWVD	1501
DB	1408	VQLFKGKFFVCOGEDTRNITNKSDCAEASVYRVYRHKYFNFDNLGOALMSLFLVLASKOGWVD	1467
QY	1502	IMYDGLDAVGVDQOPIMNHNPMWLLYFISFLLIIVAFVFLNMFVGVVVENFHKCRHQEBE	1561
DB	1468	IMYDGLDAVGVDQOPIMNHNPMWLLYFISFLLIIVAFVFLNMFVGVVVENFHKCRHQEBE	1527
QY	1562	EARRREKRLRLLEKKRRSEKQMAEQAQKPYYSYSRFRLLVHHLCTSHYLDLFTITGVI	1621
DB	1528	EARRREKRLRLLEKKRRSEKQMAEQAQKPYYSYSRFRLLVHHLCTSHYLDLFTITGVI	1587
QY	1622	GLNVVTMAMEHYOQQLDLBALAKICNYIFTVIFVFSVFKLVAFAPRRFPQDRWNOLDLA	1681
DB	1588	GLNVVTMAMEHYOQQLDLBALAKICNYIFTVIFVFSVFKLVAFAPRRFPQDRWNOLDLA	1647
QY	1682	IVLLSINGITLSEIEVNLSPINPTIIRIMRVLRIRARVLKLVKQAVGMBALLHTVMQALP	1741
DB	1648	IVLLSINGITLSEIEVNLSPINPTIIRIMRVLRIRARVLKLVKQAVGMBALLHTVMQALP	1707
QY	1742	QVGNLGLLFMLLPFIIFAALGVELFGDLECDETHPCGELGRHATFRNFGMAFLTFRVSTG	1801
DB	1708	QVGNLGLLFMLLPFIIFAALGVELFGDLECDETHPCGELGRHATFRNFGMAFLTFRVSTG	1767
QY	1802	DNWNGIMKOPSRDQDQESTCNTYVISPFIYFVSFVLTAQFVLVNVNVLAVLWKHLESNKEA	1861
DB	1768	DNWNGIMKOTLRDQDQESTCNTYVISPFIYFVSFVLTAQFVLVNVNVLAVLWKHLESNKEA	1827
QY	1862	KEBAELEAELELEWKTLSPOPHSPGSPFLWPGVEGVNSTDSPKPGAPHHTAHIGAASGF	1921
DB	1828	KEBAELEAELELEWKTLSPOPHSPGSPFLWPGVEGDPSPKPGALPAAHARASHP	1887
QY	1922	SLEHPTMTVHPBEVVPVLGPDLLTVRKSGVSRTHSLPNDSPYCRNGSTAEISLGRHWGL	1981
DB	1888	SLEHPTMQPHPTLPLP--GPDLLTVRKSGVSRTHSLPNDSPYCRNGSTAEISLGRHWGL	1944
QY	1982	PKAQSGSLSVHSQPADTSCILQPKDVHYLLQPHCAPTWTGAIPKLPFGGRSPLAQRLR	2041
DB	1945	PKAQSGSLSVHSQPADTSTYILQPKDAFHLQPHSAPTWTGTIPKLPFGGRSPLAQRLR	2004
QY	2042	ROAAIRTDSDVOGLSREDLLSEVGPSCPLTRSSSFWGGSIIQVOQRSGIOQSKVSKHI	2101
DB	2005	ROAAIRTDSDVOGLSREDLLAEVSGPPLARAYSFWGQSSTQAQHSRSHSKLSKEM	2064
QY	2102	RLPAPCPGLEPSPWAKOPPETHRSLELDTELSTWISGDLL-PSQOEPLFPRDLKCCYSVET	2160
DB	2065	TPPAPCPGPBPNGKGPETHRSLELDTELSTWISGDLLPPGQEEPPSPRDLKCCYSVEA	2124
QY	2161	QSCERRPGFWLDRQRHSTAVSCLDGSGOPLCPSPSSILGGQPLGFGSPRKKLSPPSI	2220
DB	2125	QSCORRPTSLWLDQRHSTAVSCLDGSGOPHLGTDPSNLGGQPLGFGSPRKKLSPPSI	2184
QY	2221	SIDPPRSQGRPCSPGVCLRRRAPASDSDKDPVSVPFLDSTAAASPSPKDOTLSLSGLSD	2280
DB	2185	TIIDPPSQGRPTPSPGICLURRAPASDSDKDFPLASGPPDSMAASPSPKDOVLVSLGLSSD	2244
QY	2281	PTDMOP	2286

Mon Apr 18 12:41:42 2005

2245 PADLDP 2250

RESULT 8

AA14588 standard: protein: 2268 AA:
AA14588

ID AAY14588

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 1500.

AC AAY14588;

XX
NT 07-DEC-1999 (first entry)

DT 07-DEC-1955 (11150 0001)
YX (1000-010)

Human T-type voltage-gated Ca channel α -1-G (hCav1.1C).

DE
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Human; T-type voltage-gated calcium channel; Membrane; pore; ion
KW Human; T-type voltage-gated calcium channel; Membrane; pore; ion

activation; current; rat; screen; drug; cardiomyopathy; epinephrine

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OS Homo sapiens.

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PN WO9929847-A1.

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17-TTN-1999

PD 17-JUN-1999.

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PF 30-OCT-1998: 98WO-US023161.

PF 30-OCT-1955, 2000
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XX 05-DEC-1997; 97US-00985809.
PR

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PA (LOYO) UNIV LOYOLA CHICAGO.

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PI Perez-Reyes E, Cribbs LL;

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--- 1000 204072/22

DR WPI; 1999-3949/2/33.
" DCE: 11V83483

DR N-PSDB; AAX83483.

Now T-type voltage-gated calcium channels.

PT New T-type voltage source
yy

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ps
disclosure: page 49-58; 138pp; English.

PS Disclosure: Page 100
XX = Patent not assigned calcium (C

This sequence represents a human T-type voltage-gated calcium channel.

channel alpha-1-G designated hCav1.1. Voltage-gated channels are formed of several subunits. The large

bound glycosylated proteins formed of several subunits. The enzyme is selective for a given substrate.

CC subunits form a pore in the membrane that is selective for Ca^{2+} . The subunit contains 4 domains (I, II, III and I

CC species. Each alpha subunit contains 4 domains (A, B, C, D) containing 6 putative transmembrane helical segments (

each domain contains 6 putative transmembrane domains. The L- or N-activated channels are activated at a lower voltage than L- or N-

-type Ca channels are activated as a result of the characteristics of T-type channels include short current

channels. Characteristics of Ca^{2+} -eff-
CC channels. Characteristics of Ca^{2+} -eff-
CC channels near threshold, fast inactivation kinetics
slow activation kinetics near threshold, fast inactivation kinetics

slow activation kinetics and a slow tail current. The sequences AAX83481-X83492 represent novel

CC voltage-gated Ca channel genes from humans and rats. Each of the
CC voltage-gated Ca channel genes from humans and rats. Each of the
CC voltage-gated Ca channel genes from humans and rats. Each of the
CC voltage-gated Ca channel genes from humans and rats. Each of the

CC -channels contains a putative IVS4 region comprising the amino

CC sequence AAY14598. Cells expressing the T-type voltage-gated Ca²⁺ channel for drugs which affect Ca²⁺ channel

channel proteins can be used to screen for drugs which are released for treating a disease or

QY 1322 TLSNYIFTAVFLAEMTVKVVVALGWCFCGEQAYLRSSWNVLGGLAVLISVIDILVSMVSDSG 1381
Db 1288 TLSNYIFTAVFLAEMTVKVVVALGWCFCGEQAYLRSSWNVLGGLAVLISVIDILVSMVSDSG 1347
QY 1382 TKILGMLRVLRLRLRLRLRLRAVLSRAQGLKLVVETLMSLLKPIGNIIVVICCAFFIIFGILG 1441
Db 1348 TKILGMLRVLRLRLRLRLRLRAVLSRAQGLKLVVETLMSLLKPIGNIIVVICCAFFIIFGILG 1407
QY 1442 VOLFKGKFFVCOGEDTRNITNKSDCABASRWYRHKYNFNLQALMSLFLVLSKDGWD 1501
Db 1408 VOLFKGKFFVCOGEDTRNITNKSDCABASRWYRHKYNFNLQALMSLFLVLSKDGWD 1467
QY 1502 IMYDGLDVGVDQOQPMNPNMMLLYFISPLLIVAFVLMFVGVVFNHFKCRQOEBE 1561
Db 1468 IMYDGLDVGVDQOQPMNPNMMLLYFISPLLIVAFVLMFVGVVFNHFKCRQOEBE 1527
QY 1562 EARRREKRLRLLEKKRRSEKQMA-----EAQCKPYYSYDSRFL 1603
Db 1528 EARRREKRLRLLEKKRRSEKQMA-----EAQCKPYYSYDSRFL 1587
QY 1604 VHLCTSHYLDLFTITVIGLVNVTMAHMYQOQILDEALKICNYITFTVIFVESVKLV 1663
Db 1588 VHLCTSHYLDLFTITVIGLVNVTMAHMYQOQILDEALKICNYITFTVIFVESVKLV 1647
QY 1664 AFAPRRFFODRWNOOLDLAVLSIMGITLEEIEVNLSPINPTIIRIMVLRIRARVLL 1723
Db 1648 AFGRFRFPQDQWNOOLDLAVLSIMGITLEEIEVNLSPINPTIIRIMVLRIRARVLL 1707
QY 1724 KNAVGNRALLHTVMQALPOVGNLGLLFMLFFIIFAAALGVVELFGDLECDETHPCGEGRHA 1783
Db 1708 KNAVGNRALLHTVMQALPOVGNLGLLFMLFFIIFAAALGVVELFGDLECDETHPCGEGRHA 1767
QY 1784 TRNFQMAFLTLPRVSTGDNWNGIMKDPDRDCQESTCNTVITSPYFVSFLVTAQFVLV 1843
Db 1768 TRNFQMAFLTLPRVSTGDNWNGIMKDPDRDCQESTCNTVITSPYFVSFLVTAQFVLV 1827
QY 1844 NVVIAVLMKHLRESNEKEAELEAELEEMKTLSPQHPSPGLSGPPLWPGVEGVNSTDS 1903
Db 1828 NVVIAVLMKHLRESNEKEAELEAELEEMKTLSPQHPSPGLSGPPLWPGVEGVNSTDS 1887
QY 1904 PKPGAPHTTAHIGAAAGSFLSEHPTVPHPEEVPVPLGPDLLTVRKSGVSRTHSLPNDSYM 1963
Db 1888 PKPGALHPAAHARSASHFSLHPTMQPHTELP---GPDLLTVRKSGVSRTHSLPNDSYM 1944
QY 1964 CRNGSTAERSLHRGWGLPKAAGSILSVHSQPADTSCILQPKOVHYLLQPHGAPTGA 2023
Db 1945 CRHGTAEGPLHRGWGLPKAAGSILSVHSQPADTSCILQPKADAPHLLOPHSAPTGT 2004
QY 2024 IPKLPGRSPPLAQRPLRQAAIRTDSDVQGLGSRREDLLSEVSGPSCPLTRSSSFWGS 2083
Db 2005 IPKLPGRSPPLAQRPLRQAAIRTDSDVQGLGSRREDLLSEVSGPSPPLARAYSFWGS 2064
QY 2084 SIQVQQRSGTQSVKSHIRLAPCPGLEPSSWAKDPPETRSSLELDTLSWISGDL-PS 2142
Db 2065 STQAQHSRSHKISKHMTFPAFCPEPNWKGPPETRSSLELDTLSWISGDL-PPG 2124
QY 2143 QBEPLPRDLKCYVETSCRRRPGFWDLBQRRHSIAVCLDSGQSPCLCPSPSLGQ 2202
Db 2125 QBEPPSPDLKCYVETSCRRRPGFWDLBQRRHSIAVCLDSGQSPCLCPSPSLGQ 2184
QY 2203 PLGCGSRPKKLSPPSISIDPPESQSRPPCPGVCGLRRAPASKDPSSVSPDSTA 2262
Db 2185 PLGCGSRPKKLSPPSISIDPPESQSRPPCPGVCGLRRAPASKDPSSVSPDSTA 2244
QY 2263 ASPSPKKDVLISGLSDPTDMDP 2286
Db 2245 ASPSPKKDVLISGLSDPTDMDP 2268

RESULT 9
AAE01019

AAE01019 standard; protein; 2273 AA.

AAE01019;
17-JUL-2001 (first entry)

Human T-type low voltage activated calcium channel alphaG-c protein.

Human T-type low voltage activated calcium channel alphaG-c; stress;
epilepsy; schizophrenia; depression; sleep disorder; Cushing's disease;
endocrine disorder; respiratory disorder; peripheral muscle disorder;
muscle excitability; fertilisation; contraception; hypertension;
neural firing regulation; cardiovascular disorder; gene therapy;
forensic analysis; epidemiological study; neuroleptic.

Homo sapiens.

Key Location/Qualifiers

FT Misc-difference 1138 /note= "Encoded by GAG"
FT Misc-difference 1142 /note= "Encoded by GAA"
FT Misc-difference 1680 /note= "Encoded by ACG"
FT Misc-difference 1683 /note= "Encoded by GAA"

WO200130844-A1.

03-MAY-2001.

06-OCT-2000; 2000WO-US027761.

26-OCT-1999; 99US-00426998.

(ORTH) ORTHO-MCNEIL PHARM INC.

Dubin AE, Galindo JE, Pyati J, Zhu JY, Erlander MG;

WPI; 2001-300486/31.

N-PSDB; AAD04756.

New nucleic acid encoding human calcium channel protein, useful for
identifying specific modulators and potential pharmaceuticals for
treating e.g. epilepsy.

Claim 11; Page 81-99; 115pp; English.

The invention relates to isoform of human T-type low voltage activated
calcium channel (alphaG-c) cDNA and protein. Cells transformed with
calcium channel DNA to express calcium alphaG-c channel protein are used
to identify specific modulators (antagonists or agonists). These
modulators are useful as therapeutic agents and are used for treating
wide range of calcium alphaG-c channel-mediated disorders, e.g. stress
epilepsy, schizophrenia, depression, sleep disorders, Cushing's disease,
endocrine disorders, respiratory disorder, peripheral muscle disorder,
muscle excitability, fertilisation, contraception, disorders involving
hypertension, neuronal firing regulation, potentiation of synaptic
signals and cardiovascular disorders (e.g. atherosclerosis, cardiac
hypertrophy, angina pectoris). Calcium alphaG-c channel DNA is useful
for isolating and identifying related molecule mutations. It is also
optionally used as antisense sequences, in gene therapy. Calcium channel
alphaG-c DNA, protein and antibodies are useful for forensic analysis,
diagnosis and epidemiological studies, by standard hybridisation or
immunological assays. The present sequence is T-type low voltage
activated calcium channel alphaG-c protein

Sequence 2273 AA;

Query Match 90.0%; Score 10820.5; DB 4; Length 2273;

Best Local Similarity 92.5%; Pred. No. 0;

Matches 2080; Conservative 35; Mismatches 105; Indels 29; Gaps 5;

QY 62 GAAGAGSTKDGSDSEAGLPYALAPVWFYLSQDSRPSWCLRTVCNPFVRSML 121

1322 TLNSYIFTAFLAEMTVKVALGWCFCGEOAYLRSSWNLGLLVLISVIDILVMSVDSG 1381
1288 TLNSYIFTAFLAEMTVKVALGWCFCGEOAYLRSSWNLGLLVLISVIDILVMSVDSG 1347
1382 TKILGMLRLRLRLRLPLRVLSRAQGLKLVVETLMSLSKIGNIVVICCAFFIIFGLG 1441
1348 TKILGMLRLRLRLRLPLRVLSRAQGLKLVVETLMSLSKIGNIVVICCAFFIIFGLG 1407
1442 VQLFKGKFFVCOGEDFNITNSKDCAEASRYWRVKYNFNDLGOALMSLFVLASKDGWVD 1501
1408 VQLFKGKFFVCOGEDFNITNSKDCAEASRYWRVKYNFNDLGOALMSLFVLASKDGWVD 1467
1502 IMYDGLDAVGVDQOPIINHNPNMMLLYFISFLILIVAFVFLNMPGVVVENFHKCRHQBE 1561
1468 IMYDGLDAVGVDQOPIINHNPNMMLLYFISFLILIVAFVFLNMPGVVVENFHKCRHQBE 1527
1562 EARRREKRLRLLEKRR-----SKEQMAEAOCKPYSDYSRFRLLVHLLCTS 1610
1528 EARRREKRLRLLEKRRMLDDVITAGSSASAASEAOCKPYSDYSRFRLLVHLLCTS 1587
1611 HYLDLFTVIGLVNVTMAHEHYQOQILDEALKICNYIFTVFVESVKLVAFAPRRP 1670
1588 HYLDLFTVIGLVNVTMAHEHYQOQILDEALKICNYIFTVFVESVKLVAFAPRRP 1647
1671 FQDRWNQDLAIVLLSIMGITLBEIEVNLSPINPIIIRMRVLRARVLRKLLKVAQVGR 1730
1648 FQDRWNQDLAIVLLSIMGITLBEIEVNLSPINPIIIRMRVLRARVLRKLLKVAQVGR 1707
1731 ALLTVMQALPOVGNLGLFWLLFFIFAALGVLEFGLDECEHPCEGLGRHATFRNFGM 1790
1708 ALLTVMQALPOVGNLGLFWLLFFIFAALGVLEFGLDECEHPCEGLGRHATFRNFGM 1767
1791 AFLTFLRVTGDNWNGIMKDPDRCDQESTCYNIVISPIYFVSFVLTAQVFLVNVIAVL 1850
1768 AFLTFLRVTGDNWNGIMKDPDRCDQESTCYNIVISPIYFVSFVLTAQVFLVNVIAVL 1827
1851 MKHLESKEAKEAELEAELEMKTLSPQHPGLSPFLMPGVEGVNSTDPKFCAPH 1910
1828 MKHLESKEAKEAELEAELEMKTLSPQHPGLSPFLMPGVEGVNSTDPKFCAPH 1887
1911 TTAHGAAGSFSLHPTVHPPEEVPVPLGDLITVRKSGVSRTHSLPNDSYNCRGSTA 1970
1888 PAHARSASHFSLEHTWQHPTELP---GPDLLTVRKSGVSRTHSLPNDSYNCRGSTA 1944
1971 ERLGHRGWLKPAQSGSLVHSOPADTSCILQPKDQVHLLQPHGAPTWGAIPKLP 2030
1945 EGPLGHRGWLKPAQSGSVLSVHSOPADTSTYLQPKDAPHLQPHSAPTWGTIPKLP 2004
2031 GRSPLAQRPLRQAAIRTDLSLDVQGLGSRDILLSEVSPGSPCLTRSSSGFWGSSIQVOOR 2090
2005 GRSPLAQRPLRQAAIRTDLSLDVQGLGSRDILLSEVSPGSPCLTRSSSGFWGSSIQVOOR 2064
2091 SGIOQSVKSHIRLAPCPGLEFSWAKDPETSSLELDTLSWISGDL--PSSQBEPLFP 2149
2065 SRGHSKISKHMTTPAPCPGEPENWGPPEPTESSLELDTLSWISGDL--PSSQBEPLFP 2124
2150 RDLKKCVSETQSCRRPFGMLDEQRHSHIAYSCLDGSGQRLCPSPSLGGQPLGGPGS 2209
2125 RDLKKCVSETQSCRRPFGMLDEQRHSHIAYSCLDGSGQRLCPSPSLGGQPLGGPGS 2184
2210 RPKKLSPPSISIDPPESQSGRPSPGVCLRRRPPASDSKPSVSSPLDSTAASPSPK 2269
2185 RPKKLSPPSISIDPPESQSGRPSPGVCLRRRPPASDSKPSVSSPLDSTAASPSPK 2244
2270 DTLSLSGLSSDPTMDP 2286
2245 DVLSLSGLSSDPAOLDP 2261

RESULT 11
RAY14589
ID RAY14589 standard; protein; 2243 AA.

XX AAY14589;
AC
XX 07-DEC-1999 (first entry)
DT
XX Human T-type voltage-gated Ca channel alpha-1-G (hCavTid).
DE
XX Human; T-type voltage-gated calcium channel; membrane; pore; ion;
KW activation; current; rat; screen; drug; cardiomyopathy; epilepsy.
KW
XX Homo sapiens.
OS
XX WO929847-A1.
FN
XX 17-JUN-1999.
PD
XX 30-OCT-1998; 98WO-US023161.
PF
XX 05-DEC-1997; 97US-00985809.
PR
XX (LOYO) UNIV LOYOLA CHICAGO.
PA
XX Perez-Reyes E, Cribbs LL;
PI
XX WPI; 1999-394972/33.
DR
XX N-PSDB; AAX83484.
DX
XX New T-type voltage-gated calcium channels.
PT
XX Disclosure; Page 58-67; 138pp; English.
PS
XX This sequence represents a human T-type voltage-gated calcium (Ca)
CC channel alpha-1-G designated hCavTid. Voltage gated channels are membrane
CC bound glycosylated proteins formed of several subunits. The large alpha
CC subunits form a pore in the membrane that is selective for a given ionic
CC species. Each alpha subunit contains 4 domains (I, II, III and IV) and
CC each domain contains 6 putative transmembrane helical segments (SI-S6). T
CC type Ca channels are activated at a lower voltage than L- or N-type
CC channels. Characteristics of T-type channels include short current time,
CC slow activation kinetics near threshold, fast inactivation kinetics and
CC slow tail current. The sequences AAX83481-X83492 represent novel T-type
CC voltage-gated Ca channel genes from humans and rats. Each of the novel Ca
CC channels contains a putative IVS4 region comprising the amino acid
CC sequence AAY14589. Cells expressing the T-type voltage-gated calcium
CC channel proteins can be used to screen for drugs which affect calcium
CC channels. Methods are also disclosed for treating a disease or disorder
CC associated with a deficiency in a native T-type calcium channel nucleic
CC acid, e.g. to treat cardiomyopathy, epilepsy, etc
XX
SQ Sequence 2243 AA;
Query Match 89.8%; Score 10806.5; DB 2; Length 2243;
Best Local Similarity 93.3%; Pred. No. 0;
Matches 2076; Conservative 33; Mismatches 104; Indels 13; Gaps 5;
62 GAAGAGSTKDGSDSEAGLPPALAPVVFYLSQSRPSRSCWCLRTVCNPFERSML 121
30 GRPGSGAEKDGSDSEAGLPPALAPVVFYLSQSRPSRSCWCLRTVCNPFERSML 89
122 VILLNCVTILGMPRCPEDIAQDSQRCRILOAFDDIFAFVEMVVMVALGIFGKCYLG 181
90 VILLNCVTILGMPRCPEDIAQDSQRCRILOAFDDIFAFVEMVVMVALGIFGKCYLG 149
182 DTWNRLDFFVTIAGMLEYSLDQNSVFSVARTVRVLRPLRNRVPSMRILVTLTLDLTP 241
150 DTWNRLDFFVTIAGMLEYSLDQNSVFSVARTVRVLRPLRNRVPSMRILVTLTLDLTP 209
242 MLGNVLLCFVFFIFGIVGVOLWAGLLNRNCFLENFSLPSVLDLERYOTENDESPF 301
210 MLGNVLLCFVFFIFGIVGVOLWAGLLNRNCFLENFSLPSVLDLERYOTENDESPF 269
302 ICSPRENGMRSCRVPITLGEQGGPPCSLDYETVNSSNTTCVNNNOYVYTCNSAGEHN 361

Db 270 ICSQPRENGMRS CRSVPTLRGDCGGGPPCGLDYEA YNSSNTTCVNNQYTTNCSAGEHN 329
Qy 362 PFKGAINFONIGVAMTAIFQVITLEGWDMYFVMDAHSPYNIPIYFILLIIVGSPFMNL 421
Db 330 PFKGAINFONIGVAMTAIFQVITLEGWDMYFVMDAHSPYNIPIYFILLIIVGSPFMNL 389
Qy 422 CLVVIATQFSETKORSSQLMREORVFLSNASTLASFPSPGSCYBELLKYLVLILKAAR 481
Db 390 CLVVIATQFSETKORSSQLMREORVFLSNASTLASFPSPGSCYBELLKYLVLILKAAR 449
Qy 482 RLAQVSRALGVRAGLSSPVARSQBPQSPGSCSTRSHRLSVHHLVHHHHHHHHYHLGN 541
Db 450 RLAQVSRAGVRVGLLSSPAPLGQETQSSSCSRSHRLSVHHLVHHHHHHHHYHLGN 509
Qy 542 GTLRVPASPEIQDRDANGSRRLMLPSTPTSPGPPRGAESVHFSYHADCHLEPVRCQ 601
Db 510 GTLRVPASPEIQDRDANGSRRLMLPSTPTSPGPPRGAESVHFSYHADCHLEPVRCQ 569
Qy 602 APPRCPSEASGRVTGSKYVPTVHTSPPEILKDKALVEVAPSPGPTLTSTFNIIPGPF 661
Db 570 APPRCPSEASGRVTGSKYVPTVHTSPPEILKDKALVEVAPSPGPTLTSTFNIIPGPF 629
Qy 662 SSMHKLLETQSTGACHSSCKISSPCSKADSGAGCPDSCPYCARTGAGEPESADHVMPSD 721
Db 630 SSMHKLLETQSTGACHSSCKISSPCSKADSGAGCPDSCPYCARTGAGEPESADHVMPSD 689
Qy 722 SEAVYFTQDAQSHDLRDRHSRRRQSLGPDABPSSVLAFWRLICDTFRKIVDSKYFGRG 781
Db 690 SEAVYFTQDAQSHDLRDRHSRRRQSLGPDABPSSVLAFWRLICDTFRKIVDSKYFGRG 748
Qy 782 IMAILVNTLSMGIEVHEQPEELTNALEISNIYFTSLFALEMLKLLVYVGPYIKNPYN 841
Db 749 IMAILVNTLSMGIEVHEQPEELTNALEISNIYFTSLFALEMLKLLVYVGPYIKNPYN 808
Qy 842 IFDGVIVVSWIEVQCGGSLVLTFRMLRVFLPALQRLVLMKTMNDVATP 901
Db 809 IFDGVIVVSWIEVQCGGSLVLTFRMLRVFLPALQRLVLMKTMNDVATP 868
Qy 902 CMLLMFIIFISILGMHLFCCKPASPDRDGTLPDRKNFDSLLMAIIVTVFQILTOEDWNV 961
Db 869 CMLLMFIIFISILGMHLFCCKPASPDRDGTLPDRKNFDSLLMAIIVTVFQILTOEDWNV 928
Qy 962 LYNGMASTSSWAALYFIALMTFNGYVLFNLVAILVEGQAECDATKSESEDPFSPSVD 1021
Db 929 LYNGMASTSSWAALYFIALMTFNGYVLFNLVAILVEGQAECDATKSESEDPFSPSVD 988
Qy 1022 GDGDRKRLALVALGHAELRKSLPLIHTAATPMWHPKSSSTGVEALGSGSRRTSS 1081
Db 989 GDGDRKRLALVALGHAELRKSLPLIHTAATPMWHPKSSSTGVEALGSGSRRTSS 1048
Qy 1082 SGSAEPGAHHKCPSPASRSPSPSWAASSWTSRRSRNSLGRAPSLKRRSPSGERRS 1141
Db 1049 SGSAEPGAA - HEMKSPSPASRSPSPSWAASSWTSRRSRNSLGRAPSLKRRSPSGERRS 1107
Qy 1142 LLSGEGQESQDESESEEDRASPAGSDHRRHRSLEAKSSFDLPDTLOVGLHRTASGR 1201
Db 1108 LLSGEGQESQDESESEEDRASPAGSDHRRHRSLEAKSSFDLPDTLOVGLHRTASGR 1167
Qy 1202 SSASEHQDCNGKSGARLARTLTDPPQLDGDNDDEGNLSKGERIQAWVRSLPACCCE 1261
Db 1168 GSASEHQDCNGKSGARLARTLTDPPQLDGDNDDEGNLSKGERIQAWVRSLPACCCE 1227
Qy 1262 RDSWSAYIFPPQSRFRLLCHRIITHKMFHDHVLVLIIFLNCITIAMERP KIDPHSAERIFL 1321
Db 1228 RDSWSAYIFPPQSRFRLLCHRIITHKMFHDHVLVLIIFLNCITIAMERP KIDPHSAERIFL 1287
Qy 1322 TLSNYIFTAVFLAEMTKVVALGWCCEQAYLRSSNNVLDGLLVLISVIDILYSMDSG 1381
Db 1288 TLSNYIFTAVFLAEMTKVVALGWCCEQAYLRSSNNVLDGLLVLISVIDILYSMDSG 1347
Qy 1382 TKILGMLRVLRLLRTPRVLVISAQGLKLVVLTLMSSLKPIGNIVVICAPFIIFGILG 1441
Db 1348 TKILGMLRVLRLLRTPRVLVISAQGLKLVVLTLMSSLKPIGNIVVICAPFIIFGILG 1407

Qy 1442 VOLFKGKFFVCOGEDTRNITNKSDCAEASRWYRHKYNFDNLCOALMSLFLVASKDGWVD 1501
Db 1408 VOLFKGKFFVCOGEDTRNITNKSDCAEASRWYRHKYNFDNLCOALMSLFLVASKDGWVD 1467
Qy 1502 IMYDGLDAGVGVDOQPIMNHNPMWLLYFISFLILVAFVFLNMFGVVVENPHKCRQHOEE 1561
Db 1468 IMYDGLDAGVGVDOQPIMNHNPMWLLYFISFLILVAFVFLNMFGVVVENPHKCRQHOEE 1527
Qy 1562 EARRBEKRLRLLEKRRSKEKQMAEACQCKPYYSRFRLLVHLCTSHYDLFTIGVI 1621
Db 1528 EARRBEKRLRLLEKRRSKEKQMAEACQCKPYYSRFRLLVHLCTSHYDLFTIGVI 1580
Qy 1622 GLNVVTMAHEHQOQOILDEALKICNYIFTVIFVSPVKLVAFARRFQDDRWNQDLA 1681
Db 1581 GLNVVTMAHEHQOQOILDEALKICNYIFTVIFVSPVKLVAFARRFQDDRWNQDLA 1640
Qy 1682 IVLLSIMGITLLEIEVNLSPINPTIIRIMRVLRIRARVLKLLKMAVGMRAALLTVMQALP 1741
Db 1641 IVLLSIMGITLLEIEVNLSPINPTIIRIMRVLRIRARVLKLLKMAVGMRAALLTVMQALP 1700
Qy 1742 QVGNGLLPMLLFFIPAAALGVLELFGDLECDETHPCGLGRHATFRNFGMAFLTFRVSTG 1801
Db 1701 QVGNGLLPMLLFFIPAAALGVLELFGDLECDETHPCGLGRHATFRNFGMAFLTFRVSTG 1760
Qy 1802 DWNGIMKDPDRDCDOESTCYNTVISPPIYFVSVLTAQFVLNVNVTAVLMKHEESNKEA 1861
Db 1761 DWNGIMKDPDRDCDOESTCYNTVISPPIYFVSVLTAQFVLNVNVTAVLMKHEESNKEA 1820
Qy 1862 KEAEAELEAELEEMKTLSPQHPSPGSPFLMPCVEGVNSTDSPKCAPHTTAHIGAASGF 1921
Db 1821 KEAEAELEAELEEMKTLSPQHPSPGSPFLMPCVEGVNSTDSPKCAPHTTAHIGAASGF 1880
Qy 1922 SLEHPTMPPHPEVPVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTABRSIGHRGWGL 1981
Db 1881 SLEHPTMPPHPEVPVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTABRSIGHRGWGL 1937
Qy 1982 PKAOSGIIIVSHVSOADPTSCILQLPKDVHLYLQPHCAPTWGALPKLPPGGRSPLAQRPRLR 2041
Db 1938 PKAOSGIIIVSHVSOADPTSCILQLPKDVHLYLQPHCAPTWGALPKLPPGGRSPLAQRPRLR 1997
Qy 2042 RQAARTDSDLVQGLGSRREDLLSEVSGPSCPILTRSSSFWGSSIIQVQORSIGOSKYSKHI 2101
Db 1998 RQAARTDSDLVQGLGSRREDLLSEVSGPSCPILTRSSSFWGSSIIQVQORSIGOSKYSKHI 2057
Qy 2102 RLPAPCGLEPSWAKOPPETRSLELDTLSWISGDL - PSSQEBPLFPRLDKKCYSVET 2160
Db 2058 TTPAPCPGPEPNWKGPPETRSLELDTLSWISGDL - PSSQEBPLFPRLDKKCYSVET 2117
Qy 2161 QSCRRRPGFWLDEORRHSIAVSCLDGSOPLRCPSPSSILGQPLGGGSPRPPKLSPPSI 2220
Db 2118 QSCRRRPGFWLDEORRHSIAVSCLDGSOPLRCPSPSSILGQPLGGGSPRPPKLSPPSI 2177
Qy 2221 SIDPPESQSRPPSPGVCGLRRRAPASDKDPSVSPPLDSTAASPSPKDTLSLSGLSSD 2280
Db 2178 TIDPPESQSRPPSPGVCGLRRRAPASDKDPSVSPPLDSTAASPSPKDTLSLSGLSSD 2237
Qy 2281 PTMDMP 2286
Db 2238 PADLDP 2243

RESULT 12

ADJ68819
ID ADJ68819 standard; protein; 2243 AA.

XX ADJ68819;

AC
XX 06-MAY-2004 (first entry)

DT Human heat mitochondrial protein as a therapeutic target SeqID625.
XX
XX mitochondrial; human; screening assay; diabetes mellitus;

KW Huntington's disease; osteoarthritis;
KW Leber's hereditary optic neuropathy; LHON;
KW mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
KW myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;
KW neuroprotective; nontropic; antidiabetic; anticonvulsant; antiarthritic;
KW osteopathic; ophthalmological; cytostatic.
XX Homo sapiens.
XX W02003087768-A2.
XX PD 23-OCT-2003.
XX PF 04-APR-2003; 2003WO-US010870.
XX PR 12-APR-2002; 2002US-0372843P.
XX PR 17-JUN-2002; 2002US-0389987P.
XX PR 20-SEP-2002; 2002US-0412418P.
XX PA (MITO-) MITOKOR.
XX PA (BUCK-) BUCK INST AGE RES.
XX GHOSH SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GM;
PI Warnock DE;
XX WPI, 2003-845369/78.
XX Identifying a mitochondrial target for drug screening assays and for
PT treating diseases associated with altered mitochondrial function,
PT comprises detecting a modified polypeptide in a sample and correlating
PT with the disease.
XX Claim 1; SEQ ID NO 625; 180pp; English.
XX This invention relates to novel mitochondrial targets that can be used
CC for therapeutic intervention in treating a disease associated with
CC altered mitochondrial function. Specifically, it refers to a method for
CC identifying proteins of the human heart mitochondrial proteome that are
CC useful for drug screening assays, as well as therapeutic targets. The
CC present invention describes a method for identifying such proteins that
CC can be used in the treatment of various diseases associated with altered
CC mitochondrial function including diabetes mellitus, Huntington's disease,
CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial
CC encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy
CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these
CC compositions have neuroprotective, nontropic, antidiabetic,
CC anticonvulsant, antiarthritic, osteopathic, ophthalmological and
CC cytostatic activities. This polypeptide sequence is a human heart
CC mitochondrial protein of the invention.
XX XX
SQ Sequence 2243 AA;
Query Match 89.8%; Score 10806.5; DB 7; Length 2243;
Best Local Similarity 93.3%; Pred. No. 0;
Matches 2076; Conservative 33; Mismatches 104; Indels 13; Gaps 5;
QY 62 GAACAGAGTEKDPGADSEAGSLYPALAPVVFYLSQDSRPSWCLRTVCNPFVRSM 121
DB 30 GRPGGAEKDPGADSEAGSLYPALAPVVFYLSQDSRPSWCLRTVCNPFVRISM 89
QY 122 VILNCVTLGMFRPCEDICDSQRILQAFDDFIFAFFAVENVVQWALGIFGKKCYLG 181
DB 90 VILNCVTLGMFRPCEDICDSQRILQAFDDFIFAFFAVENVVQWALGIFGKKCYLG 149
QY 182 DTNRLDFPIVIAGMLESYLDQNVFSAVRTVRVLRPLRAINRPSMRLVTLTLLDTP 241
DB 150 DTNRLDFPIVIAGMLESYLDQNVFSAVRTVRVLRPLRAINRPSMRLVTLTLLDTP 209
QY 242 MLGNVLLLCFFVFFIFGLVQWALGRNCFLENFSLPLSVDLPEYYQTENEDESP 301
DB 210 MLGNVLLLCFFVFFIFGLVQWALGRNCFLENFSLPLSVDLPEYYQTENEDESP 269
QY 302 ICSPRENGMRSRVPTRLRGGGGPPCSLDYETNSNTTCVNNQYITNCSEAGEHN 361

DB 270 ICSPRENGMRSRVPTRLRGGGGPPCSLDYETNSNTTCVNNQYITNCSEAGEHN 329
QY 362 PFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFMDAHSFVNFYIFILLIIVGSFFMINL 421
DB 330 PFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFMDAHSFVNFYIFILLIIVGSFFMINL 389
QY 422 CLVVIATOFSETKQRESQMRQVRFLSNASTLASFSEPGSCYEELLKYLVLIRKAAR 481
DB 390 CLVVIATOFSETKQRESQMRQVRFLSNASTLASFSEPGSCYEELLKYLVLIRKAAR 449
QY 482 RLAQVSRAGVRAIGLLSSPVARSGOPOPSGCTSRSHRRLSVHLLVHHHHHHHHYHLGN 541
DB 450 RLAQVSRAGVRAIGLLSSPVARSGOPOPSGCTSRSHRRLSVHLLVHHHHHHHHYHLGN 509
QY 542 GTLRVPASPEIQRDANGSRRLMLPPSTPTPGGPPRGAESVHSFYHADCHLEPVRCQ 601
DB 510 GTLRVPASPEIQRDANGSRRLMLPPSTPTPGGPPRGAESVHSFYHADCHLEPVRCQ 569
QY 602 APPPRCPSEASGRITVSGKVYPTVHTSPPELTKDALKALVEVAPSPPTLTSFNIPGPF 661
DB 570 APPPRCPSEASGRITVSGKVYPTVHTSPPELTKDALKALVEVAPSPPTLTSFNIPGPF 629
QY 662 SSMHKLLETOSTGACSSCKISSPCSKADSGAGDSCPYCARTGAGPEPSADHVMPSD 721
DB 630 SSMHKLLETOSTGACSSCKISSPCSKADSGAGDSCPYCARTGAGPEPSADHVMPSD 689
QY 722 SEAVYFTQDAQHSRLDRPHSRRRQSRSLGPDAPSSVLAFWELICDTRKIVDSYFGRG 781
DB 690 SEAVYFTQDAQHSRLDRPHSRRRQSRSLGPDAPSSVLAFWELICDTRKIVDSYFGRG 748
QY 782 IMIAILVNTLSMGIEYHEQPEELTNALEISNIVFTSLFALEMLLKVLYGPGFYIKNPYN 841
DB 749 IMIAILVNTLSMGIEYHEQPEELTNALEISNIVFTSLFALEMLLKVLYGPGFYIKNPYN 808
QY 842 IFDGVIVVISWEIVGQGGGLSVLRTFRMLRVLKLVRPALOROLVLMKTMNDVATF 901
DB 809 IFDGVIVVISWEIVGQGGGLSVLRTFRMLRVLKLVRPALOROLVLMKTMNDVATF 868
QY 902 CMLMLFTIFSIIGMLFGCKFASERDGTLPDRKNFDSLLWAIIVTVFOILODMNKV 961
DB 869 CMLMLFTIFSIIGMLFGCKFASERDGTLPDRKNFDSLLWAIIVTVFOILODMNKV 928
QY 962 LYNGMASTSSWAALFYIATMTFGNYVLFNLVAILVEGFOAGDANKSEPPFSPSVD 1021
DB 929 LYNGMASTSSWAALFYIATMTFGNYVLFNLVAILVEGFOAGDANKSEPPFSPSVD 988
QY 1022 GGDGRKRLALVALGEHAELRKSLLPPLIHTAATPMHSPKSSSTGVGEALGSGSRRTSS 1081
DB 989 GGDGRKRLALVALGEHAELRKSLLPPLIHTAATPMHSPKSSSTGVGEALGSGSRRTSS 1048
QY 1082 SGSAEPGAHHEMKCPPSARSPHSPWASASWTSRRSSRSLGRAPSLKERSPSGERS 1141
DB 1049 SGSAEPGAHHEMKCPPSARSPHSPWASASWTSRRSSRSLGRAPSLKERSPSGERS 1107
QY 1142 LLSGEGQESQDEESESDEDRAPAGSDHHRGSLEREAKSSFDLPDTLQVPLHRTASGR 1201
DB 1108 LLSGEGQESQDEESESDEDRAPAGSDHHRGSLEREAKSSFDLPDTLQVPLHRTASGR 1167
QY 1202 SSASEHQDCNGKSASGLARTLRTDDPQLDGGDDNDGNLSKGERIQAWVRSRLPACCRE 1261
DB 1168 SSASEHQDCNGKSASGLARTLRTDDPQLDGGDDNDGNLSKGERIQAWVRSRLPACCRE 1227
QY 1262 RDSWSAYIFPPQSRFRLLCHRIITHQMFVHVLVIFLNCITIAMERPKIDPHSAERIFL 1321
DB 1228 RDSWSAYIFPPQSRFRLLCHRIITHQMFVHVLVIFLNCITIAMERPKIDPHSAERIFL 1287
QY 1322 TLSNYIFTAVFLAEMTVKVVVALQWCFGEQAYLRSSNVLDGLLVLSVDIRVMSVSDSG 1381
DB 1288 TLSNYIFTAVFLAEMTVKVVVALQWCFGEQAYLRSSNVLDGLLVLSVDIRVMSVSDSG 1347
QY 1382 TKILGMRLVRLLETPLRPLRVIISRAOGLKLVVETLMSLSKPIGNIYVVICAPFIIFGILG 1441

1348	TKILGMRVLRLLRLTLRLPLRVISRAQGLKLVTETLMSLPIGNIIVVICAPFIIGILG	1400
1442	VQLFKGKFFVCOGEDTRNITNKSDCAEASRYVRHKYTNFNLQALMSLFLVASKDGWVD	1501
1408	VQLFKGKFFVCOGEDTRNITNKSDCAEASRYVRHKYTNFNLQALMSLFLVASKDGWVD	1467
1502	IMVDGLDAVGVDQOPIINHNPWMLLYPISFLLIYVAFVLMFVGVVVENFHKCRHQEEE	1561
1468	IMVDGLDAVGVDQOPIINHNPWMLLYPISFLLIYVAFVLMFVGVVVENFHKCRHQEEE	1527
1562	EARRREBKRLRLLEKKRRSEKQMAQAQCKPYTSDYSRPFLLVHHLCTSHYLDLFTIGVI	1621
1528	EARRREBKRLRLLEKKRR-----KAQCKPYTSDYSRPFLLVHHLCTSHYLDLFTIGVI	1580
1622	GLNVVTWAMEHYQQOPIIDLEALKICNYIFTVIFVFSVFKLVAFAPRRFFQDRWNQLDLA	1681
1581	GLNVVTWAMEHYQQOPIIDLEALKICNYIFTVIFVLESVFKLVAFGPRFFQDRWNQLDLA	1640
1682	IVLLSINGITLEIEIEVNLSPINPTIIRIMRVLRIRARVLKLLKMAVGMRAALLHTVQALP	1741
1641	IVLLSINGITLEIEIEVNLSPINPTIIRIMRVLRIRARVLKLLKMAVGMRAALLHTVQALP	1700
1742	QVGNLGLLFWLLFFIIPAALGVLELFGDLECDETHPCGELGRHATFRNFGMAFLTLFRVSTG	1801
1701	QVGNLGLLFWLLFFIIPAALGVLELFGDLECDETHPCGELGRHATFRNFGMAFLTLFRVSTG	1760
1802	DNWNGIMKDPSCDQESTCVNTVISIYFVSFVLTQAQFVLNVVIAVLMKHLSEENKEA	1861
1761	DNWNGIMKDTLRDCCDQESTCVNTVISIYFVSFVLTQAQFVLNVVIAVLMKHLSEENKEA	1820
1862	KEBAELBAELEMLKTLSPQHPGLSGPFIWPGVEGVNSTDSPKPGAPHTTAHIGAASGF	1921
1821	KEBAELBAELEMLKTLSPQHPGLSGPFIWPGVEGVNSTDSPKPGALHPAAHARGASHF	1880
1922	SLEHPTWVHPPEVVPPLGPDLLTVRKSGYSRTHSLNDSYMCENGSTAEKSLGRGWGL	1981
1881	SLEHPTWQHPTELP---GPDLLTVRKSGYSRTHSLNDSYMCRHGSTAEGLHGRGWGL	1937
1982	PKAQSGSILSVHSPADTSCILQPKDVHYLLQHPGAPTWGATPKLPPPGKRSPLAQRPLR	2041
1938	PKAQSGSVLSVHSPADTSYILQPKDAPHLQHPHSAPTWTGTTIPKLPPPGKRSPLAQRPLR	1997
2042	QRAAIRTSLDVQGLGSRDILLSEVSGPSCPLTRSSSFWGSSSIQVQGRSGIOSKVSKEI	2101
1998	QRAAIRTSLDVQGLGSRDILLAEVSGPSPPLARAYSFWGSSSTQAQHQHRSKSHSKHM	2057
2102	RLPAPCGLSEWAKDPPETRSSLELDELTELTSWISGDLL--PSSQEEPLFPDRLKKCYSVET	2160
2058	TPPAPCPGPEPNWKGPPETRSSLELDELTELTSWISGDLLPFGQGEPEPSPRDLKKCYVEA	2117
2161	QSCRRRPGFWLDEORRHISIAVCLDSGSPRLCPSPSSILGQPLGGPGSPKPKKLSPPSI	2220
2118	QSCQRRTPSWLDEORRHISIAVCLDSGSPHLGTDPSNLGQPLGGPGSPKPKKLSPPSI	2177
2221	SIDPPESQSGRRPPGCVGLRRRAPASDSDKDPVSSSLDTAAASPSPKDKTSLSLGSSD	2280
2178	TIDPPESQGPRTTPSPGICLRRRAPSDSDKDPPLASGPPDSWAAASPSPKDKVLSLGLSSD	2237
2281	PTMDLP 2286	
2238	PADLDP 2243	
RESULT 13		
ADQ89064		
ID ADQ89064 standard; protein; 2377 AA.		
XX	AC	ADQ89064;
XX	AC	
XX	AC	
DT	21-OCT-2004	(first entry)
XX	DE	Human urological disorder related protein 4421 SEQ:16.
XX	XX	

KW		urological disorder; uropathic; cytostatic; urinary incontinence;
KW		benign prostatic hyperplasia; human.
XX		Homo sapiens.
OS		WC2004065576-A2.
PN		
XX		
XX		05-AUG-2004.
PD		
XX		14-JAN-2004; 2004WO-US000750.
XX		
PR		15-JAN-2003; 2003US-0440318P.
PR		04-FEB-2003; 2003US-0444783P.
PR		27-MAR-2003; 2003US-0457901P.
PR		08-MAY-2003; 2003US-0468775P.
PR		19-MAY-2003; 2003US-0471614P.
PR		16-JUN-2003; 2003US-0478742P.
PR		18-JUL-2003; 2003US-0488529P.
PR		30-JUL-2003; 2003US-0491156P.
PR		02-SEP-2003; 2003US-0499594P.
PR		26-SEP-2003; 2003US-0506332P.
XX		(MILL-) MILLENNIUM PHARM INC.
PA		
PI		Karicheti V, Silos-Santiago I, Eliasof SD;
XX		
XX		WPI; 2004-562167/54.
DR		N-PSDB; ADQ89063.
XX		
PT		Use of polypeptides related to urological disorders, e.g. 44390, 54181,
PT		211 or for identifying a compound capable of treating a urological
PT		disorder or identifying and treating a subject having a urological
PT		disorder.
XX		
PS		Claim 1; SEQ ID NO 16; 542pp; English.
CC		The present invention describes the use of polypeptides related to
CC		urological disorders for identifying a compound capable of treating a
CC		urological disorder, identifying a subject having a urological disorder,
CC		or treating a subject having a urological disorder. Also described: (1) a
CC		method for identifying a compound capable of treating a urological
CC		disorder; (2) a method for identifying a subject having a urological
CC		disorder; and (3) a method for treating a subject having a urological
CC		disorder. The compound has uterine and cytotonic activities. The
CC		polypeptides related to urological disorders are useful for identifying a
CC		compound capable of treating a urological disorder, identifying a subject
CC		having a urological disorder, or treating a subject having a urological
CC		disorder. Disorders include urinary incontinence and benign prostatic
CC		hyperplasia. The present sequence represents a human urological disorder
CC		related protein, which is used in the exemplification of the present
XX		invention.
XX		
SQ		Sequence 2377 AA;
		Query Match 89.2%; Score 10732.5; DB 8; Length 2377;
		Best Local Similarity 88.3%; Pred. No. 0;
		Matches 2078; Conservative 33; Mismatches 109; Indels 133; Gaps 7;
QY	62	GAGAGSTEKDPGSADSEAEGLYPALAPVVFYLSQDSRPRNCCLRTVCNPFERSML 121
Db	30	GRPGSGAEXDPCGSADSEAEGLYPALAPVVFYLSQDSRPRNCCLRTVCNPFERISML 89
QY	122	VILLNCVTLLGMPRPCEDIACDSORCRILQAFDDFIFAFFAVEMVKVMVALGIQKKCYLG 181
Db	90	VILLNCVTLLGNFRPCEDIACDSORCRILQAFDDFIFAFFAVEMVKVMVALGIQKKCYLG 149
QY	182	DTWNRLDFFVIAGMLEYSLDLQNVSFSAVRTVRVLRLPLRAINRVPSMRILVTLTLLDTP 241
Db	150	DTWNRLDFFVIAGMLEYSLDLQNVSFSAVRTVRVLRLPLRAINRVPSMRILVTLTLLDTP 209
QY	242	MIGNVLLLCFPVFIFIGIVGVQLWAGLLNRRCFLPENFSPLSDLEPPYQTENEDESPP 301
Db	210	MIGNVLLLCFPVFIFIGIVGVQLWAGLLNRRCFLPENFSPLSDLEPPYQTENEDESPP 269

QY	1359	VLGGLLVLSVIDILVSVSDSGTKILGMLRVLRLLRTRPLRVISRAQGLKVVELTMS	1418
Db	1348	VLGGLLVLSVIDILVSVSDSGTKILGMLRVLRLLRTRPLRVISRAQGLKVVELTMS	1407
QY	1419	SLKPIGNIWVICAPFIIFGILGVOLFVKGFVQCGEDTRNITNKSDCABASYRWHRKY	1478
Db	1408	SLKPIGNIWVICAPFIIFGILGVOLFVKGFVQCGEDTRNITNKSDCABASYRWHRKY	1467
QY	1479	NFDNLGQALMSLFLVASKDQWVDIMYDGLDAGVDQDQPMNHNPMMLLYFTSFLLI VAF	1538
Db	1468	NFDNLGQALMSLFLVASKDQWVDIMYDGLDAGVDQDQPMNHNPMMLLYFTSFLLI VAF	1527
QY	1539	VLNMFGVVVENPHKCRQOESEERREKRLREKKR-----SKEQMAE	1587
Db	1528	VLNMFGVVVENPHKCRQOESEERREKRLREKKR-----SKEQMAE	1587
QY	1588	AQCKPYSDYSRRLAVHLCTSHYLDLFTITGVLNVVTMAMEHYQQOILDEALKTGN	1647
Db	1588	AQCKPYSDYSRRLAVHLCTSHYLDLFTITGVLNVVTMAMEHYQQOILDEALKTGN	1647
QY	1648	YIFTVIFVFESEVFKLVAFRFRFQDRWNQOLDLAIIVLLSIMGITILEETVNLSPINPTI	1707
Db	1648	YIFTVIFVFESEVFKLVAFRFRFQDRWNQOLDLAIIVLLSIMGITILEETVNLSPINPTI	1707
QY	1708	IRIMRVLRIRARVLKILKMAVGMALHTVMOALPOVGNLGLLFLMLFFIFAALGVLFQD	1767
Db	1708	IRIMRVLRIRARVLKILKMAVGMALHTVMOALPOVGNLGLLFLMLFFIFAALGVLFQD	1767
QY	1768	LECDETHPCGLGRHATFRNFGMAFLTFRVSTGDNWNGIMKDPDQDOESTCYNTVLIS	1827
Db	1768	LECDETHPCGLGRHATFRNFGMAFLTFRVSTGDNWNGIMKDPDQDOESTCYNTVLIS	1827
QY	1828	PIYFVSFVLTAQFVLNVNVIAVLKMLEENKAEAELEAELEEMKTLSPQHPSPLG	1887
Db	1828	PIYFVSFVLTAQFVLNVNVIAVLKMLEENKAEAELEAELEEMKTLSPQHPSPLG	1887
QY	1888	SPFLMPGVEGVNSTDSKPKGAPHTTAHIGAAAGSFSLEHPT-----	1927
Db	1888	SPFLMPGVEGVNSTDSKPKGAPHTTAHIGAAAGSFSLEHPT-----	1927
QY	1928	-----	1927
Db	1948	KLMDLAPGGQPSAPPSAPSLGSGSQDPIPLAEMALSLTSEIVSEPSCLALTDSDLDP	2007
QY	1928	-----MVPHEPVPVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAERSL	1974
Db	2008	DMHTLLLSALESNMQPHTELP---GPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAERSL	2064
QY	1975	GHRGMLPKAOGSILSVHSQPADTSCILQPLKDVHVLLOPHGAPTWCALPKLPPGRSP	2034
Db	2065	GHRGMLPKAOGSILSVHSQPADTSCILQPLKDVHVLLOPHGAPTWCALPKLPPGRSP	2124
QY	2035	LAORPLRQAAIRTDSDVOGLGSRREDLLSEVSGPSCPLTRSSFWGSSSIQVQORSIQ	2094
Db	2125	LAORPLRQAAIRTDSDVOGLGSRREDLLSEVSGPSCPLTRSSFWGSSSIQVQORSIQ	2184
QY	2095	SKVSKHRLPAPCPGLEPNAWKDPETRSSLELDELTELWISGDL- PSSQOEPLPRLK	2153
Db	2185	SKVSKHRLPAPCPGLEPNAWKDPETRSSLELDELTELWISGDL- PSSQOEPLPRLK	2244
QY	2154	KCVSVETOSCRPPGFWLDBORRHSITAVSCDGGSPRLCPSPSSILGQPLGPGSRPKK	2213
Db	2245	KCVSVETOSCRPPGFWLDBORRHSITAVSCDGGSPRLCPSPSSILGQPLGPGSRPKK	2304
QY	2214	KLSPPSISIDPPPSQSGSRPPCPGVCLRRRAPASDSDKPSVSPDLSTAAASPKKDTLS	2273
Db	2305	KLSPPSISIDPPPSQSGSRPPCPGVCLRRRAPASDSDKPSVSPDLSTAAASPKKDTLS	2273
QY	2274	LSGLSSDPTDMDP 2286	
Db	2365	LSGLSSDPTDMDP 2377	

```
RESULT 14
AAB66481
ID AAB66481 standard; protein; 2266 AA.
XX
XX AAB66481;
XX
XX 09-APR-2001 (first entry)
XX
XX Human alpha-IG T-type calcium channel protein.
XX
XX Human; antiarrhythmic; anticonvulsant; hypotensive; cardiac; nootropic;
XX T-type calcium channel subunit; cardiac hypertrophy; cardiac arrhythmia;
XX hypertension; sleep disorder; epilepsy; alpha-IG T-type calcium channel.
XX
XX Homo sapiens.
XX
XX WO200102561-A2.
XX
XX 11-JAN-2001.
XX
XX 04-JUL-2000; 2000WO-CA000794.
XX
XX 02-JUL-1999; 99US-00346794.
XX
XX (NEUR-) NEUROMED TECHNOLOGIES INC.
XX
XX Snutch TP, Baillie DL;
XX
XX WPI; 2001-123111/13.
XX
XX N-PSDB; AAF31684.
XX
XX Novel T-type calcium channel alpha-1 subunit gene useful for treating
XX cardiac hypertrophy, cardiac arrhythmia, hypertension, sleep disorder and
XX epilepsy.
XX
XX Example 3; Fig 6; 103pp; English.
XX
XX The present sequence is given in a specification providing sequences and
XX partial sequences for three types of mammalian (human and rat) T-type
XX calcium channel subunits. An expression cassette has been generated which
XX comprises a nucleotide sequence encoding a T-type calcium channel alpha_1
XX subunit operably linked to control sequences to effect its expression.
XX The novel calcium channel nucleic acids and proteins are useful for
XX treating conditions characterised by undesirable levels of T-type calcium
XX channel activity such as cardiac hypertrophy, cardiac arrhythmia,
XX hypertension, sleep disorder and epilepsy
XX
XX Sequence 2266 AA;
XX
XX Query Match 87.6%; Score 10533; DB 4; Length 2266;
XX Best Local Similarity 91.2%; Pred. No. 0;
XX Matches 2050; Conservative 38; Mismatches 125; Indels 36; Gaps 6;
XX
XX 62 GAAGAGSTEDPGSADSEAGLPALAPVFFYLSQDSRPSRCLRTVCNPNPFRVSM 121
XX
XX 30 GRPGGSAEKDPGADSEAGLPALAPVFFYLSQDSRPSRCLRTVCNPNPFRISML 89
XX
XX 122 VILLNCVTLGMFRPCEDIACDSQRCRILOAFDDFIFAFFAVEMVVMKVALGIFGKCYLG 181
XX
XX 90 VILLNCVTLGMFRPCEDIACDSQRCRILOAFDDFIFAFFAVEMVVMKVALGIFGKCYLG 149
XX
XX 182 DTNRLDFFVIAGMLEYSLDLQNVSPSAVTRVRLPLRAINRVPMSRILVTLTLLDTP 241
XX
XX 150 DTNRLDFFVIAGMLEYSLDLQNVSPSAVTRVRLPLRAINRVPMSRILVTLTLLDTP 209
XX
XX 242 MLGNVLLCCFPVFFIGLVGQWAGLNRCLFENFSLPLSDLEPYQCTENEDESP 301
XX
XX 210 MLGNVLLCCFPVFFIGLVGQWAGLNRCLFENFSLPLSDLEPYQCTENEDESP 269
XX
XX 302 ICSPRENGMRSRCSVPTLRGEGGGPPCSLDYETYNSSNTTCVNNQYNTNCAGEHN 361
XX
XX 270 ICSPRENGMRSRCSVPTLRGEGGGPPCGLDIYAYNSSKTTTCVNNQYNTNCAGEHN 329
XX
```


QY 488 RAIGVAGLSSPVAR-----SGOPEOPSGCTSRHRLSVHHLV-HHHHHHHHHYHLGN 541
Db 480 ARWQSRWRKVDPSSTVHGQPGRRPRAG-----RTASVHLLVYHHHHHHHHYHFSH 534
QY 542 GTLVPRASPEIQDORANGSRRLM--LPPSTPTFPSPGPRGABSVHSFYHADCHLEPVR 599
Db 535 GGPR--RPSPE---PCAGDNRLVRACAPSPSPGHPGPP-DSSEVHSIYHADCHVEGPQ 587
QY 600 QAPPPPCPEASORTVSGG---KYVPTV-----HTSPPEILKOKALVEVAPSP 646
Db 588 ERARVAHSIATAASLKASGLGTWNYPTILPGTVNSKGSTSSRPKGLRG-----AGAP 641
QY 647 GPPTLTSENI--PRGPFSSMKHLTQSTGACHSCK--ISSPC-----SKADSGACGPDSCP 700
Db 642 GAAVHSPSLGSPRYEKIQDVGEQGLGRASSHLSGLSVCPPLSPQAGTLTCELKSCP 701
QY 701 YCARTGAGEP--ESADVMPDSDSEAYEFTQDAQHSDLRDP-----HSRRQR 747
Db 702 YCA-SALEDEFEFSGESGSDAHGYEFTQDVHRHGDRCDPVQOPHEVGTGPHSNERR 760
QY 748 S-LGPDAPSPSVLAFWRLICDTFRKIVDSKYFGRGIMAILVNTLSMGIYHEQPEBLTN 806
Db 761 TPLRKASQPGIGIHLWASFGSKLRRIVDSKYFNRMGIMAAILVNTLSMGEVYHEQPEBLTN 820
QY 807 ALEISNIVFTSLPALEMLLKVYGPFGYIKNPYNIPOGVIIVLSVWEIVGQQGGLSVL 866
Db 821 ALEISNIVFTSMFALEMLLKLACGLPIYRNPNIFDGIIVVLSVWEIVGQADGGOSVL 880
QY 867 RTFLMRVLKVRFLPALQRLVLMKTMONVATFCMLLMFIFISILGMHFLGCKFPAS 926
Db 881 RTFLRLAVLKLVRFLPALQRLVLMKTMONVATFCMLLMFIFISILGMHFLGCKFSL 940
QY 927 ERD-GDTLPDRKPNDSLLWAIIVTFQILTOEDMNKVLVYNGMASTSSWAAALYPIALMTFGN 985
Db 941 KTDSDGTVPDRKPNDSLLWAIIVTFQILTOEDMNKVLVYNGMASTSSWAAALYFVALMTFGN 1000
QY 986 YVLNLLVAILVEGFOAGDATSESPDFSPVSDGGRKKEL-----ALVALG 1036
Db 1001 YVLNLLVAILVEGFOAGDATSESPDFSPVSDGGRKKEL-----ALVALG 1060
QY 1037 EHAELRKLSPPLIITHAATPMSPKSS-STGVGEALGSGSRRTSSSGSAEPGAAHHEMK 1095
Db 1061 GHLEGRGSLPPLIITHAATPMPTPKSSPNLDVAHAL-LDSRR--SSGSDVPQLG--DQX 1116
QY 1096 CPSPARSPPSPSAASWTSSRRNSLGRAPSLKRRSPSGERRSLLSGEGESQDEBE 1155
Db 1117 SLASLRSPCTPMGPNAGSRRSWSNLSGRAPSLKRRSPSGERRSLLSGEGKSTDE- 1175
QY 1156 SSEDRA-----PAGSDHHRGSLEREAKSSFDL-----PDTLOVPLHRTAS 1199
Db 1176 -ABDSRPSGTGHPGASPGPRATPLURRAESLDH--RSTLDLCPPRPAPPAVQV----- 1224
QY 1200 GRSSAHEQCNKGASAGRLARTURDDPOLDDDDNDENGLSKGERIQAWVRSLPACC 1259
Db 1225 -----HDCNGQWALPSEFFLRIDSHKEDAEFPDDIEDSCFLHKVLEPYAPQWC 1276
QY 1260 RERDSAYIFPPQSRFLCHRIITHKMFHDVVLVIFINCAITIAMERPKIDPHSAERI 1319
Db 1277 RSRESWALYLPQONRLRVSCQVIAHKMFHDVVLVIFINCAITIALERPIDDPGSTER 1336
QY 1320 FLTISNIVFTAVFLAEMTKVVALGWCFCGEQAYLRSSWNLVLDGLLVLSVIDILVMSVD 1379
Db 1337 FLVSNNIVFTAFVEMVMKVVALGLLWGEHAYLQSSWNLVLDGLLVLSVIDIIVANASA 1396
QY 1380 SGTIKLMLRVLRLRLRLRVISRAQGLKLVVETLMSLKPITGNVWICCAFFIIFI 1439
Db 1397 GGAKILGLVRLVRLRLRLRVISRAPGLKLVVETLISLRPIGNVILICCAFFIIFI 1456
QY 1440 LGVLFKGFVCOGEDTRNITNKSDCAEASYRWRHKNYFNPDNLGQALMSLFLVLSKDGW 1499
Db 1457 LGVLFKGFVCEGTDTRNITTKAECHAAHYRWRHKNYFNPDNLGQALMSLFLVLSKDGW 1516
QY 1500 VDIMYDGLDVGVDQOQPMNNHNPMLLYFISFLIVAFVLMFVGVVFNHFKCRHQE 1559

Db 1517 VIMYDGLDVGVDQOQPMNNHNPMLLYFISFLIVAFVLMFVGVVFNHFKCRHQE 1576
QY 1560 EEARREERKRLREKKRRSKEQMAEACKPYSDYSRFRLLVHHLCHTSHYLDLFTG 1619
Db 1577 AEARREERKRLREKKRRSKEQMAEACKPYSDYSRFRLLVHHLCHTSHYLDLFTG 1629
QY 1620 VIGLVVTVMAHEVQOQIILDEALKICNYITFVIFVESVFKLVAFAPRRFQDRWOLD 1679
Db 1630 IICLVITMSMEYHNPQKSLDEALKICNYITFVIFVESVFKLVAFAPRRFQDRWOLD 1689
QY 1680 LAIVLSIMGITLEEIEVNLSLNPINPTIIRIMVLRIRARVLKLMKMAVGRALLHTVQA 1739
Db 1690 LAIVLSIMGITLEEIEVNLSLNPINPTIIRIMVLRIRARVLKLMKMAVGRALLHTVQA 1749
QY 1740 LPQVGNLGLLFFMILLFFIFAALGVDELFGDLCEDETHPCBGLGRHATFRNFGMAFLTLFRVS 1799
Db 1750 LPQVGNLGLLFFMILLFFIFAALGVDELFGDLCEDETHPCBGLGRHATFRNFGMAFLTLFRVS 1809
QY 1800 TGDWNGIMKDPBRDC---DOESTCYNVTIVSPIYFVSFVLTAQFVLVNVVIAVLMKLE 1856
Db 1810 TGDWNGIMKDTLRECTREDKCHCLSYLPALSPYFVTFMLVAQFVLVNVVIAVLMKLE 1869
QY 1857 SNKEAEAEAELEAELEEMKTLSPQPHSLGSPPLGSPVLPWPGVEGVNSTDSPKCAPHTTAHIG 1916
Db 1870 SNKEAREDAEMDAIELEM-----AQGSTAQPPTAQES----- 1903
QY 1917 AASGFSLEHTMVPHPHEVPVPLGPDLLTVRKGSVSRTHSLPNDSYNCRNGSTAERSLGH 1976
Db 1904 -----QGTQPDPTNLLVVRKVSVRMLSLPNDSYNCRNGSTAERSLGH 1946
QY 1977 RGHGLP-----KAQSGSILSVHSQPADTSCILQLP-----KDVHLLQPHGAPTW 2021
Db 1947 -----PLQEVEMETTYGTPTVSAHSPLEPRASFQVPSAASPAKVSPLCALSPRGTP-- 1999
QY 2022 GAIPKLPKPPGCRSPLAQRPLRQAARTDSDL--VOGLGSRDLSEVSGSPCLTRSSSF 2079
Db 2000 -----RSLSLRILCRQEAHMSLESLEKVDVGG--DSIPDYTEPAENMSTSQAS 2047
QY 2080 WGG-----SSIQVQORSGIQSKVHRLPAPCPGLEPSWAKDPPETRSSLSDT 2129
Db 2048 TGAPRSPPCSPRASVTRKHTFGQRCISSR---PPTLGGDEAEAADP-----ADE 2095
QY 2130 ELWSIGDILLPSSQEBPLP-----RDLLKCYSVETQSCRRRPGFWLDE 2173
Db 2096 EVSHITSSAHPWPAEPHSPSPASPTASPVKGTWGSGRDPRFCSDAQSLDKFG-RPDA 2154
QY 2174 QRRHSIAV---SCLDSGS-----OPRLCPSPLSGQPLGGGSRPKKLSPPSIS 2221
Db 2155 QRWSSVELDNGESHLSEGEVGRASELEPAL-----GSRKKKMSPPCIS 2199
QY 2222 IDPP--ESQSGSRPPCSFG--VCLRRRAPASDS---KDPVSSSPLDSTAASP----- 2265
Db 2200 IEFTKDEGSSRPPAAEGGNTLRRRTFSCAALHRLDCPEPTGPGTGGDPVAKGERWQ 2259
QY 2266 -SPKDTLSLGSLSDDTDM 2284
Db 2260 ASCRAEHLTVNFAFEPLDM 2279

Search completed: April 13, 2005, 19:09:38
Job time : 267 secs

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OM protein - protein search, using sw model

Run on: April 13, 2005, 19:00:09 ; Search time 57 Seconds
(without alignments)
2995.130 Million cell updates/sec

Title: US-09-611-257A-24
Perfect score: 12028
Sequence: 1 MLPHRVPCRTVPLRGSAR.....KDTLSLSGLSSDPTDMDPZ 2287

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/iaa/5A COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/5B COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/6A COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/6B COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	10820.5	90.0	2273	3	US-09-426-998-5
2	10512	87.4	2220	4	US-09-949-016-9730
3	6221	51.7	2353	3	US-08-984-709A-50
4	5872	48.8	1207	4	US-09-398-322-52
5	5409	45.0	2175	3	US-09-404-650-2
6	5409	45.0	2175	4	US-09-935-541-2
7	5405.5	44.9	2188	3	US-09-404-650-4
8	5405.5	44.9	2188	4	US-09-935-541-4
9	5345	44.4	1835	3	US-09-404-650-5
10	5345	44.4	1835	4	US-09-935-541-5
11	1678	14.0	2343	3	US-09-268-163-4
12	1677	13.9	2337	3	US-08-713-118-2
13	1677	13.9	2337	1	US-09-452-007-2
14	1676	13.9	2339	1	US-08-455-543A-47
15	1676	13.9	2339	2	US-08-223-305C-47
16	1674	13.9	2339	3	US-09-268-163-6
17	1642.5	13.7	2237	1	US-08-455-543A-48
18	1642.5	13.7	2237	2	US-08-223-305C-48
19	1642.5	13.7	2236	3	US-09-268-163-10
20	1642	13.7	1985	4	US-09-495-714C-6
21	1640.5	13.6	2237	3	US-09-268-163-8
22	1634.5	13.6	1984	3	US-08-836-325-10
23	1634.5	13.6	1984	4	US-09-457-571-10
24	1631	13.6	2181	4	US-09-949-016-5981
25	1631	13.6	2188	4	US-09-949-016-8295
26	1628.5	13.5	1977	4	US-09-495-714C-4
27	1628	13.5	1873	1	US-08-435-675B-4

28	1625.5	13.5	1989	3	US-08-836-325-12
29	1625.5	13.5	1989	4	US-09-457-571-12
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32	1622	13.5	2161	1	US-07-745-206A-2
33	1622	13.5	2161	1	US-08-455-543A-49
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37	1617.5	13.4	1969	4	US-09-457-571-16
38	1616.5	13.4	1668	4	US-09-949-016-11611
39	1616	13.4	1873	1	US-08-336-257A-7
40	1614.5	13.4	1977	4	US-09-976-594-757
41	1614.5	13.4	1977	4	US-09-919-039-367
42	1614	13.4	1872	6	5386025-6
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44	1595.5	13.3	1912	4	US-09-495-714C-2
45	1589.5	13.2	2516	3	US-08-374-077C-2

ALIGNMENTS

RESULT 1

US-09-426-998-5

; Sequence 5, Application US/09426998

; Patent No. 6358706

; GENERAL INFORMATION:

; APPLICANT: DUBIN, ADRIENNE E.

; APPLICANT: PVATI, JAVASHREE

; APPLICANT: ZHU, JESSICA Y

; APPLICANT: ERANDER, MARK G

; APPLICANT: GALINDO, JOSE E

; TITLE OF INVENTION: DNA ENCODING HUMAN ALPHAIG T-TYPE CALCIUM

; TITLE OF INVENTION: CHANNEL (ALPHAIG-C)

; FILE REFERENCE: ORT-1057

; CURRENT APPLICATION NUMBER: US/09/426,998

; CURRENT FILING DATE: 1999-10-26

; NUMBER OF SEQ ID NOS: 5

; SOFTWARE: PATENTIN VER. 2.0

; SEQ ID NO 5

; LENGTH: 2273

; TYPE: PRT

; ORGANISM: HOMO SAPIENS

; US-09-426-998-5

Query Match 90.0%; Score 10820.5; DB 3; Length 2273;

Best Local Similarity 92.5%; Pred. No. 0;

Matches 2080; Conservative 35; Mismatches 105; Indels 29; Gaps 5;

Qy 62 GAAGAGSTEKDPGSADSEAGLPYPALAPVFFYLSQDSRPSRCLRTVCNPFWRVSM 121

Db 30 GRPGSAEKDPGSADSEAGLPYPALAPVFFYLSQDSRPSRCLRTVCNPFWRVSM 89

Qy 122 VILLNCVTLMGMPCEDIACDSORCRILQAFDDFPAFFAVVMVXVALGIFCKKCYLG 181

Db 90 VILLNCVTLMGMPCEDIACDSORCRILQAFDDFPAFFAVVMVXVALGIFCKKCYLG 149

Qy 182 DTWNRLDFFVIAGMLEYSLDLQNVSPSAVRTVRLPLRPLNRVPSMRILVTLTLLDTP 241

Db 150 DTWNRLDFFVIAGMLEYSLDLQNVSPSAVRTVRLPLRPLNRVPSMRILVTLTLLDTP 209

Qy 242 MLGNVLLLCFFVFFIFGIVGVQLWAGLLNRCLPENFSLPSVLDLPFYQTEDESPF 301

Db 210 MLGNVLLLCFFVFFIFGIVGVQLWAGLLNRCLPENFSLPSVLDLPFYQTEDESPF 269

Qy 302 ICSPRENGMRSCRSVPTLGECCGGPCSLDVTYSSNTTCVNNQYTNCSAGEHN 361

Db 270 ICSPRENGMRSCRSVPTLGECCGGPCSLDVTYSSNTTCVNNQYTNCSAGEHN 329

Qy 362 PFKGAINFNDIGYAWIAIFQVITLEGWVDIMYFMDAHSFYNFYIFILLIIVGSFFMINL 421

Db 330 PFKGAINFNDIGYAWIAIFQVITLEGWVDIMYFMDAHSFYNFYIFILLIIVGSFFMINL 389

QY 422 CLVVIATQFSETKORESQLMRQVRFLSNASTLASFSEPGSCYBELIKYLVITLKAAR 481
Db 390 CLVVIATQFSETKORESQLMRQVRFLSNASTLASFSEPGSCYBELIKYLVITLKAAR 449
QY 482 RLQVSRAGIVRACILSSPVARSQOPQSPGCTSHRRLSVHVLVHHHHHHHHHHLGN 541
Db 450 RLQVSRAGIVRACILSSPVARSQOPQSPGCTSHRRLSVHVLVHHHHHHHHHHLGN 509
QY 542 GTLRVPASPEIQDRDANGRRRLMLPPPTPTSGGPPRGAESVHSFYHADCHLEPVCQ 601
Db 510 GTLRVPASPEIQDRDANGRRRLMLPPPTPTSGGPPRGAESVHSFYHADCHLEPVCQ 569
QY 602 APPRCRSEASGRVSGKVPVTHSPPEILKDKALVEVAPSPGPPPTLTFTNIPPGPF 661
Db 570 APPRCRSEASGRVSGKVPVTHSPPEILKDKALVEVAPSPGPPPTLTFTNIPPGPF 629
QY 662 SSMHKLLETQGTGACHSSCKISSPCSKADSGACGPDSCPYCARTGAGEPESADHVPDSD 721
Db 630 SSMHKLLETQGTGACHSSCKISSPCSKADSGACGPDSCPYCARTGAGEPESADHVPDSD 689
QY 722 SEAVYFTQDAQSHDLRDPHRRORSIGDAPSSVLAFWRLICDTFRKIVDSKYFGRG 781
Db 690 SEAVYFTQDAQSHDLRDPHRRORSIGDAPSSVLAFWRLICDTFRKIVDSKYFGRG 748
QY 782 IMAILVNTLSNGIEYHOPELTNALEISNIVFTSLFALEMLKLLVYGFYIKNPYN 841
Db 749 IMAILVNTLSNGIEYHOPELTNALEISNIVFTSLFALEMLKLLVYGFYIKNPYN 808
QY 842 IFDGVIVISVWEIVQGGGLSVLRTFLMRVLKVRFLPALORQLVLMKTMNDVATF 901
Db 809 IFDGVIVISVWEIVQGGGLSVLRTFLMRVLKVRFLPALORQLVLMKTMNDVATF 868
QY 902 CMLLMFIFIFSLGWHLFGCKFASERDGTLPDRKNFDSLMLAIVTVFQILTOEDWNKV 961
Db 869 CMLLMFIFIFSLGWHLFGCKFASERDGTLPDRKNFDSLMLAIVTVFQILTOEDWNKV 928
QY 962 LYNMGASTSAAALFYALMTGNVFLNLLVAILVEGFOAE----- 1003
Db 929 LYNMGASTSAAALFYALMTGNVFLNLLVAILVEGFOAEISKREDASQOLSCITQP 988
QY 1004 -----GDATKSESEPPFSPVDGDRKKRLALVALGEHAEFLRKSLLPPLIHTAATPM 1058
Db 989 VDSQGGDANKSESEPPFSPVDGDRKKRLALVALGEHAEFLRKSLLPPLIHTAATPM 1048
QY 1059 SHPKSSSTGVEALGSGSRRTSSGSAEPGAAHEMKCPSPASPHSPWSAASWTSSR 1118
Db 1049 SLPKSTSTGLGALGPASRRRTSSGSAEPGAAHEMKCPSPASPHSPWSAASWTSSR 1107
QY 1119 SSRNLSGRAPSLKRRSPSGRRRLSGEGQESQDESESEEDRASPAGSDHRRHSGSLRE 1178
Db 1108 SSRNLSGRAPSLKRRSPSGRRRLSGEGQESQDESESEEDRASPAGSDHRRHSGSLRE 1167
QY 1179 AKSSFDLPDITLQVFLHRTASGRSSASEHODCNKGSAGSLARTLTDDPQDGDNDDE 1238
Db 1168 AKSSFDLPDITLQVFLHRTASGRSSASEHODCNKGSAGSLARTLTDDPQDGDNDDE 1227
QY 1239 GNLKGERIQAWTSRLPACCRDSSVSAVFPPQSRFLLRCHRIITHKMFHVLVITF 1298
Db 1228 GNLKGERIQAWTSRLPACCRDSSVSAVFPPQSRFLLRCHRIITHKMFHVLVITF 1287
QY 1299 LNCITIAMERKIDPHSAERIFLTSNYSIFTAFLAEMTVKVALGCFGEQAYLSSWN 1358
Db 1288 LNCITIAMERKIDPHSAERIFLTSNYSIFTAFLAEMTVKVALGCFGEQAYLSSWN 1347
QY 1359 VLDGLLVLSVIDILVMSVDSGTLGLMLRVLLRLTLRLRVLISRAQGLKLVVETLMS 1418
Db 1348 VLDGLLVLSVIDILVMSVDSGTLGLMLRVLLRLTLRLRVLISRAQGLKLVVETLMS 1407
QY 1419 SLKPIGNIVVICAFIFILGVLFGKFFVCGEDTRNITKNSDCAEASYEVRHKY 1478
Db 1408 SLKPIGNIVVICAFIFILGVLFGKFFVCGEDTRNITKNSDCAEASYEVRHKY 1467

QY 1479 NFDNLGOALMSLFLVASKDGVWDIMYDGLDAVGVDQOQIMHNPNMMLLYFTSFLLIIVAFF 1538
Db 1468 NFDNLGOALMSLFLVASKDGVWDIMYDGLDAVGVDQOQIMHNPNMMLLYFTSFLLIIVAFF 1527
QY 1539 VLNMFGVVVVENFHCRQHQEERREARRREKRLRLEKRRSKEKQMAEACKPYSDYS 1598
Db 1528 VLNMFGVVVVENFHCRQHQEERREARRREKRLRLEKRRSKEKQMAEACKPYSDYS 1587
QY 1599 RFLILVHHLCTSHYLDLFTITGVLGNVVTMAHEHYQQQILDEALKICNYIFTVIFVSES 1658
Db 1588 RFLILVHHLCTSHYLDLFTITGVLGNVVTMAHEHYQQQILDEALKICNYIFTVIFVSES 1647
QY 1659 VFKLVAFAFRFQDRWNQDLALVLLSTMGITLBEIEVNLSLPINPTIIRIMRVLIAR 1718
Db 1648 VFKLVAFAFRFQDRWNQDLALVLLSTMGITLBEIEVNLSLPINPTIIRIMRVLIAR 1707
QY 1719 VLKLLKAVGMRALLDVTMQLPQVNGLGLLFWLFFIIPALGVELFGDECDHPCEG 1778
Db 1708 VLKLLKAVGMRALLDVTMQLPQVNGLGLLFWLFFIIPALGVELFGDECDHPCEG 1767
QY 1779 LGRHATFRNFGMAFLTLFRVSTGDNWNGIMKDPSPRCDQESTCYNTVISPFIYVSVFLTA 1838
Db 1768 LGRHATFRNFGMAFLTLFRVSTGDNWNGIMKDPSPRCDQESTCYNTVISPFIYVSVFLTA 1827
QY 1839 QFVLNVVVIAMKHLSESKAEAELEEMKTLSPHSPGLSGPFLWPGVEG 1898
Db 1828 QFVLNVVVIAMKHLSESKAEAELEEMKTLSPHSPGLSGPFLWPGVEG 1887
QY 1899 NSTSPKPGAPHTTAHIGAASGFSLEHTVMPHPEVVPGLDPLLTVRKSGVSRTHSLP 1958
Db 1888 DSPSPKPKCALHPAARHARSASHFSLEHTVMPHPEVVPGLDPLLTVRKSGVSRTHSLP 1944
QY 1959 NDSYCRNGSTAEASRLGHRGGLPKAOSGSLSVHSPADTSCILQPKDVHYLLQPHGA 2018
Db 1945 NDSYCRNGSTAEASRLGHRGGLPKAOSGSLSVHSPADTSCILQPKDVHYLLQPHGA 2004
QY 2019 PTWGAIPKLPGRPSPLAQRPLRQAARTDLSVDQGLGREDLLSEVSGPCLTRSS 2078
Db 2005 PTWGAIPKLPGRPSPLAQRPLRQAARTDLSVDQGLGREDLLSEVSGPCLTRSS 2064
QY 2079 FWGSSISQVQSGISQKVKHRLPACRGLSPSWAKDPPETRSSLELDTLSWISGDL 2138
Db 2065 FWGSSISQVQSGISQKVKHRLPACRGLSPSWAKDPPETRSSLELDTLSWISGDL 2124
QY 2139 L-PSSOEELPFRDLKCKYVETQSCRRRPGFWLDEORRHSTIAVSLDQSGQPLCPS 2197
Db 2125 L-PSSOEELPFRDLKCKYVETQSCRRRPGFWLDEORRHSTIAVSLDQSGQPLCPS 2184
QY 2198 SLGGQPLGGPGRPKKLSPPSISIDPPESQSRPPCSPGVCLRRRAPASDKDPSVSSP 2257
Db 2185 NLGGQPLGGPGRPKKLSPPSISIDPPESQSRPPCSPGVCLRRRAPASDKDPSVSSP 2244
QY 2258 LDSTAASPSPKDITLSLGLSSDPTMDP 2286
Db 2245 PDSTAASPSPKDITLSLGLSSDPTMDP 2273

RESULT 2
US-09-949-016-9730
; Sequence 9730, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498

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; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9730
; LENGTH: 2220
; TYPE: PR1
; ORGANISM: Human
US-09-949-016-9730

Query Match      87.4%; Score 10512; DB 4; Length 2220;
Best Local Similarity 89.6%; Pred. No. 0;
Matches 2041; Conservative 32; Mismatches 112; Indels 94; Gaps 9;

Qy      11 RTPDLRGSARPSPPGRLARGWTRRRMERA---PRSRDPSVASRSSTTCGPGCAAGS 68
Db      33 RRLPLSGS--PGA-PAGORWDEEDGAGBESGQPRS-----FMRLNDLSGAGRPGGS 84

Qy      69 TEKDPGSADSEAEGLYPALAPVVFYLSQDSRPSRCLRTVCNP-WFERVSMVLILLNC 127
Db      85 AEKDPGSADSEAEGLYPALAPVVFYLSQDSRPSRCLRTVCNPWFERISMLVILLNC 144

Qy      128 VTLMFPCSDIACDSQRCRILOAFDDPIFAFFAVEMVVMVAVGIFGKKCYLGDWTNRL 187
Db      145 VTLMFPCSDIACDSQRCRILOAFDDPIFAFFAVEMVVMVAVGIFGKKCYLGDWTNRL 204

Qy      188 DFFVIAGMLEYSLDLQNVFSAVRTVRLRPLRAINRVPMSRLTVTLTLLDTLPMLGVL 247
Db      205 DFFVIAGMLEYSLDLQNVFSAVRTVRLRPLRAINRVPMSRLTVTLTLLDTLPMLGVL 264

Qy      248 LLCFFVFPIGIVGVQLWAGLLNRCLPENFSLPLSDLEPYVYQTENEDESPPICQPR 307
Db      265 LLCFFVFPIGIVGVQLWAGLLNRCLPENFSLPLSDLEPYVYQTENEDESPPICQPR 324

Qy      308 ENGRSCRSVPTLRGEGGPPCSDLYETYNSSNTTTCVNMNYYTNCAGEHNPFKGA1 367
Db      325 ENGRSCRSVPTLRGEGGPPCSDLYETYNSSNTTTCVNMNYYTNCAGEHNPFKGA1 384

Qy      368 NFNIGYAWTAI FQVITLEGWVDIMYFMDAHSYFNFIYILLIIVGSPFMINCLVIA 427
Db      385 NFNIGYAWTAI FQVITLEGWVDIMYFMDAHSYFNFIYILLIIVGSPFMINCLVIA 444

Qy      428 TQFSETKQRESQLMREQVRFLSNASTLASFPSCGYEELLKYLVLVILKAARLQAQS 487
Db      445 TQFSETKQRESQLMREQVRFLSNASTLASFPSCGYEELLKYLVLVILKAARLQAQS 504

Qy      488 RAIGVRAGLSSPVARSQBPQSGSCTRSHRRLSVHLLVHHHHHHHHYHLNGTLRVP 547
Db      505 RAAGVRVGLLSSPAPLGGQETQPSSSCSRSHRRLSVHLLVHHHHHHHHYHLNGTLRAP 564

Qy      548 RASPEIQDRDANGSRRLMLPPBSTPTSPGPPRGAESVHSFYHADCHLEPVRCQAPPPRC 607
Db      565 RASPEIQDRDANGSRRLMLPPBSTPTSPALSGAPPGGAESVHSFYHADCHLEPVRCQAPPPRS 624

Qy      608 PSASGRITVSGKYVPTVHTSPPEILKDALVEVAPSGPPTLTSFNI PPGFPSSMHKL 667
Db      625 PSASGRITVSGKYVPTVHTSPPETLKEKALVEVAASSGPPTLTSFNI PPGFPSSMHKL 684

Qy      668 LETQSTGACHSSKISSPCSKADSGACGPDSCPYCARTGAGEPESADHVPDSDSEAVYE 727
Db      685 LETQSTGACQSSCKISSPCSKADSGACGPDSCPYCARAGAGEVELADREMPDSDSEAVYE 744

Qy      728 FTODAQHSDLRDPHSRRRQRSLGPDABPSSVLAFWRLICDTFRKIVDSKYFGRGIMTIAL 787
Db      745 FTODAQHSDLRDPHS--RRQSLGPDABPSSVLAFWRLICDTFRKIVDSKYFGRGIMTIAL 803

Qy      788 VNTLSMGIETHQPEELTNALETNSIVFTSLFALEMLKLLVVGPFYIKNPYNI PDGVI 847
Db      804 VNTLSMGIETHQPEELTNALETNSIVFTSLFALEMLKLLVVGPFYIKNPYNI PDGVI 863

Qy      848 VVISWBEIVGQCGGLSVLRTFRIMRVLKLVRLPALQRLVLMKTMNDNVATFCMLLML 907
Db      864 VVISWBEIVGQCGGLSVLRTFRIMRVLKLVRLPALQRLVLMKTMNDNVATFCMLLML 923
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908 FIFISILGMHLGCKEASERDGDITLDRKNFDSLLWAIIVTVFOILTQEDNKNVLYNCMA 967
924 FIFISILGMHLGCKEASERDGDITLDRKNFDSLLWAIIVTVFOILTQEDNKNVLYNCMA 983
968 STSSWAALYFIALMTFCNYVLFNLLVAILVEGFOAEGDQATKSESEPOFFSFSVSDGDGRK 1027
984 STSSWAALYFIALMTFCNYVLFNLLVAILVEGFOAEGDQANKSESEPOFFSFSVSDGDGRK 1043
1028 KRLALVALGEBHABLRKSLPLIHTAATPMWHPKSSSTGVGEALGSGSRRTSSGSAEP 1087
1044 KCLALVSLGHPHLPRLSLPLIHTAATPMWLPKSTSTGIGALGPASRRRTSSGSAEP 1103
1088 GAHHENKCPSPASRSPSPASWTSRSPSSNSISGRAPSLKRRSPSGERRSILSGEG 1147
1104 GAA-HEMKSPSPASRSPSPASWTSRSPSSNSISGRAPSLKRRSPSGERRSILSGEG 1162
1148 QESQDEESEEEDRASPAAGSDHRRHSGSLEREAKSSFDLPDTLQVPGHLRTASGRSSASEH 1207
1163 QESQDEESEEEDRASPAAGSDHRRHSGSLEREAKSSFDLPDTLQVPGHLRTASGRSSASEH 1222
1208 QDCNGKASASRLARTLTDDPQLDGGDDNDEGNLSKGERIOAWVRSLRPLACCRERDSWSA 1267
1223 QDCNGKASASRLARALRPDDPPLDGGDDADDEGNLSKGERVRAWRARLPACCLERDSWSA 1282
1268 YIPPOSRRPRLCHRITTHKMFHVLVVIIFLNCITITAMERPKIDPHSABRIPLTLSNYI 1327
1283 YIPPOSRRPRLCHRITTHKMFHVLVVIIFLNCITITAMERPKIDPHSABRIPLTLSNYI 1342
1328 FTAVFLAEMTVKVVVALGWCFCGEQAYLRSSNVNLDGLLVLSVIDILVSMVSDSGTKILGM 1387
1343 FTAVFLAEMTVKVVVALGWCFCGEQAYLRSSNVNLDGLLVLSVIDILVSMVSDSGTKILGM 1402
1388 LRVLRLLRTRLRVLSRAQGLKLWVETLMSLKPIGNIVVICAPFIIFGILGVQLFKG 1447
1403 LRVLRLLRTRLRVLSRAQGLKLWVETLMSLKPIGNIVVICAPFIIFGILGVQLFKG 1462
1448 KFFVCOGEDPNTLNKSDCAEASVVRVHKNYFNENLGOALMSLFLVASKDGMWIMYDGL 1507
1463 KFFVCOGEDPNTLNKSDCAEASVVRVHKNYFNENLGOALMSLFLVASKDGMWIMYDGL 1522
1508 DAGVDOQPIMNHPWMLLYFISFLITVAFVLNMFVGVVFNPHKCRQOESEEARRE 1567
1523 DAGVDOQPIMNHPWMLLYFISFLITVAFVLNMFVGVVFNPHKCRQOESEEARRE 1582
1568 EKLRLRLEKRRKEKQMAEAOCKPYYSVSRFLLVHHLCTSHYLDLFTITGVLNVVT 1627
1583 EKLRLRLEKRRKEKQMAEAOCKPYYSVSRFLLVHHLCTSHYLDLFTITGVLNVVT 1642
1628 MAMEHYQOQPOLDEALKICNYIETVIFVFSVFKLVAFAPRRFQDRWNOLDLAILLSI 1687
1643 MAMEHYQOQPOLDEALKICNYIETVIFVLESVFKLVAFAPRRFQDRWNOLDLAILLSI 1702
1688 MGTITLSEIEVNLSLPNTPIIRIMRVLRIRARVLKLVGMVGMALLHTVMQALPQVGNLG 1747
1703 MGTITLSEIEVNLSLPNTPIIRIMRVLRIRARVLKLVGMVGMALLHTVMQALPQVGNLG 1762
1748 LFLMULLFFIPAAALGVLEFGLDECDETHPCBGLGRHATFRNFGMAFLTLFRVSTGDNWNGI 1807
1763 LFLMULLFFIPAAALGVLEFGLDECDETHPCBGLGRHATFRNFGMAFLTLFRVSTGDNWNGI 1822
1808 MKDPSRDCDOESTCYNTVISPVIYFVSFVLTAQFVLNVNVIATVLMKHLSEENKEAKEAEL 1867
1823 MKDTRDCDOESTCYNTVISPVIYFVSFVLTAQFVLNVNVIATVLMKHLSEENKEAKEAEL 1882
1868 EASLELEMTKLSQPSPHSLGSPFLWPGVEGVNSTDSPKGPAPHTTAHIGAASGFSLSHPT 1927
1883 EASLELEMTKLSQPSPHSLGSPFLWPGVEGVNSTDSPKGPAPHTTAHIGAASGFSLSHPT 1942
1928 MYPHPEEVPVPLGPDLLTVKSGVSRTHSLPNDPSYMCNRNGSTABRSIGHRGWGLPKAQSG 1987
1943 MQPHPTLP-- --GPDLLTVKSGVSRTHSLPNDPSYMCNRHGSTABRGWGLPKAQSG 1999
1988 SILSVHSQPADTSCIIQLPKDVHYLQPHGAPTGAIPKLP PPPGSRSPLAORPLRQAIR 2047
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Db	2000	SVLVSHQADTSTYILQPKADPHLLQPHSAPTWTGTIPKLPGRSPPLAQRLRQAAR	2059	Db	19	PPGPAALVG-----ASPSPGAPGREABRGSELGVSPSPSPAARGAELGA--DEEQ	69
Qy	2048	TDSLDVQGLGRREDLLSEVSGPCPLTRSSFWGSSIQVQORSGIQSKVSKHIRLPAPC	2107	Qy	83	LPYPALAPVFFVYLQSDSRPRSCLRVTCNPWFERYSMVLVILLNCVTLGMRPCEDIACD	142
Db	2060	TDSLDVQGLGRREDLLAE-----	2077	Db	70	VPYPALAAATVFFCLGQTRPRSCCLRLVCNPFWEHVSMLVILNCVTLGMRPCDEVECG	129
Qy	2108	PGLPSPWAKOPPSTRSSLELDTLSWISGDLPLSSQEEPLFPRLDKKCYSVETQSCRRP	2167	Qy	143	SQRCRILQAFDDFIAPFAVEMVVKVALGIFGKKCVLGDWTNRLLDFFIIVAGMVEYSLD	202
Db	2078	-----EPPSPRDLKKCYVSAQSCORP	2101	Db	130	SERCNILEAFDAFIFAFVEMVVKVALGIFGKKCVLGDWTNRLLDFFIIVAGMVEYSLD	189
Qy	2168	GFWDDEORRHIAVCLDSSQRLCPSPSLGQPLGGPSRKKLSPPSISIDPPES	2227	Qy	203	LQNTSFSAVRVRLPRLAINRVPSMRILVTLTLLDTPMLGNVLLLCFFVFFIFGIVGV	262
Db	2102	TSWLDEORRHIAVCLDSSQPLHGLTDPNGLGQPLGGPSRKKLSPPSITIDPPES	2161	Db	190	GHVNSLSAIRVRLPRLAINRVPSMRILVTLTLLDTPMLGNVLLLCFFVFFIFGIVGV	249
Qy	2228	QGSPPSPGVCRLRRAPASDKPSVSSPLDSTAASPSPKDTLSLGLSSDPTMDP	2286	Qy	263	OLWAGLNRCLPFLNFSLPLSDV-LFPYYOTENEDSPFICSPQPRNGRSCRSVTLR	321
Db	2162	QGPRTSPSGICLRRAPSSDKPLASGPPDSMAASPSFKDVLVLSGLSSDPAIDLDP	2220	Db	250	QLWAGLNRCLDLSAFVRRNNLTLFPPYYQTERGEENPFICSSRRDNGMQKCSHIP---	306
RESULT 3				Qy	322	BEGGGGPPCSLDYETYN-----SSNTTCVKNNOYTNCSAGEHNPFGKAINFDNIGY	374
US-08-984-709A-50				Db	307	GRRELMPCTLGEAYTQPAEGVGAARNACINNNQYVNCRSRGSNPHNGAINFDNIGY	366
; Sequence 50, Application US/08984709A				Qy	375	AWIAIPOVITILEGWDIMVYMDAHSFYNFIYFILLIIVGFFMINLCLVVIATQFSETK	434
; Patent No. 6320032				Db	367	AWIAIPOVITILEGWDIMVYMDAHSFYNFIYFILLIIVGFFMINLCLVVIATQFSETK	426
; GENERAL INFORMATION:				Qy	435	QRESQLMREQRVRLSNASTLASFSEPGSCYBELLKYLIVYLKAAARLAQVSRAGVRA	494
; APPLICANT: Williams, Mark E.				Db	427	QRESQLMREQRARHLSDSTLASFSEPGSCYBELLKYLIVYLKAAARLAQVSRAGVRA	486
; APPLICANT: Stauderman, Kenneth A.				Qy	495	GILLSPPVARSQEPQPSGSCSTRSHR-----LSVHHLV-HHHHHHHHHHHLGNGTLRV	546
; APPLICANT: Harpold, Michael M.				Db	487	RKKVDPVSAVOGGP-----GHRQRRAGRHTASVHHLVHHLVHHHHHHHHHSHGSPRR	538
; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND				Qy	547	PRASPEIQDRDANGSRRLML--PPSTPTPGSGPRGAEVSHSFTHACHLE--PVRQQA	602
; TITLE OF INVENTION: METHODS				Db	539	PGPEPGACD-----TRLVRAGAPPSPSPGRGPP-DAESVHSIYHADCHIEGPOERARV	591
; NUMBER OF SEQUENCES: 52				Qy	603	PPPCPSEASGR-TVGSGKV-YPTV-----HTSPPEILKDKALVEVAPSP-----	646
; CORRESPONDENCE ADDRESS:				Db	592	AHAATAAASLRLATGLTGMNYPTILPSGVGSGKSTSPGPK-----GKWAGGPPGTG	644
; ADDRESSEE: Heller Erman White & McAuliffe				Qy	647	--GPPLTTFNTPPGPSSMHKLELTQSTGAC--HSS-----CKTSSPCKSADSGACGPD	697
; STREET: 4250 Executive Square, Suite 700				Db	645	GHGPLSINS-----PDYEXI PHVVGHEGLGAPGHLGSLSVCPPLSP--PAGTILTCELK	698
; CITY: La Jolla				Qy	698	SCPYCART-GAGEPESADHVPDSEAVYETQDAQHSDLRDP-----	740
; STATE: California				Db	699	SCPYCTRALEDPRGELSGSESGSDGRGYEFTQVVRHGRDWDPTPPRATDTPGPGPS	758
; COUNTRY: US				Qy	741	HSRRORSGLPDAEPSSVLAFWRLLCOTFRKIVDSKYFGRGIMAILVNTLSMGIFYHQ	800
; ZIP: 92037				Db	759	PORRAQOORAP-GEPCWGMGLWTFTSGKLRLIVDSKYFSRGIMAILVNTLSMGIFYHQ	817
; COMPUTER READABLE FORM:				Qy	801	PEELTNALEISNIVFTSLFALEMLLKVYVPGPGYIKNPYINFDGVIVISVWEIYVQOG	860
; MEDIUM TYPE: Diskette				Db	818	PEELTNALEISNIVFTSMFALEMLLKVYVPGPGYIKNPYINFDGVIVISVWEIYVQOG	877
; COMPUTER: IBM Compatible				Qy	861	GGLSVLRTFLMRVILKLVRLPALQRLVLMKTMNVATFCMLLMFLFIFISILGHLF	920
; OPERATING SYSTEM: DOS				Db	878	GGLSVLRTFLMRVILKLVRLPALQRLVLMKTMNVATFCMLLMFLFIFISILGHLF	937
; SOFTWARE: FastSeq Version 1.5				Qy	921	GCKFASERD-GDTLPDRKNFDSLMAIIVTVFQILTQEDMNKVLNGMASTSSWAALFYA	979
; CURRENT APPLICATION DATA:				Db	938	GCKFSLKTDGTVDPDRKNFDSLMAIIVTVFQILTQEDMNKVLNGMASTSSWAALFYA	997
; FILING DATE: 02-DEC-1997				Qy	980	LMTFGNVYVFLNLLVAIIVVEGQAEQATKSESEBDFPSPVSDGDKKGLALVAL----	1035
; CLASSIFICATION: 435				Db	998	LMTFGNVYVFLNLLVAIIVVEGQAEQATKSESEBDFPSPVSDGDKKGLALVAL----	1057
; ATTORNEY/AGENT INFORMATION:				Qy	1036	-----GEHAELRKSILLPLIHTAATPMWHPKSSS-TGVGEALGSGRRRTSSSSASAPGA	1089
; NAME: Seidman, Stephanie L.				Db	1058	LAIVTPNGHLEGRGSLSPPLIMCTAATPMTPKSSPFLDAAAPSLPDRSGSSSGDPLUG-	1116
; REGISTRATION NUMBER: 33,779							
; REFERENCE/DOCKET NUMBER: 24735-9815 (formerly 6362-9815)							
; TELECOMMUNICATION INFORMATION:							
; TELEPHONE: (619) 450-8400							
; TELEFAX: (619) 587-5360							
; INFORMATION FOR SEQ ID NO: 50:							
; SEQUENCE CHARACTERISTICS:							
; LENGTH: 2353 amino acids							
; TYPE: amino acid							
; STRANDEDNESS: single							
; TOPOLOGY: linear							
; MOLECULE TYPE: protein							
; HYPOTHETICAL: NO							
; ANTI-SENSE: NO							
; FRAGMENT TYPE: internal							
; ORIGINAL SOURCE:							
US-08-984-709A-50							
Query Match							
Best Local Similarity							
Matches 1368; Conservative 209; Mismatches 530; Indels 310; Gaps 62;							
Qy	25	PPGRLARGWTRRRMERAPSRDSP--VASRSSTTCFPGCAAGAGSTKDPGSADEAEG	82				

QY	542	GTLRVRPRASPEIQDRDANGSRRLMLPPPTPTSGGPPRGAEVSHFYHADCHLEVRQ	601	QY	51	ASRSTTCGPGAGAGSTEKDPG--SADSEAEGL-----EYPALAPVVFYLS	97
Db	510	GTLRAPRASPEIQDRDANGSRRLMLPPPTPALSGAPPGAEVSHFYHADCHLEVRQ	569	Db	5	ASPPSSAAAP-AAAPGVTTEQPRFPSPPGLEPLDGDAPHVPHDPLAPIAFFCLR	63
QY	602	APPRCPSEASGRVVGSKVYPTVHTSPPPPEILKDKALVEVAPSPGPPPTLTSENIPGPF	661	QY	98	QDSRPSRCLRTVCNPFVRSVLMVILLNCVTLMFPCEDICADSORCRILQAFDDFIF	157
Db	570	APPRPSSEASGRVVGSKVYPTVHTSPPPPEILKDKALVEVAPSPGPPPTLTSENIPGPF	629	Db	64	QTTSPRNWCIRKWCNPFECVSMVILLNCVTLMGYPQCDMDCLSDRCKTLQVDFDIF	123
QY	662	SSMHKLLTQSTGACHSSCKISSPCSKADSGACQPDSCPYCARTGAGEPESADHVPDSD	721	QY	158	APFAVEMVWVALGIFGKKCYLGDWNRDLDFVIAGMLSEYSLDLQNSPSAVRTVRVL	217
Db	630	SSMHKLLTQSTGACHSSCKISSPCSKADSGACQPDSCPYCARTGAGEPESADHVPDSD	689	Db	124	IFFAMEWLVKVALGIFGKKCYLGDWNRDLDFVIAGMLSEYSLDLQNSPSAVRTVRVL	183
QY	722	SEAVVEFTQDAHQSDLRDPHRRRQSRISLGDPAESPSSVLAFWRLICDTFRKIVDSKVFGRG	781	QY	218	RLRLAINRVPMSRILVTLTLLDTPMLGNVLLLCFFVFFIFGIVGVQVWAGLLRRCFLPE	277
Db	690	SEAVVEFTQDAHQSDLRDPHRS--RRQSLGPDAPESPSSVLAFWRLICDTFRKIVDSKVFGRG	748	Db	184	RLPKAINRVPMSRILVTLTLLDTPMLGNVLLLCFFVFFIFGIVGVQVWAGLLRRCFLPE	243
QY	782	IMAILVNTLSMGIEYHQPELTNALEISNIVFTSLPALEMLKLVGPGFYKPNYN	841	QY	278	NFSLPLSLDLEPYOTENEDSPFCQSPRENGHRSCHSVPTLRGEGGGPPCSI-----	332
Db	749	IMAILVNTLSMGIEYHQPELTNALEISNIVFTSLPALEMLKLVGPGFYKPNYN	808	Db	244	NFTIQDVALPPYQPEEDDEMPFICSLSGDNGMCHEIPLPKQ-----GRECCLSKDDV	300
QY	842	IPDGVIVVISWEIVGQGGGLSVLRTFRLMRVLKLVRLPALQRLVLMKTMNDVATF	901	QY	333	-DYETVNSSNTT--CVNWNQYITNCISAGHNPPKGAINFONIGYAMIAIFQVITLEGW	389
Db	809	IPDGVIVVISWEIVGQGGGLSVLRTFRLMRVLKLVRLPALQRLVLMKTMNDVATF	868	Db	301	YDFGAGRODLNASGLCVNWNRYNVCRTGSANPHKGAINFONIGYAMIAIFQVITLEGW	360
QY	902	CMLLMFIFISILGMHLFGCKFASERDGTLPDRKNPDSLLMAIVTVFQILTQEDWNV	961	QY	390	DIMYFVMDAHSFYNFYIFILLIIVGSPFMINCLVVIATQFSETKQRESQLMREORVFL	449
Db	869	CMLLMFIFISILGMHLFGCKFASERDGTLPDRKNPDSLLMAIVTVFQILTQEDWNV	928	Db	361	EIMYVMDAHSFYNFYIFILLIIVGSPFMINCLVVIATQFSETKQRESQLMREORVFL	420
QY	962	LYNGWASTSSWAALFYALMTFGNVVFNLLVAILVEGFAEGDATKSESPDFPSVD	1021	QY	450	SNASTLASSEPGSCVEELLKYLVLTKAARLAQVSRAGRAIGVRAIGLLSSPVARSQBQ	509
Db	929	LYNGWASTSSWAALFYALMTFGNVVFNLLVAILVEGFAEGDATKSESPDFPSVD	988	Db	421	S-SSTVASAEPDCYEEIFQVCHLLKAKR-----RALGLYQALQS-----	462
QY	1022	GGDRKKRLIALVALGEHAELRKSLLPPLIIHTAATPMHSPKSSSTGVGEALGSGSRTSS	1081	QY	510	PSGSCSTRHRLSVHLLVHHHHHHHHHGLNGTLRVRPRASPEIQDRDANGSRRLMLPP	569
Db	989	GGDRKKRLIALVALGEHAELRKSLLPPLIIHTAATPMHSPKSSSTGVGEALGSGSRTSS	1048	Db	463	-----RRQAL-----GPE-----APAP	474
QY	1082	SGSAEPGAHHEMKPPSARSPHSPWASSTSRSSRSLGRAPSLKRRSPSGERRS	1141	QY	570	STPTSGGPPRGAEVSHFYHADCHLEVRQAPPRCPSEASGRVVGSKVYPTVHTSP	629
Db	1049	SGSAEPGAHHEMKPPSARSPHSPWASSTSRSSRSLGRAPSLKRRSPSGERRS	1107	Db	475	AKGPP-----HAK--EPRHYQLCPOHSPLDA-----TPHT--	502
QY	1142	LLSGEQESQDEEESSEEDRASPAGSDHRRHRSLEAREAKSFDLPDTLQVPLHRTASGR	1201	QY	630	PPEILKDKALVEVAPSPGPPPTLTSENIPPGFSSMHKLLTQSTGAC--HSSCKISSPCSK	688
Db	1108	LLSGEQESQDEEESSEEDRASPAGSDHRRHRSLEAREAKSFDLPDTLQVPLHRTASGR	1167	Db	503	-----LVQ-----PIPATLAS-----DPASCPCQCHEDGRPPSGLS	534
QY	1202	SSASEHQDCNGKSASGLARTLRTDDPOLDDGDDNDEGNL	1241	QY	689	ADSGACGPDSCPYCARTGAGEPESADHVPDSDSEAVVEFTQDAHQSDLRDPHRRRQSR	748
Db	1168	GSASEHQDCNGKSASGLARTLRTDDPOLDDGDDNDEGNL	1207	Db	535	TDGQEGSGS-----GSSAGGEDEA-----DGDGA--RSSEDDGASSELKEEEREEQ--	579
RESULT 5				QY	749	LGPDAPESPSSVLA--FWRLICDTFRKIVDSKYFGRGIMAILVNTLSMGIEYHQPELTN	806
US-09-404-650-2				Db	580	-----ADGAVMLCGDVWRETRAKRGIVDSKYFNRGIMAILVNTLSMGIEHQPELTN	635
; Sequence 2, Application US/09404650				QY	807	ALEISNIVFTSLFALEMLKLVGPGFYKPNYNIPDGVIVVISWEIVGQGGGLSVL	866
; Patent No. 6309858				Db	636	ILEICNVVFTSMFALEMLKLVGPGFYKPNYNIPDGVIVVISWEIVGQGGGLSVL	695
; GENERAL INFORMATION:				QY	867	RTPLMRVLKLVRLPALQRLVLMKTMNDVATFCMLLMFIFISILGMHLFGCKFAS	926
; APPLICANT: Dietrich, Paul S.				Db	696	RTPLMRVLKLVRLPALQRLVLMKTMNDVATFCMLLMFIFISILGMHLFGCKFAS	755
; APPLICANT: McGivern, Joseph G.				QY	927	ERD--GDTLPDRKNPDSLLMAIVTVFQILTQEDWNVLYNGMASTSSWAALFYALMTFGN	985
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;				Db	756	RTDGVIVVISWEIVGQGGGLSVLMAIVTVFQILTQEDWNVLYNGMASTSSWAALFYALMTFGN	815
; FILE REFERENCE: R0043B-REG sequence listing				QY	986	YVLFNLVAILVEGFAEGDATKSESPDFPSV-----DGDGRKKRLALVAL	1035
; CURRENT APPLICATION NUMBER: US/09/404,650				Db	816	YVLFNLVAILVEGFAEGDATKSESPDFPSV-----DGDGRKKRLALVAL	873
; CURRENT FILING DATE: 1999-09-23				QY	1036	GEHAELRKSLLPPLIIHT--AATPMHSPKSSSTGVGEALGSGSRTSSGSAEPGAH	1091
; NUMBER OF SEQ ID NOS: 12				Db	874	TPNGHLDPSL--PLGGHLLGPAAGA--PRLSLQDPMLVALGSRKSSVMSL---GRMS	926
; SOFTWARE: PatentIn Ver. 2.0							
; SEQ ID NO 2							
; LENGTH: 2175							
; TYPE: PRT							
; ORGANISM: Homo sapiens							
US-09-404-650-2							
Query Match							
Best Local Similarity							
Matches 1225; Conservative 236; Mismatches 513; Indels 450; Gaps 64;							

Qy	1092	HEMKCP	PSA	SSPHS	PSA	SSWTSS	RRSS	NSLGR	APSL	KRR	SPSG	RRSS	LLSGE	-----	QOES	1155
Db	927	YDORS	LS	SSRS	SY	YGP	WGR	SA	AS	RR	SS	WN	-----	SLKH	KP	SA
Qy	1151	QDEES	SEE	--	DRAS	PAG	SDH	-----	-----	-----	-----	-----	-----	RRGS	LE	AK
Db	981	RVCEA	VA	DE	GP	RA	PA	LPH	THA	HH	HG	PH	LA	HR	HR	HR
Qy	1194	LHRTA	GRSS	--	ASEH	OC	NG	K	S	AS	GR	LA	RTLD	--	DP	QD
Db	1041	AHPRA	AW	RA	AG	PA	P	GH	ED	C	NG	RMP	SS	--	IA	KD
Qy	1251	VRGR	L	PAC	CR	ER	D	S	W	SA	YI	FP	PO	S	R	FL
Db	1099	IDVY	K	P	D	W	C	E	R	D	S	Y	L	F	S	P
Qy	1311	IDHSA	E	R	I	F	L	T	S	N	Y	I	F	T	A	V
Db	1159	IEAG	S	T	E	R	I	F	L	T	S	N	Y	I	F	T
Qy	1371	DIUV	S	M	D	S	G	T	K	I	L	M	R	L	R	T
Db	1219	DIVU	S	L	A	S	A	G	A	K	I	L	G	V	L	R
Qy	1431	CAPFI	I	G	I	G	V	Q	L	F	K	G	F	V	C	O
Db	1279	CAPFI	I	G	I	G	V	Q	L	F	K	G	F	V	C	O
Qy	1491	FVLAS	K	D	G	W	D	I	M	V	D	G	L	D	A	V
Db	1339	FVLAS	K	D	G	W	N	I	M	Y	N	G	L	D	A	V
Qy	1551	FHKCR	H	O	E	B	E	E	A	R	R	E	K	L	R	L
Db	1399	FHKCR	H	O	E	B	E	A	R	R	E	K	L	R	L	E
Qy	1611	HYLD	F	I	T	G	I	V	I	G	N	V	T	M	A	M
Db	1452	HYLD	F	I	T	I	C	L	N	V	T	M	S	L	E	H
Qy	1671	FQDR	N	Q	L	D	I	A	V	L	L	S	I	M	G	I
Db	1512	FQDR	N	Q	L	D	I	A	V	L	L	S	I	M	G	I
Qy	1731	ALLH	T	V	M	A	O	A	L	P	Q	V	N	L	G	L
Db	1572	ALLH	T	V	M	A	O	A	L	P	Q	V	N	L	G	L
Qy	1791	AFUL	F	R	V	S	T	G	D	N	N	G	I	M	K	D
Db	1632	AFUL	F	R	V	S	T	G	D	N	N	G	I	M	K	D
Qy	1848	AVL	M	K	H	L	E	B	N	K	A	E	A	E	L	E
Db	1692	AVL	M	K	H	L	D	S	N	K	A	E	A	E	L	E
Qy	1895	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
Db	1751	EGGL	C	R	C	R	C	Y	P	A	D	S	L	E	G	E
Qy	1921	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
Db	1808	PSLNS	D	R	S	S	I	L	L	D	D	S	L	E	D	P
Qy	1953	RTHS	L	P	N	-	D	S	M	C	R	N	G	T	A	B
Db	1868	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
Qy	2012	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
Db	1919	PAVS	A	S	O	K	G	E	K	G	T	G	T	L	P	K
Qy	2061	DLISE	V	G	P	S	C	P	L	T	R	S	S	F	W	G

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Db 1973 -----PSSSAGS|QTTLEDSL|TSDSPRALGPPAPAG----- 2006
Qy 2121 TRGSLELDTEL|SWTSGDLLPSSQ|EELFPRDLKKCY|SVETQSCRRRPGFWLDEQRHSTA 2180
Db 2007 -----PRAGLS|PAARRL-----SLRGRLSRLGLRAHQRS 2038
Qy 2181 VSLDGSQRLCPSPSL-----GGQPLGGPGSRPKKLSPPSIS---IDPPESQ 2229
Db 2039 HS--SGGSTSPGCTHDSMDPSDEGRGGAGGGAGSEHSETLSSLTSLFCPPP--- 2092
Qy 2230 SRPCSPGVCLRR-----RAP-----ASDSDKPSVSSPLDSTA 2262
Db 2093 --PPAPGLTPARKFSTSSLAAPGRPHAAALAHGLARSPSWAADRSKOPPGRAPLPMGL 2150
Qy 2263 ASPSPKKDTLSLGLSSDPTDMDP 2286
Db 2151 GPLAPPPQPL-----PGELEP 2166

RESULT 6
US-09-935-541-2
; Sequence 2, Application US/09935541
; Patent No. 6589787
; GENERAL INFORMATION:
; APPLICANT: McGivern, Paul S.
; APPLICANT: McGivern, Joseph G.
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
; TITLE OF INVENTION: AND USES
; FILE REFERENCE: R0043B-REG sequence listing
; CURRENT APPLICATION NUMBER: US/09/935,541
; CURRENT FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: 09/404,650
; PRIOR FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 2175
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-935-541-2

Query Match 45.0%; Score 5409; DB 4; Length 2175;
Best Local Similarity 50.5%; Pred. No. 0;
Matches 1225; Conservative 236; Mismatches 513; Indels 450; Gaps 64;

Qy 51 ASRSSTCTCPGGAAGAGSTEKDGP--SADSEAGL-----PYPALAPVVFYLS 97
Db 5 ASPSSAAAP-AAEPGVTTTEQGPSPSPSPGLEEPDGDADPHVPHDLAPIAFCLR 63

Qy 98 QDSRPSWCLRTVCNPFWRVSMVLTLNCVTLMGMRPCEDIACDSQRILQAFDDFI 157
Db 64 QTTSPRNCWKCNPFWEFCVSMVLTLNCVTLMGTYQPCDDMDCLSDRCKLQVDDFI 123

Qy 158 APPAVENVKQVALGIFGKKCYLGD|TWNRLDFFIV|IAGLMLEYSLD|QNVSFSAVTRVRL 217
Db 124 IFTAMENVLKWVALGIFGKKCYLGD|TWNRLDFFIV|IAGLMLEYSLD|QNVLSAIRTVRL 183

Qy 218 RPLAINRVPSMRILVTLLD|TLPMLGNVLLLCFFVFFIFG|VGVLWAGLNRNRCFLPE 277
Db 184 RPLKAINRVPSMRILVNLLD|TLPMLGNVLLLCFFVFFIFG|IIGVQLWAGLNRNRCFLPE 243

Qy 278 NFSLLPLVDLEPYVQYOTENDESD|EPFICSQPRENGMRS|CRSVPTLRGEGGGPPCSL----- 332
Db 244 NFIQGDVALPPYQYPEEDDEMPF|ICSLGNDNGIMGCH|EIPPUKEQ---GRECLSKDDV 300

Qy 333 -DYETYNSSNTT--CVNNQYITNCSAGHNPFKGA|INFDNIGYAWIA|FQVITILEGW 389
Db 301 YDYGAGQDNLNAGSLCWNRYNVCRTGSANPHKGA|INFDNIGYAWI|FQVITILEGW 360

Qy 390 DIMYFVMDAHSFYNYFILLIITVGSFFMINCL|VVIATQFSETKQRESQLMREQRVFL 449
Db 361 EIMYVMDAHSFYNYFILLIITVGSFFMINCL|VVIATQFSETKQRESQLMREQRVFL 420

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Db 1752 GGLCRRCYPAQENLWLDVSLIKDSLEGELTIIDNLGSIHF---HYSSPAGCKKCHH 1808
Qy 1921 -----FSLHPTMPV-----HPEEVPV-PLG 1940
Db 1809 DKEVQLAETAEFSLNDRSSILLGDDLSLEDTACPPGRKSKGELDPPEPMRUGDLG 1868
Qy 1941 PDLLTVRKSGVSRTHSLFN-DSYMRNGSTAERSLGRHGWGLPKAQSGSILSVHSQPADT 1999
Db 1869 ECFPLSLSTAVS-----PDPENFLCEMEEIPFNPV--RSW--LKHDSSQAPPSPFSDAS 1919
Qy 2000 SCILQLPKDVHY-----LLOPHGAPTWGAIPKLPPPG-----RSPLAQRLRQAAIRT 2048
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Qy 2049 DSLDVQGLSREDLLSEVSGPSCPLTRSSFWGSSIQVQORSGIQSKVSHIRLPAPCP 2108
Db 1980 TSLDAS-----PSSAGSLQTTLEDLSLTSLSRPAALGPPAPAP 2018
Qy 2109 GLEPSPWAKPPETRSSLELDELTELWSIGDILLPSSQEBPLFPFRLDKKCYSETQSCRRPG 2168
Db 2019 G-----PRAGLSPAARRL-----SLRGGL 2039
Qy 2169 FWLDEQRHRIANVCLDSGQPRCLCPSPSL-----GGQPLGGPGRPKKLSPPSI 2220
Db 2040 FSLRLRAHORSHS--SGGSTSPGCTHDSMDPSDEEGRGAGGGAGSEHSETLSLSL 2097
Qy 2221 S---IDPPESQGRPPCPSPGVCLRR-----RAP---ASDSK 2250
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Db 2152 DPPGRAPLWGLGLAPPQPL-----PGELEP 2179
RESULT 8
US-09-935-541-4
; Sequence 4, Application US/09935541
; Patent No. 6589787
; GENERAL INFORMATION:
; APPLICANT: Dietrich, Paul S.
; APPLICANT: McGivern, Joseph G.
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
; TITLE OF INVENTION: AND USES
; FILE REFERENCE: R0043B-REG sequence listing
; CURRENT APPLICATION NUMBER: US/09/935,541
; CURRENT FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: 09/404,650
; PRIOR FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 2188
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-935-541-4
Query Match 44.9%; Score 5405.5; DB 4; Length 2188;
Best Local Similarity 50.3%; Pred. No. 0;
Matches 1225; Conservative 236; Mismatches 514; Indels 461; Gaps 64;
Qy 51 ASRSTTCPGFGAAGAGSTEDPG--SADSEAEL-----PYPALAPVVFYLS 97
Db 5 ASPSSAAAP-AAEPGVTTQPGRPSPSPPPGLERPLDGDAPHVPHDLAPFAFFCLR 63
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Db 124 IFFAEMVKNVALGIFGKCYLGDWNRLDFFVIAGMLSEYSLDLQNVLSAIRTVRL 183

Qy 218 RPLRAINRVPSMRILVTLTLLDLPMLGNVLLLCFFVFFIFGIVGVQVWAGLLNRCLPE 277
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Qy 278 NPSLPLSVLEPYQYOTENEDESPFICSQPRENMRSCRSVPTLRGEGGGPPCSL----- 332
Db 244 NFTIQGDVALPPYQYDEDEMPFICSLSGDNGIMGCHIEIPPUKEQ---GRECLSKDDV 300
Qy 333 -DYETVNSSTNT--CVNNQYITNGSAGEHNPKGAINPDNIGYAWIAIFQVITLEGWV 389
Db 301 YDFGAGRODLNASGLCVNNWRYNVCRTGSANPHKGAINPDNIGYAWIAIFQVITLEGWV 360
Qy 390 DIMYFVMDAHSFNYFYILLIIVGFFMINCLVVIATQFSETKKORESMREORVFL 449
Db 361 EIMYVMDAHSFNYFYILLIIVGFFMINCLVVIATQFSETKKOREHRLMEQORYL 420
Qy 450 SNASTLASPEPSCYEEELKYLVIYLRKAARLAQVSRAGIVRAGLLSPVARSQEPQ 509
Db 421 S-SSTVASAEPGDCYEEIFQVYCHILRAKR-----RALGLYQALQS----- 462
Qy 510 PSGSCTSRHRLSVHLLVHHHHHHHHYHLNGCTLRVPRASPEIQDRDANGSRRLMPPP 569
Db 463 -----RQAL-----GPE-----APAP 474
Qy 570 STPTPSGPPRGAESVHSFVHADCHLEPVRCQAPPRCPSEASGRTVGSKVPTVHTSP 629
Db 475 AKDGP-----HAK-----EPRHYQLCPQHSPLDA-----TPHT-- 502
Qy 630 PPLIKDKALVEVAPSGPPTLTSPNI PCGPFSSMHKLLTQSTGAC--HSSCKISSPCSK 688
Db 503 -----LVQ-----PIPATLAS-----DPASCPCCOHEDDRRPSGLGS 534
Qy 689 ADSGACPDSCPCYARTGAGEPESADHVMPDSDSEAVYEFTQDAQHSDLRDPHSRRQRS 748
Db 535 TDSGQSGSGS-----GSSAGGEDEA-----DGDGA---RSEDDGASSELKEEERQ-- 579
Qy 749 LGPDABPSSVLA--FWRLICDTFRKIVDSYFQFGIMAILVNTLSMGVHYHPOBELTN 806
Db 580 ----ADGAVMLCGDVWRETRAKLRGIVDSKYFRGIMAILVNTVSMGIEHHEQPELTN 635
Qy 807 ALBISNIVTSLFALEMLKLLVYGPFGYIKNPYNIFDGVIVVSVWEIVGQGGGLSVL 866
Db 636 ILBICNVVFTSMFALEMLKLAAGFLDYLRNPYINFDISIIVSIWEIVGQADGGLSVL 695
Qy 867 RTFLMRVLKVRFLPALQVVLVLMKTMNVATFCMLLMFIFISILGMHLFGCKPAS 926
Db 696 RTFLMRVLKVRFLPALQVVLVLMKTMNVATFCMLLMFIFISILGMHLFGCKFSL 755
Qy 927 ERD-GDTLDRKMFDSLLWAIVTVFQILTOEDWNVLYNGMASTSSWAALYFALMTFGN 985
Db 756 RTDTGDTVPDRKNFDSLLWAIVTVFQILTOEDWNVLYNGMASTSPWASYFVALMTFGN 815
Qy 986 YVLFNLLVAILVEGFOAEGDATKSESEPDFSPSV-----DGDGRRKRLALVAL 1035
Db 816 YVLFNLLVAILVEGFOAEGDANKSYDEDOSSNIEFDFKLQEGLDSSGDPK--LCFIPM 873
Qy 1036 GEHAELRKLPLPLIHT-----AATPMSHPKSSSTVGEGALGSGRRTSSSGSAEPGAH 1091
Db 874 TPNGHLDPSL--PLGHLGPAGAAGA--FRLSLQDPDPMVALGSRKSSVMSL--GRMS 926
Qy 1092 HEMKCPSPARSSPHSPWSAASWTSSRSNSIGRAPSLKRRSPSGERRILLSGE-CQES 1150
Db 927 YDORSLSRSSSYGYPWGRSAASWRRSSWN-----SLXKPPSAFHEHLSAERGGGA 980
Qy 1151 QDEEESSEE--DRASAGSDH-----RHRGSLEREAKSSFDLPDTLQVPG 1193
Db 981 RVEVARADEGPPRAAPLHTPHAHIIHGHPLAHRHRHRTLSLDNEDSDVLAELPAVG 1040
Qy 1194 LHRTASGRSS--ASEHQDCNKGASGRLAFTLRD-DPQLDGGDDDDNDEGNLSKGERQAW 1250
Db 1041 AHPRAAWRAAGPAGPHEDCNCRMP--IAQVFTKMGDRGDRGEDEEIDYTLCFRVKRM 1098
Qy 1251 VRSRLPACCRERDSWSAYIFPPQSRFLLCHRIITHKQFDHVVILVIFLNCIITIAMERP 1310

Db 1099 IDVYKPCWCEVREKSVYLFSPENRFRVLCQIIAHKLFQVIVLAFIFLNCITIALERPQ 1158
Qy 1311 IDPHSABRIFUTLSNYIPTAVFLAEMTKVVALGWCFGEQAYLRSSNVLDGLLVLSVI 1370
Db 1159 IEAGSTERIFLTVSNYIPTAIFVGEWTLKVVSGLYFGEQAYLRSSNVLDGLVLFVSII 1218
Qy 1371 DILVSMYSDCTKILGMLRVLRLLARTPLRPRVISAQGLKLVAVETLMSLLKPIGNIVIC 1430
Db 1219 DIVVSLASAGAKILGVLRVLRLLRPLRPRVISAQGLKLVAVETLMSLLKPIGNIVIC 1278
Qy 1431 CAFFIIFIGILGVOLFKGKFFVCOGEDTNRITNKSDCAEASVYRWYRHKYFNFNLCQALMSL 1490
Db 1279 CAFFIIFIGILGVOLFKGKFFVCOGEDTNRITNKSDCAEASVYRWYRHKYFNFNLCQALMSL 1338
Qy 1491 FVLASKGDVMDYDGLDAGVDQOOPINNNHNMWLLYPIISFLLIYAFVFLNMFGVVVEN 1550
Db 1339 FVLASKGDVMDYDGLDAGVDQOOPINNNHNMWLLYPIISFLLIYAFVFLNMFGVVVEN 1398
Qy 1551 FHKCRQOEAEAREERREKRLRLEKRSKEKQWAEAOCKPYYSYDSRFLVHLHCTS 1610
Db 1399 FHKCRQOEAEAREERREKRLRLEKRSKEKQWAEAOCKPYYSYDSRFLVHLHCTS 1451
Qy 1611 HYLDLFTVIGLVNVTWAMEHYQOPIILDEALKICNYIFTVIFVFSVFKLVAFAPRRF 1670
Db 1452 HYLDLFTVIGLVNVTWAMEHYQOPIILDEALKICNYIFTVIFVFSVFKLVAFAPRRF 1511
Qy 1671 FQDRWNQDLAIVLLSINGITLIEBIEVNLSPINPTIIRIMRVLRIRARVLRKLVAVGMR 1730
Db 1512 FQDRWNQDLAIVLLSINGITLIEBIEVNLSPINPTIIRIMRVLRIRARVLRKLVAVGMR 1571
Qy 1731 ALLTVMQALPQVNLGLLFWLLFFIYALGVELFGDLCEDETHPCBGLRHATFRNFGM 1790
Db 1572 ALLTVMQALPQVNLGLLFWLLFFIYALGVELFGDLCEDETHPCBGLRHATFRNFGM 1631
Qy 1791 AFLTLFVSTGDNNGIMKDSRDC-DOESTCYNTV--ISPIYVSVFLTAQFVLNVVI 1847
Db 1632 AFLTLFVSTGDNNGIMKDSRDC-DOESTCYNTV--ISPIYVSVFLTAQFVLNVVI 1691
Qy 1848 AVLKHLSEENKEAKEBAELEALEM-KTSLPQSPHPLGSP----- 1889
Db 1692 AVLKHLSEENKEAKEBAELEALEM-KTSLPQSPHPLGSP----- 1751
Qy 1890 -----FLW-----PGVEG-VNSTDSPKCAPHTTAHGAAG----- 1920
Db 1752 GGLCRYCSPAQENLWDSVSLIIDSLEGLTTIDNLSGSIHFIH--HYSSPAGCKKCHH 1808
Qy 1921 -----FSLHPTWVP-----HPEEVPV-PLG 1940
Db 1809 DKQEVQLAETAFSLNDRSSIIIGDLSLEDETPACPPGRKSKGELDPPEPMRVGDLG 1868
Qy 1941 PDLTLVRKSGVSRTHSLPN-DSYMCNRNGSTAERSLHGRWGLPKAQSGSILSVHSQPADT 1999
Db 1869 ECPPLSSTAVS-----PDENFLCEMEEIPFNVP--RSW--LKHDSQAPPSPPSPDAS 1919
Qy 2000 SCILQLPKDVHY-----LLOPHGAPTWGAIPKLPDPG-----RSPLAQRLRQAART 2048
Db 1920 SPLLPMPAEFHPAVSASQKPEKGTGTGTPKIALQGSWASLRSRPNVCTLLRQAATGSD 1979
Qy 2049 DSLDVQGLSREDLLSEVSGSPCLTRSSSPWGSSIQVQORSIQSKVSHILRAPCP 2108
Db 1980 TSLDAS-----PSSAGSLQTTLEDLSLTSPPRALGPPAPAP 2018
Qy 2109 GLEPSWAKPPETRSLLELDTLSWISGDLLPSSQEPFLPRDLKCKVSVETQCRRRPG 2168
Db 2019 G-----PRAGLSPAARRL-----SLRGL 2039
Qy 2169 FWLDEQRHRSIAVCLSGSGOPRLCPSPSL-----GQPLGGPGSRPKKLSPPSI 2220
Db 2040 FSLAGLAHQRSIS--SGGTSIPGCTHDSMDPSDEGRGAGGAGGAGSEHSETLSLSL 2097
Qy 2221 S---IDPESOGSRPPCSPGVCLR-----RAP---ASDSK 2250

Db 2098 TSLFCPPP-----PPAPGLTPARKFSSSTSLAAGCPHAAALAHGLARSWAADRSK 2151
Qy 2251 DPSVSSFLDSTAASPSPKOTLSLGLSSDDTMDP 2286
Db 2152 DPPGRAPLPMGLGPLAPPQPL-----PGELEP 2179
RESULT 9
US-09-404-650-5
; Sequence 5, Application US/09404650
; Patent No. 6309858
; GENERAL INFORMATION:
; APPLICANT: McGivern, Paul S.
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
; FILE REFERENCE: R0043B-REG sequence listing
; CURRENT APPLICATION NUMBER: US/09/404,650
; CURRENT FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 5
; LENGTH: 1835
; TYPE: PRT
; ORGANISM: Rattus sp.
US-09-404-650-5
Query Match 44.4%; Score 5345; DB 3; Length 1835;
Best Local Similarity 55.4%; Pred. No. 0;
Matches 1138; Conservative 216; Mismatches 375; Indels 324; Gaps 45;
Qy 43 PRSRDPSVARSSTTCGPGGAAGAGSTGKPGSDADSEAG-----LTPALAPVVFYLSQ 98
Db 8 PSSAABAPAPFGEITEQFGP-----RSPPPSPGPEELEGTPNPDVPHPLAPVAFCLRQ 62
Qy 99 DSRPRSCLATVCNPFERYSMVLVILNCVTLGMRFCPCDIACDSQRCRILQAQDDTFA 158
Db 63 TTSPRNWICIKWCMNPFECVSMVLVILNCVTLGMYQCDDMECLSDCKILQVDFDIFI 122
Qy 159 FFAYEMVYKVALGIFGKCYLGDTWNRLLDFFIVIAQMLEYSLDLQNVFSAVRTVLR 218
Db 123 FFAMWLVKVALGIFGKCYLGDTWNRLLDFFIVMAGMVEYSLDQNLINLSAIRTVLR 182
Qy 219 PLRINRVPKRLVTLVLLDTPMLGNVLLLCFPVFFIIGVIGVQVWAGLRNRCFLBN 278
Db 183 PLKAINRVPKRLVTLVLLDTPMLGNVLLLCFPVFFIIGVIGVQVWAGLRNRCFLBN 242
Qy 279 FSLPLSDLEPYOTENEDSPRTCSQPRENGMRCRSVPTLRGEGGGPPCSL----- 332
Db 243 FTIQGVALPPYQPEDEDEMPFICSLTGONGIMGCHEIPLKEQ---GRECCLSKDDVY 299
Qy 333 DYETYNSSNTT--CVNNQVYTNCSAGEHNPFKGAIFNDFNIGYAWIAI FQVITLEGWVD 390
Db 300 DFGAGRODLNAGSLCVNNRYNNVCRGTGNANPHKGAIFNDFNIGYAWIAI FQVITLEGWVE 359
Qy 391 IMYVMDAHGFYFIYFIILLIIVGSPFMNLCVVIATQSETQORSQMLRQRVRLS 450
Db 360 IMYVMDAHGFYFIYFIILLIIVGSPFMNLCVVIATQSETQORSQMLRQRVRLS 419
Qy 451 NASTLASFSPGSCYEELLYVILKAAARLQVSRALGVAGLSSPVARSQBPQP 510
Db 420 -SSTVASYPGDCYEIEIFQVCHILKAKR-----RALGLYQAL----- 458
Qy 511 SGSCTRSHRLSVHLLHHHHHHHHHNGTLRVPRASPEIQDRDANGSRRLMLPPPS 570
Db 459 -----QNRQA-----MGPGT-----PAPA 473
Qy 571 TPTSPGGPGRGASVHSFYHADCHLBPVRCQAPPRCPSEASGRTVSGKVYPTVHTSP 630
Db 474 KPGE-----HAK-----EPSHCKLCPRHSPLD-----PTPHT--- 500
Qy 631 PEILKDALVEVAPSPGPFTLTSFNIPPGFPSSMHKLELTQSTGACHSSCKISPCSKAD 690

501 Db -----LVO-----PISAIL----- 509
691 QY SGACPDSCPYC-----ARTGAPESADHVPDSDSEAVYFTQAOH 734
510 Db --ASDPSSCHQHEAGRRPSGLGSDSGSGSGSABE--AEANGDL-QSSEDCVS 563
735 QY SLDLRPHRRQRSLGPDABPSSVLA-----FWRLICDTRKIVDSKYFGORGIMAILVN 789
564 Db -----LGKEEBEEDGAARLCGDVWRETRKLRGIVDSKYFNKGMMAILVN 611
790 QY TLSNGIEYHEQPELITNWAIEISNIVFTSLFALEMLKLLVYGPYIKNPNYFDGVIVV 849
612 Db TVSGIHBHQBELTILNIEICNVFTSMFALEMILKLAAPGLFDYLRNPNYFDSIIVI 671
850 QY ISVWEIVQOGGGLSVLRTFLMRVLKLVFLPALORQLVLMKTMNDVNATFCMLLMFI 909
672 Db ISIWEIVQADGGLSVLRTFLRLVLKLVFPALRQLVLMKTMNDVNATFCMLLMFI 731
910 QY FIFSILGMHLFGCKFASERD-GDTLPDRKNFDSLLMAIVTVFOILTQEDWNKVLNGMAS 968
732 Db FIFSILGMHLFGCKFSLRTDGTVPDRKNFDSLLMAIVTVFOILTQEDWNKVLNGMAS 791
969 QY TSSWAALYFALMTFNGYVLFNLIVAILVEGFOAEGDATKSESEPDFSPSDVG----- 1022
792 Db TTPWASLYFVALMTFNGYVLFNLIVAILVEGFOAEGDANRSCDEQSSNLEEFKLPE 851
1023 QY --DGRKRLALVALGSHAELRSLPLLIH--TAATPMSPHKSSTGVGEALGSGRR 1078
852 Db GLDNRDLKLCIPMTENGHLDSL--PLGNHLPAGTGTAPRLSLQPPVLVALDSRK 909
1079 QY TSSGSAEPAAGAAHEMKCPSPASRSPHSASSTWTSRSSRNSLGRAPSLKRRSPGE 1138
910 Db SSVMSL---GRMSYDQSLSSRSRYGPGWGRSGTASRSMWN-----SLXHKPDSAE 960
1139 QY RRSLSGEGQES--QDEEESSE--DRASAGSDH-----RHRGSLREA 1179
961 Db HESLSGEGGSCVRACEGAREAPTATPLHAPHAAHGHPLAHRHRRHRTLSLDT 1020
1180 QY KSSFDLPTLVQVGLHRTAS--GRSSASEHQCNGKSASGLARTLTD--DPOLDGDDN 1236
1021 Db RDSVDLGLVVPVGAHSAARWAGAGAPGHEDCNGRMPN--IAKOVFTKMDRRDRGEDE 1078
1237 QY DEGNLSGERIQAWRRSLPACRERDSWASYIPPPQSRRLCHRIITHKMDHVVIVI 1296
1079 Db EEDYTLCFVRKMDIVYKPDWCEVRDWSYLFSPENKFRILQOTIAHKLFDYVVLAF 1138
1297 QY IFLNCITIAERPKIDHSAERIFLTLSNYIFTAVFLAEMTVKVALGWCFGQAVLRSS 1356
1139 Db IFLNCITIALERPOIEAGSTERIFLTVSNIYIFTAIFVGEWTLKVSGLYFGQAYLRSS 1198
1357 QY WNVLDGLLVLSVIDILVMSVSDSGTKILGMLRLRLRLRLRLRLRLRLRLRLRLRLRL 1416
1199 Db WNVLDGLVFSIIDIVSVASAGAKILGLVRLRLRLRLRLRLRLRLRLRLRLRLRL 1258
1417 QY MSSLKPTGNIVVICAPFIIFGILGVLFKGFVFCOGEDTRNITNKSQCAEASRYWRH 1476
1259 Db ISSLKPIGNIVLICAPFIIFGILGVLFKGFVFCOGEDTRNITNKSQCAEASRYWRH 1318
1477 QY KYNFDNLGOALMSFLVLASXGWDVIMYDGLDVGVDQOQPMHNPMWLLYFISFLIVA 1536
1319 Db KYNFDNLGOALMSFLVLASXGWDVIMYDGLDVGVDQOQPMHNPMWLLYFISFLIVA 1378
1537 QY FVLNMFVGVVFNHFKRQHEEAREERREKRLREKRRSKERQMAEQCKPYSD 1596
1379 Db FVLNMFVGVVFNHFKRQHEEAREERREKRLREKRRSKERQMAEQCKPYSD 1431
1597 QY YSRPRLVHLCTSHYLDLFTIGVIGLVNVTMAHEHYQQOILDALKIKNYIPTVIFVF 1656
1432 Db YCPTRLIHSNCTSHYLDLFTIFCIILNVVMTSLHYNQPTSLTALKYCNMYFTFVL 1491
1657 QY ESNPKLVAFAFRFRFQWRNOLDIAVLISLTMGTLLEEIVNLSLPNPTIIRMLVRI 1716
1492 Db EAVLKLVAFGLURFFKDRNQLDLAI VLLSVMGITLLEEINEALPNPTIIRMLVRI 1551

1717 QY ARVLKLLKMAVGNRALLHTVMQALPQVGNLGLFMLLFFIFAALGVVELFGDLCEDETHPC 1776
1552 Db ARVLKLLKMAVGNRALLHTVMQALPQVGNLGLFMLLFFIFAALGVVELFGDLCEDETHPC 1611
1777 QY EGLGRHATFRNFQMAFLTLFRVSTGDNWNGIMKDPDRDC--DQESTCNTV--LSPYFVS 1833
1612 Db EGMRSRATFRNFQMAFLTLFRVSTGDNWNGIMKDPDRDC--DQESTCNTV--LSPYFVS 1671
1834 QY FVLTAQFVLNVVAVLVMKHLBESNKEAEAELELEMKTLSPQPHSPGLGSPPLWP 1893
1672 Db FVLTAQFVLNVVAVLVMKHLBESNKEAEAELELEMKTLSPQPHSPGLGSPPLWP 1713
1894 QY GVEGVNSTDSPKPGAPHTTAHGAASGFSLEHPTWPHPEEVPV--LGPDLTV----- 1946
1714 Db AHGLGPCPCPCPG-----PCPCPCPCPCPCPCPCPCPCPCPCPCPCPCPCPCPC 1750
1947 QY RKSQVSRTHSLPNDSTWYCRN--GSTABRSILGHRGWLPKAQSGLSVHSQPADTSCILQ 2005
1751 Db RGSQVSRTHSLPNDSTWYCRN--GSTABRSILGHRGWLPKAQSGLSVHSQPADTSCILQ 1801
2006 QY PKDV-HYLLQPHG 2017
1802 Db SGSVFHHYASPDG 1814

RESULT 10

US-09-935-541-5
; Sequence 5, Application US/09935541
; Patent No. 6589787
; GENERAL INFORMATION:
; APPLICANT: Dietrich, Paul S.
; APPLICANT: McGivern, Joseph G.
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
; TITLE OF INVENTION: AND USES
; FILE REFERENCE: R0043B-REG sequence listing
; CURRENT APPLICATION NUMBER: US/09/935,541
; CURRENT FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: 09/404,650
; PRIOR FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 5
; LENGTH: 1835
; TYPE: PRT
; ORGANISM: Rattus sp.
US-09-935-541-5

Query Match 44.4%; Score 5345; DB 4; Length 1835;
Best Local Similarity 55.4%; Pred. No. 0;
Matches 1138; Conservative 216; Mismatches 375; Indels 324; Gaps 45;

QY 43 PRSRDPVASSRSTTCPCGGAAGAGSTGKDPGSADSEAG-----LPYPALAPVVFYLSQ 98
Db 8 PSAAAPAPPEPGITEQGP-----RSPSPPGLEPTEGNTDVPDPLAPVAFCLRQ 62
QY 99 DSFRSWCLRTVCNPFVRVSMVLILLNCVLTGMFRPCEDIAQSCORCRILQAFDDFIFA 158
Db 63 TTSRNCWICWNCNPFVCSMLVILLNCVLTGMFRPCEDIAQSCORCRILQAFDDFIFA 122
QY 159 FFAVWV 218
Db 123 FFAVW 182
QY 219 PLRANRVPMSRMLVTLTLLDPLMGNVLLLCFFVFFIFGIVGVQVWAGLNRRCFLPEN 278
Db 183 PLRANRVPMSRMLVTLTLLDPLMGNVLLLCFFVFFIFGIVGVQVWAGLNRRCFLPEN 242
QY 279 FSLPSLVLEPPYQTEDESPFCPSQPRENGMRSCRSVPTLRGEGGGPPCSL----- 332
Db 243 FTIQGDVALPPYQTEDESPFCPSQPRENGMRSCRSVPTLRGEGGGPPCSL----- 299
QY 333 DYETYNSSNTT--CVNNQYNTNCSAGHNPFGKAINPDNIGYAWIAIFQVITLEGWVD 390

Db 300 DFGAGRODLNAGLUCVWNRVYVCRGNANPHGAINFDNIGVAGIVFOVITLEGWVE 359
Qy 391 IMYVMDAHSYFNFIYFILLIIVGFFMINICLVVIAVATQFSETKQREBSQLMREORVFLS 450
Db 360 IMYVMDAHSYFNFIYFILLIIVGFFMINICLVVIAVATQFSETKQREHRLMLEQRQVLS 419
Qy 451 NASTLASFBGSCYEBELLKVLVILKKAARLAQVRAICVAGILSSPVARSQEQPQP 510
Db 420 -SSTVASYAEPGDCYEBIFQVCHILKAKR-----RALGLYQAL----- 458
Qy 511 SGSCTRSHRRLSVHHLVHHHHHHHVLHNGTLRVPRASPEIQORDANGSRRLMLPPPS 570
Db 459 -----QNRQA-----MGPGT-----PAPA 473
Qy 571 TPTSGPPRGABSVHGFYHADCHLEVPVRCQAPPRPCFSEASGRVSGKYVPTVHTSPP 630
Db 474 KPGP-----HAK-----EPHCKLCPRHSPLD-----PTPHT--- 500
Qy 631 PEILKDKALVEVAPSPGPTLTSFNIPGPPSSMHKLLLETQSTGACHSSCKISSPCSKAD 690
Db 501 -----LVO-----PISAIL----- 509
Qy 691 SGACGPDSCPYC-----ARTGAGEPESADHVMPDSDSEAVVEFTQAOH 734
Db 510 --ASDPSCPHCQHEAGRRPSGLASTDSGQEGSGSGSAB---AEANGDGL-QSSEBGS 563
Qy 735 SLDLPHRRRQRSLGPAEPPSSVLA-----FWRLICDTFRKIYDSYFGRGIMAILVN 789
Db 564 SD-----LGKEEBEQDCAARLCGDVMEETRKLGLGIVDSKYFNRGIMAILVN 611
Qy 790 TLSMGIEYHEQPELTHALEISNIVFTSLPALEMLLKLIVGPGYIKNPYINPDGVIV 849
Db 612 TVSMGIEHHEQPELTNILEICNVVFTSMFALENILKLAAGFLDYLRNPYINPDSIVI 671
Qy 850 ISVMEIVGQGGGLSVLRTPLRLMVLKLRPLALORQLVLMKTMNVATFCMLLMFI 909
Db 672 ISIWEIVQADGGLSVLTFRLLRVLKLVRPMPALRQLVLMKTMNVATFCMLLMFI 731
Qy 910 FIFSILOHMLPGCKPASERD-GDTPDRKPNFDSLLMAIVTVFQILTQEDMNKVLNGMAS 968
Db 732 FIFSILOHMLPGCKPASERD-GDTPDRKPNFDSLLMAIVTVFQILTQEDMNKVLNGMAS 791
Qy 969 TSSWAALYFALMTFGNYVLNLLVAILVEGQAEQDATKSESEPPFSPVDG----- 1022
Db 792 TTPWASLYFALMTFGNYVLNLLVAILVEGQAEQDANRSCDSDQSSNLEBFDKLPE 851
Qy 1023 --DGRKRLALVALGEHAEIRKSLPLIITH--TAATPMHSPKSSSTGVGEALGSGSR 1078
Db 852 GLDNRDLKLCPIWTPNGHLDPSL--PLGAHLPGAGTMGTAPRLSLQPPDVLVALDSRK 909
Qy 1079 TSSGSAEPGAHHEMKCPSPASPHSPWSAASWTSRSSRNSLGRAPSLKRRSPSGE 1138
Db 910 SSVMSL---GRMSYDQRLSSSRSSYYGPMGRSGTWASRRSWN-----SLKHKPPSAE 960
Qy 1139 RRLSLSGEQBS--QDEBESSEE--DRASPAGSDH-----RHRSGLREEA 1179
Db 961 HESLLSGEGGSCVRACEGAREEAPTAPLHAPHAAHGHGPHLAHRHRRHRLTSLDT 1020
Qy 1180 KSSFDLPDLOVGLHRTAS--GRSSASEHODCKGASGLARTLRTD-DPOLDDGDDN 1236
Db 1021 RDSVDLDELVPVGAHRAWRGAGQAPGHEDCGRMPN--IANDVFTKMDRRDRGRDE 1078
Qy 1237 DEGNLSKGERIQAWVRSLPACCRERDSWSAYIFPPQSRFRLLCRIITHKMFQHVVLVI 1296
Db 1079 ESDYTLCFVRKMDVYKPDWCVEVDWSVYLSFSPENKFRILCQTIIAHKLFDYVVLAF 1138
Qy 1297 IFLNCITIAMRPRKIDPHSABRIFLTLSNYIFTAVFLAEMTVKVVVALGWCFCGEQAYLRSS 1356
Db 1139 IFLNCITIALRPOQIEAGSTERIFLTYSNYIFTAVFVGMTLKVVSILGLYFEGEAYLRSS 1198
Qy 1357 WNVLDGLLVLSVTDILVMSVSDSGTKILGMLRVLLRLTLRLPLRVISRAOGLKLVVETL 1416

Db 1199 WNVLDGLVFSVFIIDIIVSVASAGGAKILGVLRVLRLLRLTLRLPLRVISRAPGLKLVVETL 1258
Qy 1417 MSSLKPTIGNIVVICCAFFIIFGILGVOLFPGKFFVCOGEDTRNITNKSDCAEASYRWVRH 1476
Db 1259 ISSLKPTIGNIVVICCAFFIIFGILGVOLFPGKFFVCOGEDTRNITNKSDCAEASYRWVRH 1318
Qy 1477 KYNFDNLGOALMSIFVLASXGQWVDINVDGLDAGVDOOPIMNHNPMWLLYFISFLIIVA 1536
Db 1319 KYNFDNLGOALMSIFVLASXGQWVDINVDGLDAGVDOOPIMNHNPMWLLYFISFLIIVA 1378
Qy 1537 FFVLNMFVGVVVENFHKCRQHEEERREERREERREERREERREERREERREERREERRE 1596
Db 1379 FFVLNMFVGVVVENFHKCRQHEEERREERREERREERREERREERREERREERREERRE 1431
Qy 1597 YSRFRLVHLLCTSHYLDLFTIGVIGLVNVTMAHEHYQQOILDEALKICNYITVIVPVF 1656
Db 1432 YCPTRLLIHSNCTSHYLDLFTIGVIGLVNVTMAHEHYQQOILDEALKICNYITVIVPVF 1491
Qy 1657 ESVFKLVAFAPRRFFODRWNOLDLAIVLISIMGTLEIEVNLSPINPTIIRMRVLR 1716
Db 1492 EAVUKLVAFGLRRFFODRWNOLDLAIVLISIMGTLEIEVNLSPINPTIIRMRVLR 1551
Qy 1717 ARVLKLLKMAVGRALLHTVMQALPOVGNLGLLPMLEFFIFAAALGVELFGDCEDETHPC 1776
Db 1552 ARVLKLLKMAVGRALLHTVMQALPOVGNLGLLPMLEFFIFAAALGVELFGDCEDETHPC 1611
Qy 1777 EGLGRHATPFRNFGMAFLTLFRVSTGDNWNGIMKDPDRDC-DQESTCVNTV--ISPIYFVS 1833
Db 1612 EGMRSRATFENFGMAFLTLFRVSTGDNWNGIMKDPDRDC-DQESTCVNTV--ISPIYFVS 1671
Qy 1834 FVLTAQFVLNVVAVLMLKHEBSNKEAEAELEAELEEMKTLSPQPHSPGLSPFLWP 1893
Db 1672 FVLTAQFVLNVVAVLMLKHEBSNKEAEAELEAELEEMKTLSPQPHSPGLSPFLWP 1713
Qy 1894 GVEGVNSTDSPKGPAPHTTAHGAASGFSLEHPTMVPHPPEVPVP-LQPDLLTV----- 1946
Db 1714 -AHGLGPCPCPG-----FCPCPCPCAGPRLPTSSPGAP 1750
Qy 1947 RKSQSVRTHSLPNDNSYCMRN-GSTAERSLGRHGLPKAOSGSLSVHSQPADTSCILQL 2005
Db 1751 RGSAGAGAGG-DTESHLCRCYSPAQETL-----W-----LDSVSLIIKDSLEGELTIIDNL 1801
Qy 2006 PKOV-HYLLLOPHG 2017
Db 1802 SGVFFHHYASPDG 1814
RESULT 11
US-09-268-163-4
; Sequence 4, Application US/09268163B
; Patent No. 6353091
; GENERAL INFORMATION:
; APPLICANT: Lipecombe, Diane
; APPLICANT: Schorge, Stephanie
; TITLE OF INVENTION: HUMAN N-TYPE CALCIUM CHANNEL ISOFORM AND USES THEREOF
; FILE REFERENCE: B1055/7000
; CURRENT APPLICATION NUMBER: US/09/268,163B
; CURRENT FILING DATE: 1999-03-12
; EARLIER APPLICATION NUMBER: US 60/077,901
; EARLIER FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 2343
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-268-163-4
Query Match 14.0%; Score 1678; DB 3; Length 2343;
Best Local Similarity 23.3%; Pred. No. 4.9e-126;
Matches 625; Conservative 354; Mismatches 828; Indels 872; Gaps 81;
Qy 59 PGCAAGAGSTKDPGSADEAGLPYPALAPV-----VFFYLSQDSRPRSWCLRT 109

Db 32 PGEGLOGQGVLYKQSIAGARTMALYNPIPKQNCFTVNRSLVFSEDNVVRKAKRI 91
Qy 110 VCNPFERVMVLNLCVTLMPFCPCDIACQSRCLIQAFDD---FIFAFVAVEMV 166
Db 92 TENPPFEYMLATIANICIVLAL---EOHLPDGDKTPMSERLDDTEPYGIGCFEAGI 147
Qy 167 KVALG-IFGKKCVLGTWRDLDPFIVIAGLMYS---LDLQNVSPSARTVAVLAPLRA 222
Db 148 KIIALGVFPHKGYLRNGMVMDFVVLTLGILATAGTDFDLR-----TLRAVAVLRLPKL 202
Qy 223 INRVPMRILVTLTLLDTPMLGNVLLCFFVFFIGVQVLWAGLLRNRCLFLENFSLP 282
Db 203 VSGIPSOVLVKSIMKANVLLQIGLLFFAILMFAIGLEFYNGRHKACF-----P 255
Qy 283 LSVLDPEYYQTEBESPFICQSPRENGMRSRCSVPTLRGEGGGPPCSDLDYTYNSSN 342
Db 256 NSTDAEPV-----GDFPCGKEAPARLCEGD 280
Qy 343 TTCVNNQYVYNSCAGEHNPFGKAINFDNIGYAWIAIFOVITLEGWVDIMYFVMD-AHSP 401
Db 281 TEC-----GNFGITNFDNILFALTVOICITMEGWTDIYNTNDAAGNT 330
Qy 402 YNFTYILLIIVGFFMINCLVIAQFSETKQES-----QLMREQRVRFSLNASTL 455
Db 331 WNWLYFIPLIIGSFFMLNLVGLSGEFAKERERVENRRAFLKLRQOQIE-----382
Qy 456 ASFSEPGSCVEELKYLVIYLRKARLAQVRAIGLRLSPVARSQOEPOPPSSCT 515
Db 383 -----RELNGYLEWIFKABEVMLEABD-----RNAEKSPLDLVK 417
Qy 516 RSHRLSVHILVHHHHHHHHYHNGTLRVPRASPEIQORDANGSRRLMLPPSTPTPS 575
Db 418 RAATKSRNDLIH-----AEEGEDRPAD-----440
Qy 576 GGPREGAESVHSFYHADCHLEPRVCOAPPPRCPSSEASRTVSGKGYPTVHTSPPPILK 635
Db 441 -----440
Qy 636 DKALVEVAPSGPPTLTSFNIPGPPFSMHKLLTQSTGACHSSCKTSSPCSKADSGACG 695
Db 441 -----LCVAGSPPARAS-----452
Qy 696 PDCPYCARTGAGBPESADHVPDSDSEAVYEFQDAQHSDLRDPHRRRORSILGPDAP 755
Db 453 -----LKSGETESSYF-----RRKEK-----469
Qy 756 SSVLAFWRLICDTPRKIVDSKYFGRGIMAILVNTLSGIBYHQPBELTNALBISNIVP 815
Db 470 --MERFF-----IRRMVKAQSFYVWVLCVVALNTLCVAMVYHQPRRLTTLFYABFVF 521
Qy 816 TSLFALEMLLKLIVYGPFGYIKNPNIFDGVIVISVWEIVGQ-----QGGGLSVLATER 870
Db 522 LGLEFTEMSLKMYGLGPRSYFRSSFCDFGVIVGSVFVWVAIKPGSSFGISVLRALR 581
Qy 871 LMRVLKVRFLPALORQVLWLMKMDNVAITFCMLIMLFIIFISILGMFLFCCKEASERDG 930
Db 582 LLRIFKVTYKWSLENLVVLLNSKMSIISLLFLFLFVIVFALLGMQLFGQNFQDET 641
Qy 931 DTLPRKNPDSLMAIVTVFOILTODWNKVLYNGM-----ASTSSWAALFYIALMTFGN 985
Db 642 PT---TNFDTPPAAILTVFOILTGEDWNVAMVHGIESQGGVSKGMFSSFFIVLTLFGN 697
Qy 986 VYLENLLVAILVEGFOAEGDATKSEPDFFSPVSDGDRKRLALVALGEHAELRKS 1045
Db 698 YTLNVFLAIVADNLANAQELTKDEEMEEAA-----NQRLAQAKEVALEV--SP 746
Qy 1046 LPPLIHTAATPMWHPKSSSTGVGEA-----1071
Db 747 MSAANIISAARQONSAKARSVWEORASQLRLQNLRASCEALYSEMDPEERLRFATTHLR 806
Qy 1072 -----LGSGRRTSSSGSAPGNA-----HH-----EMKCP-----1097

Db 807 PDMKTHLDRLVVELGRDGCARGVGGKARPEAAEAPEGVDPRRHRRHRDKDKTTPAAGQ 866
Qy 1098 -----PSARSS---PHSPWASAASWTSSRSKNSLGRAPSLKRRRSPSGERRSL 1142
Db 867 DRAEAPKAESGPGAREERPRHRSHKEAA--GPPEARSEGRGP-----CPGEGRRH 919
Qy 1143 LSGEQESODEB-----ESSEEDRASPAGSDHRRHRSLE---REAKSSFDLPDTL 1189
Db 920 RRGSPDEAAERPRHRAHRHODPSKECAGAKGERRARRHGGPRAGPREAESG-----972
Qy 1190 QVPG-LHRTASGRSASE--HQCNGKSASGLA-----RTLRTDDPOLDDDDNDE 1238
Db 973 EBPARRHRAHKAQPAHEAVEKETTEKEATEKEABIVEADKEKELRNHQBREPHCDLETS 1032
Qy 1239 GNLKGERIQAWVRSLPACCRER-----DSW-----1265
Db 1033 GTVTGVP-----MHTLPSTCLOKVEEOPEDADQNVRTRMGSPQDPDNTIIVHVPMLTG 1086
Qy 1266 -----SAYIFPQSRPRLCHRI 1283
Db 1087 PLGEATVPVSGNVDLLESQAEGKEVEADDVMSRGPPIVPYSSMFCLSPTNLLRRECHYI 1146
Qy 1284 ITHKMPDHVVLIIIFLNCITIAMERPKIDPHSAERIFLTLSNVIFTAVFLAEMTVKVVVAL 1343
Db 1147 VTMRYFEVVLVIALSSIALAEDP-VRTDSPRNALKYLDYIFTGVTFEFEMVIMIDL 1205
Qy 1344 GWCFGEOAYLRGSWNVLDGLLVLSVIDI-LVSMVSDSGTKILGMLRLRLRLTLPLRV 1402
Db 1206 GLLHHPCAFRLWNILDFIVVSGALVAFSPFVSGSGKDINTIKSLRVLRLPLKT 1265
Qy 1403 ISRAOGLKLVETLMSLSLPIGNIVVICAPFIIFGILVOLFKGFFVCOGE-----D 1456
Db 1266 IKELPKLAVFDCVNSLKNVILIVYMLFIFAVIAVOLFKGFFCTDESKELELD 1325
Qy 1457 TRN--ITNKSDCAEASYR--WVRHKNFNDLGOALMSLFVLASKDGVWDIMYDGLDVGVD 1513
Db 1326 CRGQYLDYKEBEVEAOPROWKKYDHYDNVWALLTLFTVSTGEGPFWLKHSDATYEE 1385
Qy 1514 QQIMNHNPMWLLYFTISLLIYAFFVNLNMFVGVVVENFHKCRQHOEBEERREKRLRR 1573
Db 1386 QGSPGYRMELSIIFYVYVFWVPFFVFNIFVALIITF-----QBQDKWSE-----CS 1435
Qy 1574 LEKRSKKEQMAEACKPYSDYSR--FRLLVHLLCTSHYLDLFTITGVLGNVVTWAME 1631
Db 1436 LKNERACIDFPAISAKPLTRYMPQNRQSFQYKTTFTVSPFPFFIFIMALTNTVLMWK 1495
Qy 1632 HYQOQPOLDEALKICNVIFTVIEVFEVSFKLVAFAPRRFPQDRWNOLDLAILVLSIMGIT 1691
Db 1496 FYDAPYEYELMLKCLNIVFTSMESMECVLKIAGVNLNFRDANVDFVTVLGSITDIL 1555
Qy 1692 LEBIE-----VNLSPINPTIIRIMVLRVARVLKLLKMAVGMRALHTWQALPOVGNL 1746
Db 1556 VTEIAETNNFINLS-----FLRLFRAARLIKLLRQGYTIRILLTWTVQSFKALPYV 1606
Qy 1747 GLLFMLLFFIIFALGVLELFGDLCEDETHPCGEGHATERNFGWAFILTRVSTGDNWNG 1806
Db 1607 CLLIAMLFFYIYALIGMVFQGNIALDDD---TSINRHNFFTLQALMLLFRSATGEAWHE 1663
Qy 1807 IMKD--PSRCDDBE--STCVNTVISPIYFVSFVLTAQFVLNVNVIAYLM-----1851
Db 1664 IMLSCLNQACDQANATECGSDFAFYFVSFIFLCSFLMLNLFVAVIMDNFEYLTRDSS 1723
Qy 1852 ----KHLBE-----1856
Db 1724 ILGPHLHDEFIRVWAEYDPAACGRISYNDMFEMFKHMSPPGLGKCKPARVAYKRLVRMN 1783
Qy 1857 -----SNKEAKEAELEAEL-----ELEMKTLS- 1879
Db 1784 MPTSNEDMTVHTSTLMALIRTALEIKAPAGTKHQHCDALRKEISVWVANLPQKTLDL 1843
Qy 1880 -POHSP-----LGSPP-----LWPGVEGVNSTDSKPGAPHTTAHIGAASGSLEHPTWVP 1930
Db 1844 LVPHKFDENTVGKVAALMIFDYFKQNTTRDQMOPQAGLSQMGVPSLF---HPLKAT 1900

698	YTLNVLPLATAVDNLANAQELTKDEBEMEEAA-----NOKLALQKAKEVAEV--SP	746
1046	LPPLLIHTAATPMSPHKSSSTGVGEA-----	1071
747	MSAANISIAARQONSAKARGSWEQRASQRLQNLRASCEALYSEMDEPERLRATTHRR	806
1072	-----LQSGSRERTSSGSAEGAA-----HH-----EMKCP-----	1097
807	PDWKTHLDRLVVLGRDARGPVGGKARPEAAEAPGVDPPPRRHHRRDKDKTPAAGDQ	866
1098	-----PSARSS-----PHSPMSAASWTSRRSSRNSLGRAPSLKRRSPSGERRSL	1142
867	DRAEAPKAESGEPGAREERPRPHRSKSEA--GPPEARSERGRGP-----GREGGERHH	919
1143	LSGEGESQDEE-----ESSBEDRASPGSDHRHRGSLE--REAKSFDLPDTL	1189
920	RRGSPEAAERPRHRAHRHODPFSKECAKAGERRARRHGGPRAGPREAESG-----	972
1190	QVPG-LHRTASGRSSASE--HODCNGKSASGRLLA-----RTLRTDDPOLDGDNDDE	1238
973	EEFARRHRAHKAQPAHEAVEKETTEKEATEKAEIVEADKEKLNHQPREPHCDLETS	1032
1239	GNLSKGERIQAWVRSRLPACRRR-----DSW-----	1265
1033	GTVTGVP-----MHTLPSTCLOKVEQBEDADNQNRVTRMGSPQDPNTIVHIPVMLTG	1086
1266	-----BAYIFPPOSRRFLCHRI	1283
1087	PLGEATVVPNGVNDLSQAEGKKEVADVWRSGPRPIVPYSSMFCULSPNLNLRFRCHYI	1146
1284	ITHKMFHDVVLVLIIFLNCITITAMERPDKIDPHSAERIFLTLNSNIFTAVFLAEMTVKVVAL	1343
1147	VTWKYFEWILVIALSSIALAAEDP--VRTDSPRNNALKYLDYIFTGVFTFEMVIMIDL	1205
1344	GWCFGQAYLRSWNVLDELVLISVIDILVSMV--SDSGTKILGLMARVLRLTLRLPLRV	1402
1206	GLLHHPGAYFRDLWNITLD----FIVVSGALVAFAGSGKGDINTTKSLRVLEVLRLPKT	1261
1403	ISRAOQKLKVVETLMSLKPIGNIVICCAFFIIFGILGVOLPKGFFVFCQG-----D	1456
1262	IKELPKLKAFCVDCVNSLKNVNLILVYMLFMFIFAVIAVOLPKGFFYCTDSEKLERD	1321
1457	TRN--ITNKSDCABASYR--WVRHKYFNPNLGOALMSLFVLASKDGWVDIMYDGLDVGVD	1513
1322	CRGOYLDYEEVEAOPROWKKYDFHYDNLVWALLTLFTVSTGEGPWLKHSVDATYEE	1381
1514	QQPIMNHNPMMLLYFSLFLLIVAFFVLNMPGVVNFHFKCRQHOEEEAARREEKRLRR	1573
1382	QGPSGYRMELSYFYVYFVFFVFFVFNIFVALIITP-----QSGQDKWSE----CS	1431
1574	LEKRRSKEKQMAEACKPYYSYSR--FRLLVHHLCTSHYLDLFTIGVIGLNVVTWAME	1631
1432	LEKNERACIDFAISAKPLTRYMPQNRQSFOYKWTWTVVSPPEFYFIMAILNTVVLMMK	1491
1632	HYOQPILDEALKICNYFIVTVIFVPSVFKLVAFAFRPFQDRWNQOLDIAVLLSIMGIT	1591
1492	FYDAPYEYELMLKCLNIVFTSMFSMECVLKIIAAGVLNFRDANNVDFVTVLGISTDIL	1551
1692	LEBIEVNLSPINPTIIRIMRVLRIARVLKLLKWAVCMRALLTHVTMQUALPQVGNLGLFM	1751
1552	VTBIANNF---IN---LSFLRLFRAARLILKLAQQYTIRILLWTFFQSPKALFYVCLLIA	1605
1752	LLFFIPAALGVELFGDLECDETHPCBGLGHATFRNFGMAFLTLFRVSTGDNNWNGIMKO-	1810
1606	MLEFFIYAIGMVGFGNIALDDD---TSINRHNFRFTLQALMLLFRSATGEAHWEIMLSC	1662
1811	-PRDCCDOE--STCYNTVISPYPVGSFVLTAQFVLVNVNVLAVLM-----K	1852
1663	LSNQACDBQANAECCSDFAFYFVFSFIFLCSFLMLNLFVAVIMDNFEYLTRDSSITLGP	1722
1853	HLBEE-----	1856
1723	HLDEFIRVWAEYDPAACGRISYNDMPFEMLKHMSPPGLGKCKCARVAYKGLVRMNPISN	1782

RESULT 13

RESULT 13
US-09-452-007-2

US-09-452-007-2
: Sequence 2: Application US/09452007: sequence 2, Application
: Patent No. 6140485

FACEBOOK NO. 6140483
: GENERAL INFORMATION:

APPLICANT: Franco, Rodrigo

APPLICANT: Franco, Rodrigo

APPLICANT: Sun Chen, Al Ku
APPLICANT: Smev David J.

APPLICANT: Suey, David J.
TITLE OF INVENTION: NUCLEIC ACID ENCODING HUMAN NEUTRONAL.

;	TITLE OF INVENTION:	NUCLEIC ACID ENCODING HUN
;	TITLE OF INVENTION:	CALCIUM CHANNEL SUBUNITS

; TITLE OF INVENTION: CAL
: NUMBER OF SEQUENCES: 6; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton Brook Smith & Reynolds P C

ADDRESSEE: Hamilton, Brook
STREET. Two Militia Drive

STREET: TWO MILL
CITY: ARLINGTON

; CITY: Lexi
CITY: Lexi
CITY: Lexi

; STATE: MA

; COUNTRY: USA

ZIP: 02173-4799

; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk

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;
COMPUTER: IBM PC compatible

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OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, V

; CURRENT APPLICATION DATA:

APPLICATION N

FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/713,118

FILING DATE: 16-SEP-1996

NAME: Mata, Elizabeth W.	REGISTRATION NUMBER: 38,236	REFERENCE/DOCKET NUMBER: ACC96-01	TELEPHONE: 617-861-6240	TELEFAX: 617-861-9540	INFORMATION FOR SEQ ID NO: 2:	SEQUENCE CHARACTERISTICS:	LENGTH: 2337 amino acids	TYPE: amino acid	TOPOLOGY: linear	MOLECULE TYPE: protein	US-09-452-007-2
Query Match	13.9%;	Score 1677;	DB 3;	Length 2337;							
Best Local Similarity	23.4%;	Pred. No. 5.9e-126;									
Matches 627;	Conservative 350;	Mismatches 829;	Indels 868;	Gaps 82;							
QY	59	PGGAGAGAGSTEKDPGASDSEAEGLPYPALAV	-----VFYLSQDSRPRSWCLRT	109							
DB	32	PGGGGLQPGQVLYKQSIQAQARTMALVNP	IPVKQNCFTVNRSLRSLFVSEDVNRKYAKRI	91							
QY	110	VCPNPFERYSMVLILNCVTLGWFRCED	ACDSQRCILQAFDD---FIFAFVAVMVV	166							
DB	92	TEWPPPEYMLATIANCIIVLAL---	EQHLPGDKTMSERLDDTBTFYIGICFEAGI	147							
QY	167	KMVALG-IFGKKCYLGDTWNRLDFF	VIAGMLEYS---LDLQNVFSFSAVRTVRVLRPLRA	222							
DB	148	KIIALGFVFKHGSYLRNGWVDFVVL	TGILATAGTDFDLR-----TIRAVRVLRPLKL	202							
QY	223	INRVPSMRILVLLDPTLMLGNVLL	CCFFVFFIFGIVGVQLWAGLNRNCFLPENFSLP	282							
DB	203	VSGIPSLQVVLKSIKMAVPLQIGLL	FPAILMFAIIGLEPYMGKPHKACF-----P	255							
QY	283	LSVDLEPYQTENEDESFPICQPRE	NGMRCRSVPTLRGGGGGPPCSDLYEYINSSSN	342							
DB	256	NSTDAPFV-----	GDFFPCGKEAPARLCEGD	280							
QY	343	TTCVNNQYVTCGAGEHPNFKGAIN	FDNIGVATIAFOVITLEGWVDIMYFVMD-AHSF	401							
DB	281	TEC---REVTP-----	GNFGITNFDNLFAILTVFCITMEGWTDILYNTDAAGNT	330							
QY	402	YNFIYFILYIVGSPFMNLCVLVIAT	QFSETKQRES-----QLMRQVRVFLSNASTL	455							
DB	331	MNWLXFIPLIIGSPFMLNLVLG	SLGSEFAKERVENRRAFLKRRQOIE-----	382							
QY	456	ASPSFGCVSEBLLKYLIVILKAAR	LRAQVRSALGVRAGLSSPVARSQGPQPSGCT	515							
DB	383	-----RELNGYLEWIFKAEV	YMLAEED-----RNABESPLDLVK	417							
QY	516	RSRRRLSVHHLVHHHHHHHHYH	LNGTLRVPRASPEIQDRDANGSRRLMLPPSTPPS	575							
DB	418	RAATKKSRLDLH-----	AEEGEDRPAD-----	440							
QY	576	GGPPRGABSVHSPYHADCHLEP	VRVCOAPPPPCPSASGRTVGSKVYPTVHTSPPEILK	635							
DB	441	-----	-----	440							
QY	636	DKALVEVAPSGPPTLTSTNIP	PPGPPSSMHKLLETQSTGACHSSCKISSPCSKADSGACG	695							
DB	441	-----	-----	452							
QY	696	PDSCPCYARTGAGEPESADHVP	SDSEAVYEFTQDAQHSDLRDPHSRRQRSLGPDAP	755							
DB	453	-----	-----	469							
QY	756	SSVLAFLRLICDTFRKIVDSKYF	GRGIMAILVNTLSMGIEYHEQPEELITNALEISNIVF	815							
DB	470	--MFRF-----	IREWKAQSPYVVLVCVALNTLCVAMVHYNQPRLLITLYAEFVF	521							
QY	816	TSVLALEMILLKLVYGPFGYK	NPVNIPOGVIVISVWEIVQO-----QGGGLSVLRTFR	870							
DB	522	LGFLELMSLKMVGLGRSVYFRSS	FNCFDFGVIGVSPVEVWAAIKPGSSFGISVLRALR	581							

Db 2077 MDGAPSSAVGGLPPGEGPTCCRERERRRGRSQRQPPSSSSSEKQRF---YSCDRF 2133
Qy 2187 GSQPRLCFSPS-----SLGGQPL-----GGPGSRPKK 2213
Db 2134 GGREPPKPKSLSHPTSPTAGQPGPHPGSGSVNGSPLLSTSGASTPGRGRRQLPQT 2193
Qy 2214 KLSP-PSISIDPPBS-----QGRPPPCSPG-----VCLRRAPASD----- 2248
Db 2194 PLTERPSITYKTANSPIHFAGATSLPAPSPGRLSRGLSEHNALLQDDPLSQPLAPGSR 2253
Qy 2249 -SKDPSVSSPLDSTAAPSFKUTLSL-----SLSS 2279
Db 2254 IGSDPYLQRLDSEASVHALPEDTLTFEEAVATNSGRSS 2292

RESULT 15

US-08-223-305C-47
; Sequence 47, Application US/08223305C
; Patent No. 5851824
; GENERAL INFORMATION:
; APPLICANT: Harpold, Michael
; APPLICANT: Ellis, Steven
; APPLICANT: Williams, Mark
; APPLICANT: Feldman, Daniel
; APPLICANT: McCue, Ann
; APPLICANT: Brenner, Robert
; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
; METHODS
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/223,305C
; FILING DATE: April 4, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/868,354
; FILING DATE: April 10, 1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/745,206
; FILING DATE: 15-AUG-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/620,250
; FILING DATE: 30-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/482,384
; FILING DATE: 20-FEB-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/603,751
; FILING DATE: 04-APR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US89/01408
; FILING DATE: 04-APR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/176,899
; FILING DATE: 04-APR-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L.
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 52516 (P519739)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619)238-0999
; TELEFAX: (619)238-0062

; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2339 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-08-223-305C-47

Query Match 13.9%; Score 1676; DB 2; Length 2339;
Best Local Similarity 23.4%; Pred. No. 7.1e-126;
Matches 627; Conservative 350; Mismatches 826; Indels 876; Gaps 82;

Qy 59 PGPGAAGAGSTEXDPCGSADSEAGLPYPALAPV-----VFFYLSQDSRRSRSCWLR 109
Db 32 PGPGGLQPGQRVLYKQSIQARTMALNPVYKQNCFTVNRSLVFSEDNVVRKYAKRI 91
Qy 110 VCNPFERFVSMVLVILNLCVTLGMFRPCEDIACDSQRCLILQAFDD---FIAFAFAEMVV 166
Db 92 TEWPPFENMILATIIANCIVLAL---EQHLDPGDKTPMSERLDDTEPYFIGIFCFEAGI 147
Qy 167 KMVALG-IFGKCYLGDTNRNLDFFIVIAQMLYS---LDLQNVSFSAVTVRVLRLRA 222
Db 148 KIIALGFVPHKGSYLRNGWNVDFVVVLTGILATAGTDFDLR-----TLRAVRVLRLKL 202
Qy 223 INRVPSMRILVTLTLLDPLMLGNVLLCPVFFIFIGVGVQLWAGLLNRNCFLENFSLP 282
Db 203 VSGIPSLQVVLKSIKAMVPLLIQILLLPAILMFAILGLEFYNGKFKACF-----P 255
Qy 283 LSVLDLEPYQTENEDESPFICSPQRENGMRSCRSVPTLRGEGGGPPPCSLDYETYNSSN 342
Db 256 NSTDAEPV-----GDFPCGKEAPARLCEGD 280
Qy 343 TTCVNNQYNTCSAGEHNPFGKAINFDNIGYAWIAIFQVITLEGWVDIMYFMD-AHSF 401
Db 281 TEC---REYWP-----GPNFGITNFDNLIFALTVOICITMEGWDILYNTNDAAGNT 330
Qy 402 YNFIYFILLIIVGSPFMINLCLVVIATQFSETKQRES-----QLMREQRVRLSNASTL 455
Db 331 WNWLYFIPLIIGSFEMNLNLVGLVSGEFAKERERVENRRAFLKLRQOQIE----- 382
Qy 456 ASFSEPGCVBELLYLVILKKAARRLAQVRAIGVRAGLJSSPVARSQGPQSGSCT 515
Db 383 -----RELNGYLEWIFKAEVWLAED-----RNAEEKSPLDVLX 417
Qy 516 RSHRRLSVHHLVHHHHHHHHHNGTLRVPRASPEIQDRDANGSRRLMLPPSPPTPS 575
Db 418 RAATKKSRNDLIH-----AEEGEDRFAD----- 440
Qy 576 GGPARGAESVHSFYHADCHLEPVRCQAPPPRCPSASGRTVGSGKVYPTVHTSPPEILK 635
Db 441 ----- 440
Qy 636 DKALVEVAPSGPPTLTSFNIPPGFSPMHKLELTOSTGACHSSCKISPCSKADSGACG 695
Db 441 -----LCAVGSPPFARAS----- 452
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Db 453 -----LKSQKTESSYF-----RRKEK----- 469
Qy 756 SSVLAFWRLICDTFRKIVDSKYFGRGIMIAILVNTLSMGIEVHEQPEELTNALEISNIVF 815
Db 470 --MREFF-----IREMKAQSFYVWVLCVVALNTLCVAMVHVNQPRRLTLYFAEFVF 521
Qy 816 TSLFALEMLLKLIVYOPFGYIKNPYINFGVIVVISWEIVGO-----QGGGLSVLRTFR 870
Db 522 LGLFLTEMLKMYGLGPRSYFRSSFCDFGVIVGSVFVFWAAAIKPGSSFGISVLRLR 581
Qy 871 LMRVLKLVRLPALORQLVVLMTKMDNVATFCWMLMLFIFISILGMHLFGCKPFASERDG 930
Db 582 LRIIFKVTYKWSLRLNLVSLNSMKSIIISLLFLFLFVIVFALLGMQLFGGQFNQDET 641

Qy		931	DTLPDRKNFOSLWAIIVTVPFIITQBBDWKVLYNGM-----ASTSSWAALYFTIALMTFGN	985
Dd		642	PT---TNEFTFPAAILTVPIIITGEDDNAVMTGHGIESQGSGVKGMFSFYFTVLTLFGN	697
Qy		986	YVLFNLLVALLVGSFQAEGDATSESEPDPFPSVDGDGRKKRLALVALGEHAELRKSIL	1045
Dd		698	YTLLNVFLATAVNDLANAQELTKDEEMEBEAA-----NOKLAQLKAKEVAEV--SP	746
Qy		1046	LPLLIITHAATPMSPHKSSSTGVGEA-----	1071
Dd		747	MSAANISIAARQQNSAKARSWEQRASQLRLQNLRASCEALYSEMPEERLERPATTRLHLR	806
Qy		1072	-----LGSGSRRTSSSGBAEAGAA-----HH-----EMKP-----	1097
Dd		807	PDMKTHLDRLPVVELCRDGARGVGKGARPEABEAPEGVDPPRRHHRHDKDXTPAAGDQ	866
Qy		1098	-----PSARSS-----PHSPWSAASWTSSRSSRSLSRAPSLKRKRRSPSGERRSL	1142
Dd		867	DRAEAPKAESGFPCAREERPFRHSRHISEAAA--GPPEARSERGRP-----GREGRRHH	919
Qy		1143	LSGEGEQSDOE-----ESSBEDRASPGSDHRHRGSLE-----REAKSFSDLPTDL	1189
Dd		920	RGSPEAEAREPRHRAHRHQDSPKECACAGERRARRHGGRPRAGPREAESG-----	972
Qy		1190	QVPG-LHRTASGRSSASE--HQDCNGKSASGLA-----RTLRTDDPOLDDGGDDNDE	1238
Dd		973	EBPARRHRAHRHKAQAPAHEAVEKETTEKBATEKEAEIVEADKEKELRNHOHPREPHCDLET	1032
Qy		1239	GNLSKGERIQAWVRSLRPACCRR-----DSW-----	1265
Dd		1033	GTVTVP-----MHTLPTSICLKVBEOPEDANDQRNVTRMGSQPDNPNTIVHI	1086
Qy		1266	-----SAYIFPPQSFRLLCHRI	1283
Dd		1087	PLGEATVPSGNVDLESQAEGKEVEADDVMRSGPRPIVPSYMFCLSPNTLLRRRFCHI	1146
Qy		1284	ITHCMPDHVVULVIIPNCITIIMERPKI DPHSAERIPTLSNVIPTAVFLAEMTKVVAL	1343
Dd		1147	VTRYFEWLTVIAUSSIALAADBP-VRTDSRPNNALKYLDVIFTGYVFTEMVIIKMIDL	1205
Qy		1344	GWCFGEQAYLRSSWNVLDDLVLISVIDIIIVSMV-SDSGTYKILCMLRVLRLLTLRLPRV	1402
Dd		1206	GLLLHPCAIFYDLWNILD----FIVYSBALVAFAPSGSKGDIINTIKSLERVLRVLRPKLT	1261
Qy		1403	ISRQOGLKVUETLMGSLKPIDIGNIVI TC AFF I IFGLIGVOLPKGFVFCQGE-----D	1456
Dd		1262	IKEPLKXKAVFDCCVMXSNKLNLIIYMFMETFAVIAVIOFKGKFYYCTDESKELED	1321
Qy		1457	TRN--ITNKSDCAEASVR-VWRHKYNFDNLGOALMSLFVLASKDGVMDIMYDGLDAVGVD	1513
Dd		1322	CRCQYL DY E KE BE A Q P R M K Y D F H V N L W A L L T L T V S T G E G M P W L U G H S V D A T Y E E	1381
Qy		1514	QQPIMHNPNMWLIYFISFLIIIVAFFVLNMVGVVVVENFHRCROHBEEBAAREEKRLLR	1573
Dd		1382	QGPSGVMELSI FYVVYFVFFVFFFVNIFVALLITF-----QEQDKWME-----CS	1431
Qy		1574	LEKRRSKEKOMABAQCXPYSYSR--FRLLVHLCITSYLDLFTGTVIGLVNVTWAME	1631
Dd		1432	LEKNERACIDFAISAKPLTRIYMPQNRQSFOYKTWTFVVSPPPFIYMIAMITALNTVVLMMK	1491
Qy		1632	HYOOQILLDEALKICNYFITVIVFVESVFKLAFAPRRPFQDNQWLDLAIVLLSIGIT	1691
Dd		1492	FYPAPYEYELMKCLNIIVFTSMFSMECVLKIIFAGVLNYPRAWNVDFFTVLGISTDIL	1551
Qy		1692	LEEIE-----VNLISLPINPTIIIRMRVLRVARVLKLKMAVGRMALHTVMQALPOVGNL	1746
Dd		1552	VTEIATAENTNFINLS-----FLRLFRAARLIKULARQGYTIRILLMTFVQSFKALPYV	1602
Qy		1747	GLLFLMLFFTFAALGVELFGDCEDETHPECEGLGRHATFRNFQM AFLUTLP RV ST GD NW NG	1806
Dd		1603	CLTIAMLFFYTAIGMQVFNIA LD DD --TS IN RH NN FT TF QA LM LL FS RT SA WH E	1659

Search completed: April 13, 2005, 19:17:08
Job time : 102 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 13, 2005, 19:11:35 ; Search time 215 Seconds
(without alignments)
3535.497 Million cell updates/sec

Title: US-09-611-257A-24

Perfect score: 12028

Sequence: 1 MLPHRVRCVTPPLRGSAR.....KDTLSLGLSSDPTDMDPZ 2287

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1421835 seqs, 332370683 residues

Total number of hits satisfying chosen parameters: 1421835

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*

2: /cgn2_6/ptodata/2/pubpaa/PTCT_NEW_PUB.pep.*

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4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*

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19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*

20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	11542.5	96.0	2425	10	US-09-383-894-4
2	11532	95.9	2374	10	US-09-383-894-2
3	10806.5	89.8	2243	16	US-10-408-765A-625
4	10732.5	89.2	2377	16	US-10-757-262-16
5	6222	51.7	2353	16	US-10-408-765A-1128
6	5872	48.8	1207	17	US-10-930-301-52
7	5409	45.0	2175	9	US-09-935-541-2
8	5409	45.0	2175	14	US-10-425-800-2
9	5405.5	44.9	2188	9	US-09-935-541-4
10	5405.5	44.9	2188	14	US-10-425-800-4
11	5345	44.4	1835	9	US-09-935-541-5
12	5345	44.4	1835	14	US-10-425-800-5
13	3950	32.8	1853	9	US-09-030-482B-19

14	3553	29.5	1657	15	US-10-369-493-6836	Sequence 6836, Ap
15	1680.5	14.0	2264	15	US-10-627-370-2	Sequence 2, Appli
16	1678	14.0	2343	13	US-10-033-026-4	Sequence 4, Appli
17	1676	13.9	2339	15	US-10-375-253-12	Sequence 12, Appli
18	1674	13.9	2339	13	US-10-033-026-6	Sequence 6, Appli
19	1647.5	13.7	2313	16	US-10-322-696-178	Sequence 178, App
20	1642.5	13.7	2237	15	US-10-375-253-14	Sequence 14, Appli
21	1642.5	13.7	2237	13	US-10-033-026-10	Sequence 10, Appli
22	1640.5	13.6	2237	13	US-10-033-026-8	Sequence 8, Appli
23	1638	13.6	2251	15	US-10-375-253-38	Sequence 40, Appli
24	1637.5	13.6	2270	15	US-10-375-253-40	Sequence 84, Appli
25	1636	13.6	2251	16	US-10-322-696-84	Sequence 176, App
26	1635.5	13.6	2270	16	US-10-322-696-176	Sequence 10, Appli
27	1634.5	13.6	2270	10	US-09-457-571-10	Sequence 10, Appli
28	1631	13.6	2181	13	US-10-029-413A-18	Sequence 18, Appli
29	1631	13.6	2181	13	US-10-029-413A-20	Sequence 20, Appli
30	1631	13.6	2181	14	US-10-205-823-50	Sequence 50, Appli
31	1631	13.6	2181	13	US-10-411-010-29	Sequence 29, Appli
32	1631	13.6	2181	16	US-10-322-696-54	Sequence 54, Appli
33	1631	13.6	2181	17	US-10-953-264-29	Sequence 29, Appli
34	1630.5	13.6	2166	13	US-10-029-413A-4	Sequence 4, Appli
35	1628	13.5	1873	13	US-10-029-413A-22	Sequence 22, Appli
36	1625.5	13.5	1989	10	US-09-457-571-12	Sequence 12, Appli
37	1618	13.5	2141	17	US-10-875-892-4	Sequence 4, Appli
38	1617.5	13.4	1969	10	US-09-457-571-16	Sequence 16, Appli
39	1617	13.4	2161	15	US-10-375-253-2	Sequence 2, Appli
40	1614.5	13.4	1977	10	US-09-919-039-367	Sequence 367, App
41	1614	13.4	2161	17	US-10-875-892-6	Sequence 6, Appli
42	1607	13.4	1745	15	US-10-627-370-4	Sequence 4, Appli
43	1599	13.3	1815	17	US-10-856-122-22	Sequence 22, Appli
44	1598.5	13.3	2016	16	US-10-632-342-2	Sequence 2, Appli
45	1598.5	13.3	2016	16	US-10-632-342-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1

US-09-383-894-4
; Sequence 4, Application US/09383894
; Publication No. US20030125269A1
; GENERAL INFORMATION:
; APPLICANT: Li, Ming
; TITLE OF INVENTION: T-Type Calcium Channel
; FILE REFERENCE: 004.00191
; CURRENT APPLICATION NUMBER: US/09/383.894
; CURRENT FILING DATE: 1999-08-26
; EARLIER APPLICATION NUMBER: US 60/098.004
; EARLIER FILING DATE: 1998-08-26
; EARLIER APPLICATION NUMBER: US 60/117.399
; EARLIER FILING DATE: 1999-01-27
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; TYPE: PRT
; LENGTH: 2425
; ORGANISM: Rattus sp.
US-09-383-894-4

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						Gaps	4
Qy	3	PHRVRCVTPPLRGSARPSDPPGRLARGWTRRRMERAPRSRDSVARS	-----	54			
Db	21	PTGVPLREDTSLEGRSLFGPGAPAG	-----	QRWDEEDGAGEESGQPSFTQ	72		
Qy	55	-STTCPGFGAAGSGTEKDPGSDADSEAGLPYPALAPVFFYLSQDSRRSWCLRTVCNP	113				
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Db	73	LNLSGAGRGQPGSGTEKDPGSDADSEAGLPYPALAPVFFYLSQDSRRSWCLRTVCNP	132				
Qy	114	WFRVSMVLIVCNVTILGMERPCEDICDSORCILQAFDDFIAPFAFVEMVVKWALGI	173				

Db 133 WFERVSNLVLLNCVTLGMFRPCEDTACDSQRILQAFDDFIFFAFVAVMVKWVALGI 192
Qy 174 FGKKCYLGDWNRLLDFEVIAGLMLEYSLDLQNVFSFSAVTRVLRPLRAINRVPMSRILV 233
Db 193 FGKKCYLGDWNRLLDFEVIAGLMLEYSLDLQNVFSFSAVTRVLRPLRAINRVPMSRILV 252
Qy 234 TLLDLDLPLMGNVLLLCFFVFFIFIGVQVLMAGLNRNCFIPENFSLVDLPEYQY 293
Db 253 TLLDLDLPLMGNVLLLCFFVFFIFIGVQVLMAGLNRNCFIPENFSLVDLPEYQY 312
Qy 294 ENEDESFFICQRENGMRCRSPVTLRGEGGGPPCSLDYETYNSSNTTCVNNQY 353
Db 313 ENEDESFFICQRENGMRCRSPVTLRGEGGGPPCSLDYETYNSSNTTCVNNQY 372
Qy 354 NCSAGHNPKGAINFONIGYAMIAIPQVITLGGWVDIMYFVMDAHSFYNFIYFILLIIV 413
Db 373 NCSAGHNPKGAINFONIGYAMIAIPQVITLGGWVDIMYFVMDAHSFYNFIYFILLIIV 432
Qy 414 GSFFMINCLVVIATQFSETKQRESQLMRQVRFLSNASTLASFEPGSCYEELKYL 473
Db 433 GSFFMINCLVVIATQFSETKQRESQLMRQVRFLSNASTLASFEPGSCYEELKYL 492
Qy 474 YILKAARRLAQVSRAGLSSPVARSQGOBOPSGCTSRHRLSLVHLVHHHHH 533
Db 493 YILKAARRLAQVSRAGLSSPVARSQGOBOPSGCTSRHRLSLVHLVHHHHH 552
Qy 534 HHHYHLNGTLVRPRASPEIQDRDANGSRRLMLPPSTPTPPSGPPRGASVHSFYHADC 593
Db 553 HHHYHLNGTLVRPRASPEIQDRDANGSRRLMLPPSTPTPPSGPPRGASVHSFYHADC 612
Qy 594 HLEPVRCAOPPCPSEASGRTVSGKYPVHTSPPEILKOKALVEVAPSGPPTLTS 653
Db 613 HLEPVRCAOPPCPSEASGRTVSGKYPVHTSPPEILKOKALVEVAPSGPPTLTS 672
Qy 654 FNIIPGPSSMHKLEITQSTGACHSSCKISPPCKADSGACGPDSCYCARAGAGEPESA 713
Db 673 FNIIPGPSSMHKLEITQSTGACHSSCKISPPCKADSGACGPDSCYCARAGAGEPESA 732
Qy 714 DHVMPDSDSEAVYETQDAQHSIDLDPHSRRRQSLGDAEPSSVLAFWRLICDTPRKIV 773
Db 733 DHVMPDSDSEAVYETQDAQHSIDLDPHSRRRQSLGDAEPSSVLAFWRLICDTPRKIV 792
Qy 774 DSKYFGRGIMAILNVTLSMGIEYHEQPEELTNALEISNIVFTSLFALEMLLKVYGP 833
Db 793 DSKYFGRGIMAILNVTLSMGIEYHEQPEELTNALEISNIVFTSLFALEMLLKVYGP 852
Qy 834 GYIKNPYNIFDGVIVVISWEIVGQGGGLSVLRTFRLMRVLKLVRFJALQROLVLMK 893
Db 853 GYIKNPYNIFDGVIVVISWEIVGQGGGLSVLRTFRLMRVLKLVRFJALQROLVLMK 912
Qy 894 TMDNATFCMLLMLEIFISILGMLFGCKFASERDGTLPDRKNFDSLLWALVTVFQIL 953
Db 913 TMDNATFCMLLMLEIFISILGMLFGCKFASERDGTLPDRKNFDSLLWALVTVFQIL 972
Qy 954 TQEDWNKVLNGMASTSSWAALYFIALMTFGNYVLFNLLVAILVGGPOAE----- 1003
Db 973 TQEDWNKVLNGMASTSSWAALYFIALMTFGNYVLFNLLVAILVGGPOAE----- 1032
Qy 1004 -----GDATKSEBPDFSPVDCGDKKELALVALGEHAELKSLPLLI 1050
Db 1033 QLSICQLPVNSQGDATKSEBPDFSPVDCGDKKELALVALGEHAELKSLPLLI 1092
Qy 1051 IHTAATPMGHPKSSSTGVGEALGSGSRRTSSGSAEPGAAHEMKCPPSARSSPHSWA 1110
Db 1093 IHTAATPMGHPKSSSTGVGEALGSGSRRTSSGSAEPGAAHEMKCPPSARSSPHSWA 1152
Qy 1111 ASSWTSRRSRNLSGRAPSLKRPSGERRSLISGEGQSEDESEEDRASPGSDHR 1170
Db 1153 ASSWTSRRSRNLSGRAPSLKRPSGERRSLISGEGQSEDESEEDRASPGSDHR 1212
Qy 1171 HRGSLEREAKSFDPDPTLQVPGILHRTASGRSSASEHQCNGKSGASGRILARTLRD 1230
Db 1213 HRGSLEREAKSFDPDPTLQVPGILHRTASGRSSASEHQCNGKSGASGRILARTLRD 1272

Qy 1231 DGGDDNDEGNLSKGERIOAWVRSLPACCRERDSWSAYIFPPQSRFLLCHRIITHOMFD 1290
Db 1273 DGGDDNDEGNLSKGERIOAWVRSLPACCRERDSWSAYIFPPQSRFLLCHRIITHOMFD 1332
Qy 1291 HVLVIIIFLNCITITAMERPKIDPHSABRIIFLTISNYIFTAVFLAEMTVKVVALGWC 1350
Db 1333 HVLVIIIFLNCITITAMERPKIDPHSABRIIFLTISNYIFTAVFLAEMTVKVVALGWC 1392
Qy 1351 AYLRSSWNVDGLVLSVIDILVSMVSDSGTKILGMLRVLRLLRTPRVRVISAQGLK 1410
Db 1393 AYLRSSWNVDGLVLSVIDILVSMVSDSGTKILGMLRVLRLLRTPRVRVISAQGLK 1452
Qy 1411 LWETLMSLXIPGINIVVICCAFFIIFGILGVQLFKGFFVCOGEDPRNITNKSDCABAS 1470
Db 1453 LWETLMSLXIPGINIVVICCAFFIIFGILGVQLFKGFFVCOGEDPRNITNKSDCABAS 1512
Qy 1471 YRVRHKYNFNLGQALMSLFLVSLASKDGDWIMYDGLDVGVDQOQPMNHNPMWLLYFIS 1530
Db 1513 YRVRHKYNFNLGQALMSLFLVSLASKDGDWIMYDGLDVGVDQOQPMNHNPMWLLYFIS 1572
Qy 1531 FLLIVAFVFLMVFVNVVENFHKCRQHOEBEAREERREKRLRLEKKRR----- 1579
Db 1573 FLLIVAFVFLMVFVNVVENFHKCRQHOEBEAREERREKRLRLEKKRR----- 1632
Qy 1580 SKEKQMAEAOQCKPYYSYDSYRFRLLVHHLCTSHYLDLFTITVIGLVNVTMAMEHYQO 1639
Db 1633 SSASAASEAOQCKPYYSYDSYRFRLLVHHLCTSHYLDLFTITVIGLVNVTMAMEHYQO 1692
Qy 1640 DEALKICNYIFTVIFVFSVFKLVAFARFRFQDRWNOLDLAILVLSIMGTLEBIEVNL 1699
Db 1693 DEALKICNYIFTVIFVFSVFKLVAFARFRFQDRWNOLDLAILVLSIMGTLEBIEVNL 1752
Qy 1700 SLPIINPTIIRMRVLRIRARVLKLVQAVCMRALHTVMOALPOVGNLGLLFWLFFIAA 1759
Db 1753 SLPIINPTIIRMRVLRIRARVLKLVQAVCMRALHTVMOALPOVGNLGLLFWLFFIAA 1812
Qy 1760 LGVELFGDLECDETHPCGELGRHATFRNFGMAFLTFRVSTGDNWNGIMKDPSPRDCDOES 1819
Db 1813 LGVELFGDLECDETHPCGELGRHATFRNFGMAFLTFRVSTGDNWNGIMKDPSPRDCDOES 1872
Qy 1820 TCNTVTISPIYFVSFVLTAQFVLNVNVIAMKMLEESNKEAKEAEAELEEMKTL 1879
Db 1873 TCNTVTISPIYFVSFVLTAQFVLNVNVIAMKMLEESNKEAKEAEAELEEMKTL 1932
Qy 1880 PQPHSPLGSPFLMPGVEGVNSTDSPKPGAPHTTAHGAASGFSLEHPTMVPHPEVPVL 1939
Db 1933 PQPHSPLGSPFLMPGVEGVNSTDSPKPGAPHTTAHGAASGFSLEHPTMVPHPEVPVL 1992
Qy 1940 GPDLLTVRKSGVSRTHSLPNDSTYMCNNGSTABERSLGHRCWGLPKAQSGSILSVHSPADT 1999
Db 1993 GPDLLTVRKSGVSRTHSLPNDSTYMCNNGSTABERSLGHRCWGLPKAQSGSILSVHSPADT 2052
Qy 2000 SCITLQPKDVHYLLQPHGAPTWGAIIPKLPPGSPPLAQRLRQAAIRTDSDVQGLGR 2059
Db 2053 SCITLQPKDVHYLLQPHGAPTWGAIIPKLPPGSPPLAQRLRQAAIRTDSDVQGLGR 2112
Qy 2060 EDLLSEVSGSPCDITRSSSFWGSSITQVORSGIQSKVSKHRLPAPCPGLEPSWAKOPP 2119
Db 2113 EDLLSEVSGSPCDITRSSSFWGSSITQVORSGIQSKVSKHRLPAPCPGLEPSWAKOPP 2172
Qy 2120 ETRSSLELDTLSELSGDLPLPSSQEBPLFPRDLKCKYCVETQSCRRRPGFWLDEQRHSI 2179
Db 2173 ETRSSLELDTLSELSGDLPLPSSQEBPLFPRDLKCKYCVETQSCRRRPGFWLDEQRHSI 2232
Qy 2180 AVSCLDSSGSPRILCPSPSSILGGQPLGPGSPRKKLSPPSISIDDPESQSGSRPPCPGVC 2239
Db 2233 AVSCLDSSGSPRILCPSPSSILGGQPLGPGSPRKKLSPPSISIDDPESQSGSRPPCPGVC 2292
Qy 2240 LRRRAPASDKDPVSVSPFLDSTAASPSPKKDTLSLSGLSSDPTDMDP 2286
Db 2293 LRRRAPASDKDPVSVSPFLDSTAASPSPKKDTLSLSGLSSDPTDMDP 2339

RESULT 2

US-09-383-894-2

; Sequence 2, Application US/09383894

; Publication No. US20030125269A1

; GENERAL INFORMATION:

; APPLICANT: Li, Ming

; TITLE OF INVENTION: T-Type Calcium Channel

; FILE REFERENCE: 004.00191

; CURRENT APPLICATION NUMBER: US/09/383.894

; CURRENT FILING DATE: 1999-08-26

; EARLIER APPLICATION NUMBER: US 60/098.004

; EARLIER FILING DATE: 1998-08-26

; EARLIER APPLICATION NUMBER: US 60/117.399

; EARLIER FILING DATE: 1999-01-27

; NUMBER OF SEQ ID NOS: 11

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 2

; LENGTH: 2374

; TYPE: PRT

; ORGANISM: Rattus sp.

US-09-383-894-2

Query Match 95.9%; Score 11532; DB 10; Length 2374;

Best Local Similarity 97.7%; Pred. No. 0;

Matches 2206; Conservative 1; Mismatches 18; Indels 34; Gaps 2;

Qy	62	GAAGAGSTEDKPGSADSEAGLPYPALAPVVFYLSQDSRPSRCLRTVCNPNPFRVSM	121
Db	30	GRQPGSTEDKPGSADSEAGLPYPALAPVVFYLSQDSRPSRCLRTVCNPNPFRVSM	89
Qy	122	VILLNCVTLMGFRCEDIACDSQRCRILOAFDDIFAFFAVEMVQVVALGIFKCKYLG	181
Db	90	VILLNCVTLMGFRCEDIACDSQRCRILOAFDDIFAFFAVEMVQVVALGIFKCKYLG	149
Qy	182	DTWNRDFFVIAGMLYSLDLQNVFSVAVTAVLPLRAINRVPSMRILVLLDTLP	241
Db	150	DTWNRDFFVIAGMLYSLDLQNVFSVAVTAVLPLRAINRVPSMRILVLLDTLP	209
Qy	242	MLGNVLLCFFVFFIFGIVGVLWAGLLRNCFLPENFSLPSVDLBPYYQTENEDSPF	301
Db	210	MLGNVLLCFFVFFIFGIVGVLWAGLLRNCFLPENFSLPSVDLBPYYQTENEDSPF	269
Qy	302	ICSQPRENGHRSRCSVPTLRGEGGGPPCSLDYETYNSSNTTCVNNQYTYNCAGEHN	361
Db	270	ICSQPRENGHRSRCSVPTLRGEGGGPPCSLDYETYNSSNTTCVNNQYTYNCAGEHN	329
Qy	362	PFKGAIPNDNIGYAWIAIFOVITLEGWVDIMYFVMDAHSFYNRTYFILLIIVGSFFMINL	421
Db	330	PFKGAIPNDNIGYAWIAIFOVITLEGWVDIMYFVMDAHSFYNRTYFILLIIVGSFFMINL	389
Qy	422	CLVVIATQFSETKQRESQMRQVRFLSNASTLASFPSCGYEEELKLVILYLRKAAR	481
Db	390	CLVVIATQFSETKQRESQMRQVRFLSNASTLASFPSCGYEEELKLVILYLRKAAR	449
Qy	482	RLAQVSAIGVRAGLSSPVARSQEPQSGCTRSRRRLSVHLLVHHHHHHHHYHLGN	541
Db	450	RLAQVSAIGVRAGLSSPVARSQEPQSGCTRSRRRLSVHLLVHHHHHHHHYHLGN	509
Qy	542	GTLRVPRASPEIQDRDANGSRRLMLPPSTPTPSGGPPRGAEVSHSFVHADCHLEPVRCQ	601
Db	510	GTLRVPRASPEIQDRDANGSRRLMLPPSTPTPSGGPPRGAEVSHSFVHADCHLEPVRCQ	569
Qy	602	APPPRCSEASGRVTSKGVYPTVHTSPPPPEILKDKALVEVAPSGPPTLTSFNIPPGPF	661
Db	570	APPPRCSEASGRVTSKGVYPTVHTSPPPPEILKDKALVEVAPSGPPTLTSFNIPPGPF	629
Qy	662	SSMHKLLTOSTGACHSCKISSPCSKADGACGPDSCPYCARTGAGEPSADHVPDSD	721
Db	630	SSMHKLLTOSTGACHSCKISSPCSKADGACGPDSCPYCARTGAGEPSADHVPDSD	689
Qy	722	SEAVYEFTQAOHSDLRDPHSRRORSIGPDAEPSSVLAFWRLICDTFRKIVDSKYFGRG	781

Db	690	SEAVYEFTQAOHSDLRDPHSRRORSIGPDAEPSSVLAFWRLICDTFRKIVDSKYFGRG	749
Qy	782	IMTIALVNTLSMGIEYHEQPEELTNALEISNIVFTSLFALEMLKLLVYGPFGYKNPYN	841
Db	750	IMTIALVNTLSMGIEYHEQPEELTNALEISNIVFTSLFALEMLKLLVYGPFGYKNPYN	809
Qy	842	IFDGVIIVISWEIVGQGGGLSVLRTFRLMRVLKLYRFLPALQROQLVLMKTDNVAIF	901
Db	810	IFDGVIIVISWEIVGQGGGLSVLRTFRLMRVLKLYRFLPALQROQLVLMKTDNVAIF	869
Qy	902	CMLLMLFIFIFSLGMLHFGCKPASERDGDTLPDRKNFDSLWAIWTVFQILLTOEDWNKV	961
Db	870	CMLLMLFIFIFSLGMLHFGCKPASERDGDTLPDRKNFDSLWAIWTVFQILLTOEDWNKV	929
Qy	962	LYNGMASTSSWAALYFIALMTFGNYVLFNLLVAILVEGFOAE-----	1003
Db	930	LYNGMASTSSWAALYFIALMTFGNYVLFNLLVAILVEGFOAEETGKREDASGQLSCIPL	989
Qy	1004	-----GDATKSESEPDFSPVDGDKRKRLLALVALGEHAELRKSLLPPLIIHTAATPM	1058
Db	990	VNSQGGDATKSESEPDFSPVDGDKRKRLLALVALGEHAELRKSLLPPLIIHTAATPM	1049
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Db	1050	SLPKSSTGVGEALGSGSRRTSSGSAEPGAHHEMKCPPSARSSPHSPMSAASWTSRR	1109
Qy	1119	SSRNSLGRAPSLKRRSPGERRLLSGEGQESODEESSBEDRASPGSDHRRHGSLERE	1178
Db	1110	SSRNSLGRAPSLKRRSPGERRLLSGEGQESODEESSBEDRASPGSDHRRHGSLERE	1169
Qy	1179	AKSSFDPDPTLOVPGHLRTASGRSSASEHODCKGKSAGRLARTLRTDDOLDGDDNDE	1238
Db	1170	AKSSFDPDPTLOVPGHLRTASGRSSASEHODCKGKSAGRLARTLRTDDOLDGDDNDE	1229
Qy	1239	GNLSKGERIQAWVRSLPACCRERDSMSAIFFPQSRFLLCHRIITHKMFHDVVLVIF	1298
Db	1230	GNLSKGERIQAWVRSLPACCRERDSMSAIFFPQSRFLLCHRIITHKMFHDVVLVIF	1289
Qy	1299	LCNITIAMERPKIDPHSAERIIFLTLSNYIFTAVPLAEMTVKVVALGCFGEQAYLRSSN	1358
Db	1290	LCNITIAMERPKIDPHSAERIIFLTLSNYIFTAVPLAEMTVKVVALGCFGEQAYLRSSN	1349
Qy	1359	VLGGLLVLSVIDILVSMVSDSGTKILGMLRVLRLLTLRPLRVISRAQGLKVVELTMS	1418
Db	1350	VLGGLLVLSVIDILVSMVSDSGTKILGMLRVLRLLTLRPLRVISRAQGLKVVELTMS	1409
Qy	1419	SLKPIGNIIVICCAFFIIFGILGVQLFKGFFVCGQEDTRNITNKSDCAEASYRWVRHKY	1478
Db	1410	SLKPIGNIIVICCAFFIIFGILGVQLFKGFFVCGQEDTRNITNKSDCAEASYRWVRHKY	1469
Qy	1479	NFDNLGQALMSLVLASQGWVDIMYDGLDAGVDQGPIMNHNPMWLLYFISFLLIIVAFP	1538
Db	1470	NFDNLGQALMSLVLASQGWVDIMYDGLDAGVDQGPIMNHNPMWLLYFISFLLIIVAFP	1529
Qy	1539	VLANMFVGVVFNHFKCHQHOEEAEAREEKKRLRLEKKR-----SKEQMAE	1587
Db	1530	VLANMFVGVVFNHFKCHQHOEEAEAREEKKRLRLEKKR-----SKEQMAE	1589
Qy	1588	AQCKPYYSYDSRFRLLVHLLCTSHYLDLFTIGVLNVVWAMEHYQOQOTILDALKICN	1647
Db	1590	AQCKPYYSYDSRFRLLVHLLCTSHYLDLFTIGVLNVVWAMEHYQOQOTILDALKICN	1649
Qy	1648	YIFTVIVFVSFVKLVAFARFRFFQDRWNOLDLAILVLLSIMGITLSEIEVNLSPINPTI	1707
Db	1650	YIFTVIVFVSFVKLVAFARFRFFQDRWNOLDLAILVLLSIMGITLSEIEVNLSPINPTI	1709
Qy	1708	IRIMRVLRIRARVLKLLKMAVGMALLHTVMQALPOVGNLGLLFPIFAALGVELFGD	1767
Db	1710	IRIMRVLRIRARVLKLLKMAVGMALLHTVMQALPOVGNLGLLFPIFAALGVELFGD	1769
Qy	1768	LECDETHPCBGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMKDPDRCDQESTCYNTVIS	1827
Db	1770	LECDETHPCBGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMKDPDRCDQESTCYNTVIS	1829

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QY 1828 PIYFVSFLTAQVFLVNNVIAVLKHLERSNKEAELEAELEMKTLSPQHPSLG 1887
Db 1830 PIYFVSFLTAQVFLVNNVIAVLKHLERSNKEAELEAELEMKTLSPQHPSLG 1889
QY 1888 SPFLWPGVEGVNSTGDPKPGAPHTTAHGAAGSFLSLEHPTWPHPEVPVPLGPDLLTVR 1947
Db 1890 SPFLWPGVEGVNSTGDPKPGAPHTTAHGAAGSFLSLEHPTWPHPEVPVPLGPDLLTVR 1949
QY 1948 KSGVSRTHSLPNDSYMCRNGSTAESRGLHGRGWGLPKAQSGSILSVHSQPADTSCILQLPK 2007
Db 1950 KSGVSRTHSLPNDSYMCRNGSTAESRGLHGRGWGLPKAQSGSILSVHSQPADTSCILQLPK 2009
QY 2008 DVHYLLQPHGAPTGAIPKLPGRSPLAORPLRROAAITDSDVQGLGSRREDLSEVS 2067
Db 2010 DVHYLLQPHGAPTGAIPKLPGRSPLAORPLRROAAITDSDVQGLGSRREDLSEVS 2069
QY 2068 GPSCLTRSSSFWGGSSIQVQORSIGQSKVSKHIRLPAPCPGLEPSWAKDPPETRSSLEL 2127
Db 2070 GPSCLTRSSSFWGGSSIQVQORSIGQSKVSKHIRLPAPCPGLEPSWAKDPPETRSSLEL 2129
QY 2128 DTLSWISGDLPLSSQEEPLFPRDLKCYSVETQSCRRRPGFWLDEORHSIAVSCLDG 2187
Db 2130 DTLSWISGDLPLSSQEEPLFPRDLKCYSVETQSCRRRPGFWLDEORHSIAVSCLDG 2189
QY 2188 SQPLCPSPSLGGQPLGGGSRPKKLSPPSISIDPPESQSGRRPPCSGVCVCLRRRAPAS 2247
Db 2190 SQPLCPSPSLGGQPLGGGSRPKKLSPPSISIDPPESQSGRRPPCSGVCVCLRRRAPAS 2249
QY 2248 DSKDPSVSSPLDSTAASFPKKTLSLSGLSSDPTMDP 2286
Db 2250 DSKDPSVSSPLDSTAASFPKKTLSLSGLSSDPTMDP 2288

RESULT 3
US-10-408-765A-625
; Sequence 625, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Faly, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Waddock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 625
; LENGTH: 2243
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-625

Query Match 89.8%; Score 10806.5; DB 16; Length 2243;
Best Local Similarity 93.3%; Pred. No. 0;
Matches 2076; Conservative 33; Mismatches 104; Indels 13; Gaps 5;

QY 62 GAAAGAGTEKDPGSADEAGLPPALAPVVFVYLSQDSRPRSCVCLRTVCNPFWRYSML 121
Db 30 GRPGGSAEKDPGSADEAGLPPALAPVVFVYLSQDSRPRSCVCLRTVCNPFWRYSML 89

QY 122 VILLNCVTLGMRPCEDIACDSQRILQAFDDTIFAFVAVMVVMVAVGIFPKCYLG 181
Db 90 VILLNCVTLGMRPCEDIACDSQRILQAFDDTIFAFVAVMVVMVAVGIFPKCYLG 149

QY 182 DTWNRDLFFIATAGMLEYSLDLQNVFSFSAVTRVRLRLRAINRVPSMRILVTLTLLDTP 241

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Db 150 DTWNRDLFFIATAGMLEYSLDLQNVFSFSAVTRVRLRLRAINRVPSMRILVTLTLLDTP 209
QY 242 MLGNVLLLCFFVFFIFGIVGVLWAGLLNRNCFLENFSLPLSVLDLEPYQTEDESEFP 301
Db 210 MLGNVLLLCFFVFFIFGIVGVLWAGLLNRNCFLENFSLPLSVLDLEPYQTEDESEFP 269
QY 302 ICSPRENGMRSRCSVPTLRGEGGGPPCSDLYETYNSSNTTCVNMNQYTYNCAGEHN 361
Db 270 ICSPRENGMRSRCSVPTLRGEGGGPPCGLDYEAYNSSNTTCVNMNQYTYNCAGEHN 329
QY 362 PFKGAINFDNIGYANIAIIFOVITLISGWDIMYFVMDAHSFYNFIFILLIIVGSPFMINL 421
Db 330 PFKGAINFDNIGYANIAIIFOVITLISGWDIMYFVMDAHSFYNFIFILLIIVGSPFMINL 389
QY 422 CLVVIATQSETKQESQLMRQVRFLSNASTLASFSEPGSCYBELLYVILRKAAR 481
Db 390 CLVVIATQSETKQESQLMRQVRFLSNASTLASFSEPGSCYBELLYVILRKAAR 449
QY 482 RLQAQVSRAITGVRAGLLSPPVARSGQPSGCTSHRRRLSVHHLVHHHHHHHHYHLGN 541
Db 450 RLQAQVSRAAGVRVGLLSPPAPLGGQETQPSSCSRSHRRRLSVHHLVHHHHHHHHYHLGN 509
QY 542 GTLRVPASPEIOTDRDANGSRRLMLPPSTPTPGPPRGAESVHSFYHADCHLEPVRQ 601
Db 510 GTLRVPASPEIOTDRDANGSRRLMLPPSTPALSGAPPGGAESVHSFYHADCHLEPVRQ 569
QY 602 APPRCPSEASGRTVGSGKYPTVHTSPPPEILKOKALVEVAPSPGPPTLTLSNIPPGPF 661
Db 570 APPRCPSEASGRTVGSGKYPTVHTSPPPEILKOKALVEVAPSPGPPTLTLSNIPPGPF 629
QY 662 SSMHKLETTOSTGACHSSCKISSPCKADSGAGDDSCPCYCATGAGEPESADHVPDSD 721
Db 630 SSMHKLETTOSTGACHSSCKISSPCKADSGAGDDSCPCYCATGAGEPESADHVPDSD 689
QY 722 SEAVYFTODAOHSDLRDPHSRRRORSIGDPDAEPSSVLAFWRLICDTFRKI VDSKYFGRG 781
Db 690 SEAVYFTODAOHSDLRDPHSRRRORSIGDPDAEPSSVLAFWRLICDTFRKI VDSKYFGRG 748
QY 782 IMIAILVNTLSMGIEYHEQPEELTNALEISNIVFTLSFALEMLKLLVTVGPGYIKNPYN 841
Db 749 IMIAILVNTLSMGIEYHEQPEELTNALEISNIVFTLSFALEMLKLLVTVGPGYIKNPYN 808
QY 842 IFDGVIVISWWEIVGQGGGLSVLRTFRLMRVLKLVRELPALOROLVLMKTMNDVATF 901
Db 809 IFDGVIVISWWEIVGQGGGLSVLRTFRLMRVLKLVRELPALOROLVLMKTMNDVATF 868
QY 902 CMLLMFIFITFSLGMLHFCCKFASERDGTLPDRKNFDSLWAIIVTFQILTQEDWNKV 961
Db 869 CMLLMFIFITFSLGMLHFCCKFASERDGTLPDRKNFDSLWAIIVTFQILTQEDWNKV 928
QY 962 LYNMGMASTSSWAALYFIALMTFGNYVLFNLLVAILVEGQAEQDADATKSESEPPFSPVD 1021
Db 929 LYNMGMASTSSWAALYFIALMTFGNYVLFNLLVAILVEGQAEQDADATKSESEPPFSPVD 988
QY 1022 GDGRKKRLALVALGEHAEIRKSLPLIHTAATPMWPKSSSTGVGAALGSGSRRTSS 1081
Db 989 GDGRKKRLALVALGEHAEIRKSLPLIHTAATPMWPKSSSTGVGAALGSGSRRTSS 1048
QY 1082 SGSAEPGAHHEMKCPSPSARSSPHSPWSAASSWTSSRRNSLGRAPSLKRRSPSGERRS 1141
Db 1049 SGSAEPGAHHEMKCPSPSARSSPHSPWSAASSWTSSRRNSLGRAPSLKRRSPSGERRS 1107
QY 1142 LLSGEGQESQDESESEEDRASPAGSDHRRHRSGLERAKSSFDLPDTLQVPGHRTASGR 1201
Db 1108 LLSGEGQESQDESESESEEDRASPAGSDHRRHRSGLERAKSSFDLPDTLQVPGHRTASGR 1167
QY 1202 SSASEHQCNGKSGASGRARTLTDDPDQDGDNDDEGNLSKGERIQAWVRSLPACCRE 1261
Db 1168 GSASEHQCNGKSGASGRARTLTDDPDQDGDNDDEGNLSKGERIQAWVRSLPACCRE 1227
QY 1262 RDSWSAYIFPPQSRFRLLCHRIITHKMFHDHVLVILFNCITTIAMERPKIDPHSAERIFL 1321
Db 1228 RDSWSAYIFPPQSRFRLLCHRIITHKMFHDHVLVILFNCITTIAMERPKIDPHSAERIFL 1287

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Qy 1322 TLSNYIFTAVFLAMTVMKVVVALGWCFCGEQAYLRSSNVNVLGGLLVLIISVIDILVSMVSDSG 1381
Db 1288 TLSNYIFTAVFLAMTVMKVVVALGWCFCGEQAYLRSSNVNVLGGLLVLIISVIDILVSMVSDSG 1347
Qy 1382 TKILGMLRVLRLLRTLRLPLRVISRAOGLKLVVETLMSLKPIGNIVVICAFFIIFGILG 1441
Db 1348 TKILGMLRVLRLLRTLRLPLRVISRAOGLKLVVETLMSLKPIGNIVVICAFFIIFGILG 1407
Qy 1442 VOLFKGFFVQCQEDTRNITNKSCABASYRWVRHKYNFNLGQALMSLFLVASKOGWVD 1501
Db 1408 VOLFKGFFVQCQEDTRNITNKSCABASYRWVRHKYNFNLGQALMSLFLVASKOGWVD 1467
Qy 1502 IMYDGLDAVGVDQOPIINHPNMLLYIFISLLIIVAFVFLNMVFCVVVFENHFKCRQOHEE 1561
Db 1468 IMYDGLDAVGVDQOPIINHPNMLLYIFISLLIIVAFVFLNMVFCVVVFENHFKCRQOHEE 1527
Qy 1562 EARRREKRRLRLEKREKREKQMAEAOCKPYSDYSRFLLVHHLCTSHVLDLFIITGVI 1621
Db 1528 EARRREKRRLRLEKREKREKQMAEAOCKPYSDYSRFLLVHHLCTSHVLDLFIITGVI 1580
Qy 1622 GLNVVTWAMEHYQOQILDEALKICNYIFTVIFVFSVFKLVAFAPRRFFQDRWNQDLA 1681
Db 1581 GLNVVTWAMEHYQOQILDEALKICNYIFTVIFVFSVFKLVAFAPRRFFQDRWNQDLA 1640
Qy 1682 IVLLSINGITLLEEIVNLSIPNPTIIRIMRVLRIRARVLKLLKQAVGMRLALLTVMQALP 1741
Db 1641 IVLLSINGITLLEEIVNLSIPNPTIIRIMRVLRIRARVLKLLKQAVGMRLALLTVMQALP 1700
Qy 1742 QVGNLGLLFWLLPFIIPALGVLELPGDLECDETHCEGLGRHATPRNFGMAFLTIFRVSTG 1801
Db 1701 QVGNLGLLFWLLPFIIPALGVLELPGDLECDETHCEGLGRHATPRNFGMAFLTIFRVSTG 1760
Qy 1802 DNWNGIMKDSRDCQESTCYNTVISPIYFVSFVLTAAQFVLNVNVIIVLAKHLEESKEA 1861
Db 1761 DNWNGIMKDTLRDCQESTCYNTVISPIYFVSFVLTAAQFVLNVNVIIVLAKHLEESKEA 1820
Qy 1862 KEAELEBAELEMLEMTLSPQSPHSPGSPFLWPGEVGNSTSDSPKPGAPHTTAHIGAASGF 1921
Db 1821 KEAELEBAELEMLEMTLSPQSPHSPGSPFLWPGEVGNSTSDSPKPGALHPAAHARSASHF 1880
Qy 1922 SLEHPTVMPHEEVVPVPLGPDLLTVKSGVSRTHSLPNDSTMCRNGSTAESRSLGRCWGL 1981
Db 1881 SLEHPTMQPHTPLP---GPDLLTVKSGVSRTHSLPNDSTMCRNGSTAGSLGHRGWGL 1937
Qy 1982 PKAQSGSILSVHSQFADTSCITLQPKDVHYLLQPHGAPTWGAIPKLPPLPPGSRPLAQRPLR 2041
Db 1938 PKAQSGSVLHVHSQFADTSYILQPKAPHLQPHSAPTWTGTIPKLPPLPPGSRPLAQRPLR 1997
Qy 2042 RQAAIRTDSDVQGLGSRDILLSEVSGPSCPLTRSSSFWGSSITQVQORSGIOSKVSXHI 2101
Db 1998 RQAAIRTDSDVQGLGSRDILLAEVSGSPPLARAYSFWGSSITQAAQOHSRSHSKISXHM 2057
Qy 2102 RLPAAPCPGLPSMAKDPPTRSSLSLELDELTELISWISGDL--PSSOREPLPFDLKKCYSVET 2160
Db 2058 TTPAPCPGPENWGKGPETRSSLSLELDELTELISWISGDLPLPGQBEPPSPRDLKKCYVEA 2117
Qy 2161 QSCRRRPFGLDEQRHRSIAVSCLDGSGQRLCPSPSSLGQPLGGPGSRPKKLSPPSI 2220
Db 2118 QSCORRTSWLDEQRHRSIAVSCLDGSGQHLGTDPSNLGGQPLGGPGSRPKKLSPPSI 2177
Qy 2221 SIDPPESQGRPPCPGVCVLARRAPASDQPSVSSPLDSTAASPPSKKOTLSLSGLSSD 2280
Db 2178 TIDPPESQGRTPSPGICLRRRAPSDDKPLASGPPDSMAASPPSKKQDVLISLSGLSSD 2237
Qy 2281 PTDMDP 2286
Db 2238 PADLOP 2243
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RESULT 4

US-10-757-262-16

; Sequence 16, Application US/10757262

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; Publication No. US20040197825A1
; GENERAL INFORMATION:
; APPLICANT: Karicheti, Venkateswarlu
; APPLICANT: Silos-Santiago, Immaculada
; APPLICANT: Eliasof, Scott D.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: UROLOGICAL DISORDERS USING 44390, 54181, 211, 5687, 884,
; TITLE OF INVENTION: 1405, 636, 4421, 5410, 30905, 2045, 16405, 18560, 2047,
; TITLE OF INVENTION: 33751, 52872, 14063, 20739, 32544, 43239, 44373, 51164,
; TITLE OF INVENTION: 53010, 16852, 1587, 2207, 22245, 2387, 52908, 69112, 14990,
; TITLE OF INVENTION: 18547, 115, 579, 15985, 15625, 760, 18603, 2395, 2554, 8675,
; TITLE OF INVENTION: 32720, 4809, 14303, 16816, 17827, 32620, 577, 619, 1423,
; TITLE OF INVENTION: 2158, 8263, 15402, 16209, 16386, 21165, 30911, 41897, 1643,
; TITLE OF INVENTION: 2543, 9626, 13231, 32409, 84260, 2882, 8203, 32678 OR
; TITLE OF INVENTION: 55053
; FILE REFERENCE: MP103-007PIRNONMIN
; CURRENT APPLICATION NUMBER: US/10/757,262
; CURRENT FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: US 60/440,318
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/444,783
; PRIOR FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: US 60/457,901
; PRIOR FILING DATE: 2003-03-27
; PRIOR APPLICATION NUMBER: US 60/468,775
; PRIOR FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: US 60/471,614
; PRIOR FILING DATE: 2003-05-19
; PRIOR APPLICATION NUMBER: US 60/478,742
; PRIOR FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: US 60/488,529
; PRIOR FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 60/491,156
; PRIOR FILING DATE: 2003-07-30
; PRIOR APPLICATION NUMBER: US 60/499,594
; PRIOR FILING DATE: 2003-09-02
; PRIOR APPLICATION NUMBER: US 60/506,332
; PRIOR FILING DATE: 2003-09-26
; NUMBER OF SEQ ID NOS: 136
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 2377
; TYPE: PRT
; ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens
US-10-757-262-16
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Query Match 89.2%; Score 10732.5; DB 16; Length 2377;
Best Local Similarity 88.3%; Pred. No. 0;
Matches 2078; Conservative 33; Mismatches 109; Indels 133; Gaps 7;
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Qy 62 GAAGAGSTKXDPGSADEAGLPYPALAPVFFYLSQDSRPSRCLRTVCNPNWFERVSM 121
Db 30 GRPGSAEKDPGSADEAGLPYPALAPVFFYLSQDSRPSRCLRTVCNPNWFERISML 89
Qy 122 VILLNCVTLGMPFCEDIACDSORCRILQAFDDFIFAFFAVMVVGVVAGLIFGKKCYLG 181
Db 90 VILLNCVTLGMPFCEDIACDSORCRILQAFDDFIFAFFAVMVVGVVAGLIFGKKCYLG 149
Qy 182 DTWNRLDFFTVIAGMLEYSLDLQNVSPSAVRTVRLRPLRINRVPMSRILVTLTLLDTP 241
Db 150 DTWNRLDFFTVIAGMLEYSLDLQNVSPSAVRTVRLRPLRINRVPMSRILVTLTLLDTP 209
Qy 242 MLGNVLLLCFFVFFIFGIVGVQWAGLLNRCLPENFSLPLSVLDLPYYQTEDESSPF 301
Db 210 MLGNVLLLCFFVFFIFGIVGVQWAGLLNRCLPENFSLPLSVLDLPYYQTEDESSPF 269
Qy 302 ICSPRENGHRSRCSVPTLRGEGGGPCSLDITYNSSNTTTCNNQYNTNCSAGEHN 361
Db 270 ICSPRENGHRSRCSVPTLRGEGGGPCSLDITYNSSNTTTCNNQYNTNCSAGEHN 329
Qy 362 PFKGAINFDNIGVAMIAIFQVITILEGWVDIMYFVMDAHSFYNFYFTILLIIVGSFFMINL 421
Db 330 PFKGAINFDNIGVAMIAIFQVITILEGWVDIMYFVMDAHSFYNFYFTILLIIVGSFFMINL 389
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QY	422	CLVVIATQFSETKORBSQLMREORVFLSNASTLASFPSCYEBLLKYLVIILKKAAR	481
DB	390	CLVVIATQFSETKORBSQLMREORVFLSNASTLASFPSCYEBLLKYLVIILKKAAR	449
QY	482	RLAQVSRAGVRAGLLSSPVARGOPPOPGSGSTRSHRRLSVHLLVHHHHHHHHVHLGN	541
DB	450	RLAQVSRAGVRAGLLSSPVARGOPPOPGSGSTRSHRRLSVHLLVHHHHHHHHVHLGN	509
QY	542	GTLRVPASPEIORDDANGRRMLPPPSTPTSGGPPRCAGAESVHSHFYHADCHLEPVRCQ	601
DB	510	GTLRVPASPEIORDDANGRRMLPPPSTPTSGGPPRCAGAESVHSHFYHADCHLEPVRCQ	569
QY	602	APPRCPSEASGRVTGSKYVPTVHTSPPEILKDKALVEVAPSPGPPTLTSTNIPGPP	661
DB	570	APPRCPSEASGRVTGSKYVPTVHTSPPEILKDKALVEVAPSPGPPTLTSTNIPGPP	629
QY	662	SSMHKLETSQSTGACHSSCKTSSPCSKADSGAGCPDSCPCYACARTGAGEPESADHVPDSD	721
DB	630	SSMHKLETSQSTGACHSSCKTSSPCSKADSGAGCPDSCPCYACARTGAGEPESADHVPDSD	689
QY	722	SEAVYEFTQDAHQSDLRDPHSRRRQSLGPDAPSSVLAFWRLICDTFRKIVDSKYFGRG	781
DB	690	SEAVYEFTQDAHQSDLRDPHSRRRQSLGPDAPSSVLAFWRLICDTFRKIVDSKYFGRG	748
QY	782	IMIAILVNTLSNGIYEHQPELTNALEISNIVFTSLFALEMLKLLVYGFYKPNYN	841
DB	749	IMIAILVNTLSNGIYEHQPELTNALEISNIVFTSLFALEMLKLLVYGFYKPNYN	808
QY	842	IFDGVIIVISWEIVGQGGSLVLRTPRLMRVLKLVRFPLPALORQLVLMKTMNDVATF	901
DB	809	IFDGVIIVISWEIVGQGGSLVLRTPRLMRVLKLVRFPLPALORQLVLMKTMNDVATF	868
QY	902	CMLMLFIFISILGMHLFGCKPASERDGDTLPDRKPFDSLLWAVTVFQILTOEDWNKY	961
DB	869	CMLMLFIFISILGMHLFGCKPASERDGDTLPDRKPFDSLLWAVTVFQILTOEDWNKY	928
QY	962	LYNGWASTSSWAALYFIAMFTFGNVLFNLVAILVEGFOAE	1003
DB	929	LYNGWASTSSWAALYFIAMFTFGNVLFNLVAILVEGFOAE	988
QY	1004	-----GDATKSESEDPFSPVSDGDRKRLALVALGEHAELKSLPPLIIHTAATPM	1058
DB	989	VDSQGGDANKSESEDPFSPVSDGDRKRLALVALGEHAELKSLPPLIIHTAATPM	1048
QY	1059	SHPKSSSTGVEALGSGSRRTSSGSAEPGAHEMKCPPSARSPHSPWAAASWTSSR	1118
DB	1049	SLPKSTSTGLGALGPASRRTSSGSAEPGAHEMKCPPSARSPHSPWAAASWTSSR	1107
QY	1119	SRNSILGRAPSLKRRSPGERRSLLSGEGQESDEESSEEDRASPGSDHRRHGSLERE	1178
DB	1108	SRNSILGRAPSLKRRSPGERRSLLSGEGQESDEESSEEDRASPGSDHRRHGSLERE	1167
QY	1179	AKSSFDLPDQLVPGHLRTASGRSASHODCNGSASGRILARTDPODGDGDDONDE	1238
DB	1168	AKSSFDLPDQLVPGHLRTASGRSASHODCNGSASGRILARTDPODGDGDDONDE	1227
QY	1239	GNLSKGERIQAMVRSRLPACCRSDWSAYIIPPQSRFLLCHRIITHKMFHDVVLVIF	1298
DB	1228	GNLSKGERVIRAMIRAPLACCLERSWSAYIIPPQSRFLLCHRIITHKMFHDVVLVIF	1287
QY	1299	LNCITIAMERPKIDPHASERIFLTISNYIFTAVFIAEMTVKVALGWCFOAYLRSSWN	1358
DB	1288	LNCITIAMERPKIDPHASERIFLTISNYIFTAVFIAEMTVKVALGWCFOAYLRSSWN	1347
QY	1359	VLDGLVILSVIDILVSMVSDSKTLGMLRVLRLRLRLPRLVLSRAQGLKVVELTMS	1418
DB	1348	VLDGLVILSVIDILVSMVSDSKTLGMLRVLRLRLRLPRLVLSRAQGLKVVELTMS	1407
QY	1419	SLKPIGNIVVICCAFFIIFGILGVLFKGFYFCQGEDTRNTNKSDCAEASVWRVHKY	1478
DB	1408	SLKPIGNIVVICCAFFIIFGILGVLFKGFYFCQGEDTRNTNKSDCAEASVWRVHKY	1467

QY	1479	NFDNLGQALMSLFLVASKDQWVDIMYDGLDAVGVDQOQIMNHNPMWMLLYFISFLIIVAF	1538
DB	1468	NFDNLGQALMSLFLVASKDQWVDIMYDGLDAVGVDQOQIMNHNPMWMLLYFISFLIIVAF	1527
QY	1539	VLMFVGVVNFHFKCHQHOEEERREARRERKRLRLEKKR-----SKEKQMAE	1587
DB	1528	VLMFVGVVNFHFKCHQHOEEERREARRERKRLRLEKKR-----SKEKQMAE	1587
QY	1588	AQCKPYTSDYERFLLVHLLCTSHYLDLFTGVIGLVNVTWAMEHYQOQPIQLDEALKICN	1647
DB	1588	AQCKPYTSDYERFLLVHLLCTSHYLDLFTGVIGLVNVTWAMEHYQOQPIQLDEALKICN	1647
QY	1648	YIFTVIFVFESVFKLVAFAPFRFFQDRWNQDLDAIVLLSIMGITIEIEVNLSPINPTI	1707
DB	1648	YIFTVIFVLESVFKLVAFGRFFQDRWNQDLDAIVLLSIMGITIEIEVNLSPINPTI	1707
QY	1708	TRIMEVLRARVLLKLVAVGMRALLHTVMQALPQVGNLGLLPMLLFFIFAALGVLEFGD	1767
DB	1708	TRIMEVLRARVLLKLVAVGMRALLHTVMQALPQVGNLGLLPMLLFFIFAALGVLEFGD	1767
QY	1768	LECDETHPCBGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMKDTLRLDCDQESTCVNTVIS	1827
DB	1768	LECDETHPCBGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMKDTLRLDCDQESTCVNTVIS	1827
QY	1828	PIYFVSFVLTAQFVLVNVVIAVLMKHLSESNKEAEAELEMLEMKTLSPOPHSPUG	1887
DB	1828	PIYFVSFVLTAQFVLVNVVIAVLMKHLSESNKEAEAELEMLEMKTLSPOPHSPUG	1887
QY	1888	SPFLMPGVEGVNSTDSKPKGAPHTTAHIGAAAGSFLSHEPT-----	1927
DB	1888	SPFLMPGVEGVNSTDSKPKGAPHTTAHIGAAAGSFLSHEPT-----	1947
QY	1928	-----KLMDELAPGQGPSAPPSAPSLGSDPQIPLAEMALSITSEIVSEPSCLALTDSDLPD	2007
DB	1928	-----KLMDELAPGQGPSAPPSAPSLGSDPQIPLAEMALSITSEIVSEPSCLALTDSDLPD	1974
QY	2008	DMHTLLLSALESNMOPHTTELP---GPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAERSL	2064
DB	1975	GHRGWLCPKAQSGSLSVHSQPADTSCILQLPKQVHYLLQPHGAPTWGAIPKLPGRSP	2034
QY	2065	GHRGWLCPKAQSGSLSVHSQPADTSCILQLPKQVHYLLQPHGAPTWGAIPKLPGRSP	2124
DB	2035	LAORPLRQAAIRTDSDLVQGLSGREDLLSEVSGSPCLTRSSSFWSGSSIOVQORSQIQ	2094
QY	2125	LAORPLRQAAIRTDSDLVQGLSGREDLLSEVSGSPCLTRSSSFWSGSSIOVQORSQIQ	2153
DB	2095	SKYSKHRLPAPCPGLEPSWAKDPPETRSLSLELDTLSWISGDL--PSSQEBPLFPDRLK	2244
QY	2185	SKYSKHRLPAPCPGLEPSWAKDPPETRSLSLELDTLSWISGDL--PSSQEBPLFPDRLK	2244
DB	2154	KCYSVTQSCRRRPGFWLDEQRHRSIAVSCDLSGSPRLCPSPSSLGSGOPLGGPSRPPK	2213
QY	2245	KCYSVTQSCRRRPGFWLDEQRHRSIAVSCDLSGSPRLCPSPSSLGSGOPLGGPSRPPK	2213
DB	2214	KLSPSSITIDPPSQSRPPSPGVCLRRRAPASDKDPSVSPDLSDTAASPSPKDITLS	2273
QY	2305	KLSPSSITIDPPSQSRPPSPGVCLRRRAPASDKDPSVSPDLSDTAASPSPKDITLS	2273
DB	2274	LSGLSSDPTDMDP 2286	2364
QY	2365	LSGLSSDPTDMDP 2286	2364

RESULT 5
US-10-408-765A-1128
; Sequence 1128, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing


```
Db 1803 RVSTGDNWNGIMKDTTRECREDKHCLSVLPALSPVFTFVLVAQFVLNVVAVLMKH 1862
Qy 1854 LEESNKEAEAELEAELEEMKTLSPQPHSPGLSPFMPGVEGVNSTSPKPGAPHTTA 1913
Db 1863 LEESNKEAREDAELDAIELEMA-----QGPGSARRVDADRP----- 1899
Qy 1914 HIGASGFSLEHTMTWPHPEVPVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTA--- 1970
Db 1900 -----PLPQESPCARDAPNLVARKVSVSRMLSLPNDSYMFRVVPASAP 1943
Qy 1971 -----ERSLGRGWGLPKAQSGSILSVHSOPADTSCILQPKDVH-----YLLQP 2015
Db 1944 HPRPLQEVETVAGTP---LGSVASVHSPRAESCASLQIPLAVSSPARSGEPLHALSP 2000
Qy 2016 HGAPTWGAIPKLPPPGSPSLAQPRLRQAIRTDSDVGLGSRDILLSEV-----SGPSC 2071
Db 2001 RGT-----ARSPSLRLLCQEAHVHTDSLEK-IDSPRDTLDPAPGCKTPVR 2047
Qy 2072 PLTRSSFWGSSLOVQORSGIQSKV--SKH-----IRLPAPCPGLEPSWAKDPPETRS 2123
Db 2048 PVTQ-----GGSLQSPRPRPASVTRKHTFGQHCVSRRPAAPGGEAEASDP----- 2096
Qy 2124 SLELDTLSMTSGDLLP--SSQEEPLFP-----RDLKKCYSVETQSCRRRPGFWLDE 2173
Db 2097 ---ADEEVSHITSSACWQPTAEHPGPEASPVAGGERDLRLYSVDAQGLDKPG-RADE 2152
Qy 2174 QRRHSIAVCLDSGSPRLCPSPSLGGQPLGP--GSRPKKLSPPSISIDPP-BSQGS 2230
Db 2153 QWRPSAE---LGSGE-----PGEAKWG-PEAEFALGARKKKMSPPCISVEPPAEDEGS 2203
Qy 2231 -RPCSQG--VCLARRAPA-----SDSKOPSVSSPLDSTAAS-----PSPKQDTLSL 2274
Db 2204 ARPAAGEGSTLRRRTSPCEATPHRUSLEPTEGSGAGGPPAKGERWGOASCAEHLTV 2263
Qy 2275 SGLSSDPTDM-----DP 2286
Db 2264 PSFAPEPLDLGVPSGDP 2280

RESULT 6
US-10-930-301-52
; Sequence 52, Application US/10930301
; Publication No. US20050026207A1
; GENERAL INFORMATION:
; APPLICANT: Issa, Jean-Pierre
; TITLE OF INVENTION: CACNAIG POLYNUCLEOTIDE POLYPEPTIDE AND
; FILE REFERENCE: JHU1590
; CURRENT APPLICATION NUMBER: US/10/930.301
; CURRENT FILING DATE: 2004-08-30
; PRIOR APPLICATION NUMBER: US/09/398,522
; PRIOR FILING DATE: 1999-09-15
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52
; LENGTH: 1207
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: CACNAIG - a gene encoding a T-type calcium channel
US-10-930-301-52

Query Match 48.8%; Score 5872; DB 17; Length 1207;
Best Local Similarity 95.2%; Pred. No. 0;
Matches 123; Conservative 11; Mismatches 44; Indels 2; Gaps 2;

Qy 62 GAAGAGSTKOPGSDADSEAGLUPYPALAPVVFYFYLQSDSRPSWCLRTVCNPFWRVSM 121
Db 30 GRPGSGAEKDPGSDADSEAGLUPYPALAPVVFYFYLQSDSRPSWCLRTVCNPFWRVSM 89
Qy 122 VLLNCVTLMGFRPCEDIACDSQRILQAFDDFIFAFVAVMVVVKVVALGIFGKCKYLG 181
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Db 90 VLLNCVTLMGFRPCEDIACDSQRILQAFDDFIFAFVAVMVVVKVVALGIFGKCKYLG 149
Qy 182 DTWNELDFFIIVAGMLEYSLDLQNVFSAVTRVLRPLRAINRVPSMILVTLTLLDLP 241
Db 150 DTWNELDFFIIVAGMLEYSLDLQNVFSAVTRVLRPLRAINRVPSMILVTLTLLDLP 209
Qy 242 MLGNVLLCCFFVFFIFIGIVGVLWAGLLRNRCFLPENFSLPLSDVLEPYOTENEDSEFP 301
Db 210 MLGNVLLCCFFVFFIFIGIVGVLWAGLLRNRCFLPENFSLPLSDVLEPYOTENEDSEFP 269
Qy 302 ICSPRENGMSCRVPPTLRGEGGGPCSLDYETYNSSNTTCVNMNYYTNCAGSHN 361
Db 270 ICSPRENGMSCRVPPTLRGEGGGPCSLDYETYNSSNTTCVNMNYYTNCAGSHN 329
Qy 362 PFKGAINFDNIGYAMIAIFQVITTLLEGWVDIMYFVMDAHSFYNYFIILLIIVGSFMINL 421
Db 330 PFKGAINFDNIGYAMIAIFQVITTLLEGWVDIMYFVMDAHSFYNYFIILLIIVGSFMINL 389
Qy 422 CLVVIATQFSETKQRESQLMREQVRFLSNASTLASFPSEPGSCYEELLYVILRKAAR 481
Db 390 CLVVIATQFSETKQRESQLMREQVRFLSNASTLASFPSEPGSCYEELLYVILRKAAR 449
Qy 482 RLAQVSRAGVRAGLLSPPVARSQOPSGSCTSRHRLSVHLLVHHHHHHHHVHLGN 541
Db 450 RLAQVSRAGVRAGLLSPPVARSQOPSGSCTSRHRLSVHLLVHHHHHHHHVHLGN 509
Qy 542 GTLRVPRAPEIQDRDANGSRRLMLPPSTPTPPSGPPRGAESVHSFYHADCHLBPVRQC 601
Db 510 GTLRAPRASPEIQDRDANGSRRLMLPPSTPTPPSGPPRGAESVHSFYHADCHLBPVRQC 569
Qy 602 APPRCPSASQRTVSGSKVYPTVHTSPPELTKOKALVEVAPSPGPTLTSTFNIPPGPF 661
Db 570 APPRCPSASQRTVSGSKVYPTVHTSPPELTKOKALVEVAPSPGPTLTSTFNIPPGPF 629
Qy 662 SSMHKLLETQSTGACHSSCKISSPCSKADSGACDPSCPYCATGAGEPESADHVPDSD 721
Db 630 SSMHKLLETQSTGACHSSCKISSPCSKADSGACDPSCPYCATGAGEPESADHVPDSD 689
Qy 722 SEAVYFTQDAQHSDLRDPHSRRRORSLGPDAPSSVLAFWRLICDTFRKIIVDSKYFGRG 781
Db 690 SEAVYFTQDAQHSDLRDPHS--RRQSLGPDAPSSVLAFWRLICDTFRKIIVDSKYFGRG 748
Qy 782 IMTALVNTLSMGIEVHEQPEELTNALEISNVFTSLFALEMLLLVTVGPGFYKNPNYN 841
Db 749 IMTALVNTLSMGIEVHEQPEELTNALEISNVFTSLFALEMLLLVTVGPGFYKNPNYN 808
Qy 842 IFDGVIVVISWEIVGQGGGLSVLTFRLMRVLLKLVRLPALQROLVVLMTMDNVATF 901
Db 809 IFDGVIVVISWEIVGQGGGLSVLTFRLMRVLLKLVRLPALQROLVVLMTMDNVATF 868
Qy 902 CMLLMFLIFIFSLGMHLFGCKFASERDGTLPDRKNFDSLWAIIVTVFQILTQEDWNKV 961
Db 869 CMLLMFLIFIFSLGMHLFGCKFASERDGTLPDRKNFDSLWAIIVTVFQILTQEDWNKV 928
Qy 962 LYNMGASTSSWAALYFIALMTFGNYVLFNLLVAILVEGQAECDATKSESEDPFSPSVD 1021
Db 929 LYNMGASTSSWAALYFIALMTFGNYVLFNLLVAILVEGQAECDANKSESEDPFSPSLD 988
Qy 1022 GDGDRKRLALVALGHEALRKSLLPLIHTAATPMSPKSSSTGVGEALGSGSRRTSS 1081
Db 989 GDGDRKRLALVALGHEALRKSLLPLIHTAATPMSPKSTSTGLGEALGPASRTSS 1048
Qy 1082 SGAEPCAAHEMKCPSPASRSPHSWASASTWTSRRSNSLGRAPSLKRRSPSGERRS 1141
Db 1049 SGAEPCAA--HEMKSPSPASRSPHSWASASTWTSRRSNSLGRAPSLKRRSPSGERRS 1107
Qy 1142 LLSGEGQESQDEBESSEDESRASPGSDHRRHGRSLEREAKSSFDLPDTLQVPGHLRTASGR 1201
Db 1108 LLSGEGQESQDEBESSEDESRASPGSDHRRHGRSLEREAKSSFDLPDTLQVPGHLRTASGR 1167
Qy 1202 SSASEHQCNGKSGASGRRLATLRTDDPOLDDDDNDEGNL 1241
Db 1168 GSASEHQCNGKSGASGRRLAPALRPDPPLDDDDADDEGNL 1207
```

RESULT 7

US-09-935-541-2
; Sequence 2, Application US/099335541
; Patent No. US2002015091A1
; GENERAL INFORMATION:
; APPLICANT: Dietrich, Paul S.
; APPLICANT: McGovern, Joseph G.
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
; TITLE OF INVENTION: AND USES
; FILE REFERENCE: R0043B-REG sequence listing
; CURRENT APPLICATION NUMBER: US/09/935,541
; CURRENT FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: 09/404,650
; PRIOR FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 2175
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-935-541-2

Query Match 45.08; Score 5409; DB 9; Length 2175;
Best Local Similarity 50.58; Pred. No. 0;
Matches 1225; Conservative 236; Mismatches 513; Indels 450; Gaps 64;

Qy	51	ASRSSTTCPCGAGAGAGSTKDPG--SADSEAEGL-----PYPALAPVVFYLS	97
Db	5	ASPPSSAAAP-AAEPGVTTQCPGPRSPSPGLEPPLDGDADPHVPHDLPIAFCLR	63
Qy	98	QDSRPSWCLRTVCNPFVSMVLVLLNCVTGLGMPFPCSDIACDQRCLIQAFDDIF	157
Db	64	QTTSPRNCIKMVCNPFVSMVLVLLNCVTGLGMPFPCSDIACDQRCLIQAFDDIF	123
Qy	158	AFPAVEMVMKVALGIEGKCYLGDWNRLLDFFVIAGMLEYSLDLQNVFSARVTVRL	217
Db	124	IFPAMENVLMKVALGIEGKCYLGDWNRLLDFFVIAGMLEYSLDLQNVFSARVTVRL	183
Qy	218	RPLRINRVSMLRVLTLDDTLPMLGNVLLCFVFFIFIGIVGQVWAGLLNRCLPE	277
Db	184	RPLKAINRVSMLRVLNLLDTPMLGNVLLCFVFFIFIGIVGQVWAGLLNRCLPE	243
Qy	278	NFLSLVDLEPYQYQTEDESPICSPQRENGMRSCRSVPTLREGGGGPPCSL----	332
Db	244	NFTIQGDVALPPYQYQTEDESPICSLGDNQIMGCHIEPPLKEQ---GRECCLSKDDV	300
Qy	333	-DYETYNSSNTT--CVNNQYITNCAGHNPKGAINEDNIGYAMIAIQTITLEGW	389
Db	301	YDFGAGRQDLNAGLCVNNWRYNVCRTGSANPHKGAINEDNIGYAMIAIQTITLEGW	360
Qy	390	DIMYFVMDAHSFYNYFIYILLIIVGSPFMNLCVLTATOFSETKQESOLMRQRVRL	449
Db	361	EIMYVMDAHSFYNYFIYILLIIVGSPFMNLCVLTATOFSETKQESOLMRQRVRL	420
Qy	450	SNASTLASFSPGSCYBELLYLILKARLAQVSRIGVRAGLLSLSPVARSQEPQ	509
Db	421	S-SSTVASAEPGDCYEIEFYVCHILRKAKR-----RALGLYQALQS-----	462
Qy	510	PSGCTSHRLSVHVLVHHHHHHHHHLLNGTILRVPRASPEIQDRDANGSRRLMLPPP	569
Db	463	-----RQAL-----GPE-----APAP	474
Qy	570	STPTSGGPPRGABSVHSFYHADCHLEPVRCAQPPPCPSASGRVTSKGVYPTVHTSP	629
Db	475	AKCP-----HAK-----EPHYQLCPQHSPLD-----TPHT--	502
Qy	630	PPEILKDKALVEVAPSGPPTLTSTFNIPGPFSSMHKLETTQSTGAC-HSSCKTSSPCSK	688
Db	503	-----LVQ-----PIPATLAS-----DPASCPCCOHEGDRRPSGLGS	534
Qy	689	ADSGACGPDSCPYCARTGAGEPESADHVPDSDSEAVYFTQDAQHSDLRDPHRRQRS	748

Db	535	TDSCQEGSGS-----GSSAGGEDEA-----DGDCA-----RSEDGASSELGKEBEREQ--	579
Qy	749	LGPDAEPSSVLA--FWRLICDTFRKIYDSKYFGRGIMAILVNTLSMGIEYHEQPEELTN	806
Db	580	---ADGAVWLCGDVWRETRAKLGIYDSKYFNRGIMAILVNTVSMGIEHHEQPEELTN	635
Qy	807	ALBISNIVFTSLFALEMLLKLIVYGPYIKNPNIFDGVIVWISVWEIVCOQGGLSVL	866
Db	636	ILBICNVFTSMFALEMLLKLAAFGFLYLRNPNIFDSIIVISWEIVCOQGGLSVL	695
Qy	867	RTFLMRVLKVRFLPALORQLVVMKTMNVATFCMLLMFLIFISITLGHMLFGCKPAS	926
Db	696	RTFLMRVLKVRFLPALORQLVVMKTMNVATFCMLLMFLIFIFILGNHIFGCKPSL	755
Qy	927	ERD-GDTLPDRKNPDSLLMAIVTVFQILTQEDMNKVLVYNGMASTSSWAALYFIALMTF	985
Db	756	RTDTGDTVPDRKNPDSLLMAIVTVFQILTQEDMNKVLVYNGMASTSPWASLYFVALMTF	815
Qy	986	YVLFNLLVAILVEGFOAEGDATKSESEPDFFSPV-----DGDGDKKRLALVAL	1035
Db	816	YVLFNLLVAILVEGFOAEGDANRSYDEQSSNIEFQKLEGLDSSGDPK--LCPIPM	873
Qy	1036	GEHAELRKSLPLLIHT----AATPMSPKSSSTGVGEALGSGSRRSTSSGSAEPGAH	1091
Db	874	TPNGHLDPSL--PLGHLGPAGAAGPA--PRLSLOPDMVLVALGSRKSSVMSL---GRMS	926
Qy	1092	HEMKCPPSARSSPHSPMSAASWTSRRSSRNSLGRAPSLKRSPSGRRSLLSGE--GOES	1150
Db	927	YDQRSLSRSSSYGPMGRSAASWTSRRSSRNSLGRAPSLKRSPSGRRSLLSGE--GOES	980
Qy	1151	QDEEESSE--DRASPAGSDH-----RHRGSLERAKSSPDLPTQLQVPG	1193
Db	981	RVCEVADEGPRAAPLPHPHHIIHGHPLAHRHRRHTLSLDNDRSDVLAELVPVAVG	1040
Qy	1194	LHRTASGRSS--ASEHODCNKGSASGLARTLTD-DPQLDGDNDNDEGNLSKGERIAQW	1250
Db	1041	AHPRAAWRAAGAPGHEDCNGRMP--IAKOVFTMGDRGDRGEDEIDYTLCFVRKM	1098
Qy	1251	VRSLPACCRERDSWSAYIFPPQSRFLCHRIITHQFDDHVLVLIIFLNCITIAMERPK	1310
Db	1099	IDVYKPDWCVEEDWSVYLFSPENRFRVLCQITIAHLFDYVVLAFILNCITIALERPQ	1158
Qy	1311	IDPHSAERIFLTLSNYIFTAVFLAEMTVKVALGWCQEGQAYLSSNVLDGLLVSIV	1370
Db	1159	IEAGSTERIFLTLSNYIFTAVFGEMTLKVLSGLYEGQAYLSSNVLDGLFLVFSII	1218
Qy	1371	DILVSMVSDSGTKILGMLRVLLRLTLRPLRVISRAOGLKLVVETLMSLLKPIGNIVIC	1430
Db	1219	DIVVSLASAGAKILGVLRVLRLLRPLRVISRAOGLKLVVETLMSLLKPIGNIVIC	1278
Qy	1431	CAFFIIFGILGVQLFKGKFFVCOGEDTRNTNKSDCAEASYRVRHRYKFNFDNLGOALMSL	1490
Db	1279	CAFFIIFGILGVQLFKGKFFVCHGLGVDTNRNTRSDCMAANYRWVHHKYFNFDNLGOALMSL	1338
Qy	1491	FVLASKDQWDIMVLDGLDVGVDQOOPIMNPNMMLLYFISFLLIIVAFVFLNMFVGVVEN	1550
Db	1339	FVLASKDQWNIWYNGLDVAVDQOPVTNPNMMLLYFISFLLIIVAFVFLNMFVGVVEN	1398
Qy	1551	FHKCRQHEEEARRRREKRLRLEKRRSKEKQMAEAQCKPYSDYSRFRLLVHLLCTS	1610
Db	1399	FHKCRQHEEARRRREKRLRLEKRR-----KAQRLPYVATYCHTLLHSMCTS	1451
Qy	1611	HYLDLFTIGVIGLVNVTMAHEYYQQPQILDEALKICNYIETVIVFVFSVFKLVAFAPRRF	1670
Db	1452	HYLDIFITFIICLVNVTMSLEHYNQPTSLTALKYCNVMTPTVPVLEAVLKLVAFLRRP	1511
Qy	1671	PDQRWOLDIAVLSTLSTGTLLEBIEVLSLPTINPTIIRINRVLRIARVLKLLQAVGR	1730
Db	1512	PDQRWOLDIAVLSTLSTGTLLEBIEVLSLPTINPTIIRINRVLRIARVLKLLQAVGR	1571
Qy	1731	ALLHTVQALPOVGNLGLLFFLFFIIFAALGVLEFGLECDETHPCGELGRHATFRFGM	1790

Db 1572 ALLDTVVQALPOVGNLGLLPMLLFFIYAALGVLELFGKLVNCDENPCGMSRHATPENFCM 1631
Qy 1791 AFLTLFRVSTGDNWNGIMKDPDRDC-DQBSTCYNV--ISPIYFVFLVTAQFVLVNVVI 1847
Db 1632 AFLTLFQVSTGDNWNGIMKDTLDRCTHDSRCLSLQFVSPLFVFLVTAQFVLVNVV 1691
Qy 1848 AVLKMLHEENKEAELEAELEEM-KTLSPQPHSLPGSPFLWPG----- 1894
Db 1692 AVLKMLHDDSDNKAQDAEAELEMAHGLGPGRLPTGSPGA-PGRPGGAGGGDT 1750
Qy 1895 -----VEG-VNSTDSPKPGAPHTTAHGAASG----- 1920
Db 1751 EGGLECRRCYPAQDSLEGEU1IDNLGSIFFH---HYSSPAGCKKCHDKQEVOLAETA 1807
Qy 1921 -----FSLBHTWVP-----HPEVVP-PLGPDLLTVRSGVYS 1952
Db 1808 FSLNSDRSSILLGDDLSLEDPACTPPGRKDSKGLDPPPEPMRVGDIGECFFLSSTAVS 1867
Qy 1953 RTHSLPN-DSVMCRNGSTAERSLGRWGMLPKAQSGSILSVHSOPADTSCILQPKDVHY 2011
Db 1868 -----PPENFLCEMEIIPNV--RSL--LKHDSSQAPSPSPDASSPLLPMPAEFFH 1918
Qy 2012 -----LLQPHGAPTWGAIPKLPPPG-----RSLAQRLRRQAIRNDSLDVOGLSRE 2060
Db 1919 PAVSASQKGEKGTGTGLPKIALQGSWASILRSPVNCVTLRQATGSDTSLDAS----- 1972
Qy 2061 DLLSEVSGPCPLTRSSSFWGSSIQOQRSGIQSKVSHIRLPAPCPGLEPSPWAKDPPE 2120
Db 1973 -----PSSAGSLQTTLEDLSLSDSPRALGPPAPAG----- 2006
Qy 2121 TRSLELDELTSWISGDLPLSSQBEPLPRDLKCYSVETQSCRRRPFGLDQRHSA 2180
Db 2007 -----PRAGLSPAARREL-----SLRGLFSLRGLRAHQRS 2038
Qy 2181 VCLSDSGQRLCPSPSSL-----GGPLOGGSRPKKLSPPSIS---IDPPESQG 2229
Db 2039 HS---SGGSTSPGCTHDSMDPSDEGRGAGGAGGAGSEHSETLSLSLTSFLCPPP--- 2092
Qy 2230 SRPSCSQVCLRR-----RAP---ASDSKDPSSVSPDLSTA 2262
Db 2093 ---PPAPGLTPARKFSSTSSLAARCPHAAALHGLARSWAADRSKDPPGRAPLPMGL 2150
Qy 2263 ASPSPKDKTSLSGSLSDPTMDP 2286
Db 2151 GLAPPPQPL-----PGELEP 2166

RESULT 8
US-10-425-800-2
; Sequence 2, Application US/10425800
; Publication No. US20030180886A1
; GENERAL INFORMATION:
; APPLICANT: Dietrich, Paul S.
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
; TITLE OF INVENTION: AND USES
; FILE REFERENCE: R0043B-REG sequence listing
; CURRENT APPLICATION NUMBER: US/10/425,800
; CURRENT FILING DATE: 2003-04-29
; PRIOR APPLICATION NUMBER: US/09/404,650
; PRIOR FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 2175
; TYPE: PR1
; ORGANISM: Homo sapiens
US-10-425-800-2

Query Match 45.0%; Score 5409; DB 14; Length 2175;
Best Local Similarity 50.5%; Pred. No. 0;
Matches 1225; Conservative 236; Mismatches 513; Indels 450; Gaps 64;

Qy 51 ASRSSTTCFPGAGAGAGSTKDPG--SADSABGL-----PYDALAPVVFYLS 97
Db 5 ASPSSSSAAP-AAEPGVTTQPGPRSPSPSPGLEEDLGDGADPHVPHDLAPIAFFCLR 63
Qy 98 QOSRPRSCLRTVCMNPFERVSMLVILLNCVTGLNFRCEDIACDSQRCRILQADDDTF 157
Db 64 QTTSPNNCMKVCNPFECVSMVILLNCVTGLNMQPCDDMDCLSDCKILQVDDDF 123
Qy 158 AFPAVEMVMVALGIFGKCYLGDWTNRLOPFIIVIAGMLEYSLDLQNVFSFVAVRTVYL 217
Db 124 IFPAMEVMVLKVALGIFGKCYLGDWTNRLOPFIIVMAGVSEISDLQNLNSAIRTVYL 183
Qy 218 RPLRAINRVPMSRILVTLTLLDPLMGNVLLCFPVFFIFIGVQVQVQVQVQVQV 277
Db 184 RPLKAINRVPMSRILVTLTLLDPLMGNVLLCFPVFFIFIGVQVQVQVQVQV 243
Qy 278 NFSPLSLVDLEPYQTEDEDESPFICSPRENGMESCSPVTLRGECCGGPPCSL- 332
Db 244 NFTIQGDVALPYQPEDEDEPFICSLGSDNGIMGCHIEIPPLEQ---GRECCLSKDDV 300
Qy 333 -DYETVNSSNTT--CVNMNOYTNCSAGEHNPFGAINFDNIGYAWIAFOVITLEGV 389
Db 301 YDFGACRODLNAGLGVNWRYYNVCRTGSANPHKGAINDNIGYAWIVFOVITLEGV 360
Qy 390 DIMYFMDAHSFYNTFYFILLIIVGSFFMINCLVVIATOFSETKORESQVRL 449
Db 361 EIMYYVMDAHSFYNTFYFILLIIVGSFFMINCLVVIATOFSETKOREHRLMEOQVRL 420
Qy 450 SNASTLASFSESGSCVEELKYLVTILKAARLQVSRAGVRAGLLSSPVARSQBPQ 509
Db 421 S-SSTVASAEPCDCYEETFCVCHILRAKR-----RALGLYQALQS----- 462
Qy 510 PSGSCTRSHRRLSVHHLVHHHHHHHHLNGTLFVPRASPEIQDRDANGRRMLPPP 569
Db 463 -----RRQAL-----GPE-----APAP 474
Qy 570 STPTPGGPRGASVHSFYHADCHLEPVRCQAPPCPSEASGRVGVGVVYVHTSP 629
Db 475 AKPGP-----HAK-----EPHYQLCPOHSLDA-----THT-- 502
Qy 630 PBEILKDKALVEVAPSPGPTLTSTFNIPPGFSSMEKLETTOSTGAC-HSSCKISPCSK 688
Db 503 -----LVQ-----PIPATLAS-----DPASCPCQCHEDGRRPSGLGS 534
Qy 689 ADSGACGPDSCPYCARTGAGEPESADHVPDSDSEAVYEFTQAOQSLDLDPSRRORS 748
Db 535 TDSGQSGSGS-----GSSAGGEDEA-----DGDGA---RSEDCASSELGKEEBEQ-- 579
Qy 749 LGPDAEPSSVLA--FWRLICDTERKIVDSKYFCRGIMIALVNTLSNGIYEHQPEELTN 806
Db 580 ---ADGAVMLCGDVWRETRAKURGIIVDSKYFNRGIMAILVNTVNGIEHHEQPEELTN 635
Qy 807 ALBISNIVFTSLFALEMLKLLVYGPFGYIKPNYINFDGVIVVISVWEIVQOQGGLSVL 866
Db 636 ILBICNVVFTSMFALEMLKLLAAFGFLDYLRNPNYINFDGVIVVISVWEIVQOQGGLSVL 695
Qy 867 RTFRLMRVLKVRPLPALQOLVLMKTMNDVATFCMLMFIIFISILGMLHFGCKFAS 926
Db 696 RTFRLMRVLKVRPLPALQOLVLMKTMNDVATFCMLMFIIFISILGMLHFGCKFAS 755
Qy 927 ERD-GDTLPDRKNFDSLLWAVTVFOILTQEDWNKVLNGMSTSSWAALFYIALMTFGN 985
Db 756 RTDGTDTVPDRKNFDSLLWAVTVFOILTQEDWNKVLNGMSTSSWAALFYIALMTFGN 815
Qy 986 YVLFNLLVAILVEGFOAEGDATKSESEPDFFSPSV-----DGDGRKRLALVAL 1035
Db 816 YVLFNLLVAILVEGFOAEGDANRSYDEQSSNIEFDFKLOGLDSSGDPK--LCPIPM 873
Qy 1036 GEHAELRKSILLPLIHT-----AATPMHPSKSTGTGVEALGSGSRRTSSSGSAEPGAH 1091
Db 874 TPNGLHDPSL--PIUGHLGPAGAAGPA--PRLSLQDPDMVLGSRKSSVMSL---GRMS 926
Qy 1092 HEMKCPPSARSSPHSPWSAASWTSRRSRNSLGRAPSLKRRSPSGRRSLLSGE-QGES 1150

Db 927 YDQSLSSRSYYPWGRSAWASRRSSWN-----SLKHKPSAHESSLASRGGGA 980
Qy 1151 QDEESSEE--DRASPPAGSDH-----RHRGSLEREAKSSFDLPPTLQVPG 1193
Db 981 RVCEVAADGPPRAAPLHTTAAHIIHGHPLAHRHRRHTLSLDNRSDVLAELPAVG 1040
Qy 1194 LHRTAGRSS--ASEHODCKGKSASGLARTLRD-DPOLDGDDNDNENGLSKGERLOAW 1250
Db 1041 AHPPAAWRAAGPAGBHDCCGRMPS--IAKDVFTKMGDRGDRGEDEEIDYTLFCFRK 1098
Qy 1251 VRSLPACCRERDSWASIIYPPQSRFLCHRIITHKMFHVVLVLIIFLNCITIAMERPK 1310
Db 1099 IDVYKPDWCEVREDWSYVLESPENRFVLQOTIIAHLFDYVLAFIFLNCITIALERPQ 1158
Qy 1311 IDPHASRIIFLTISNYIFTAVFLAEMTVKVVALGWCFCGEQAYLRSSWNVDGLVLISVI 1370
Db 1159 IEAGSTERIFLTISNYIFTAIFVGMTLKVVSGLYFGEQAYLRSSWNVDGLFLVFSII 1218
Qy 1371 DILVSMVSDSGTKILGMLRLVRLRLRLRLRLRLRLRLRLRLRLRLRLRLRLRLRL 1430
Db 1219 DIVVSLASAGAKILGVLRLRLRLRLRLRLRLRLRLRLRLRLRLRLRLRLRLRLRL 1278
Qy 1431 CAFFIIEGILGVOLFCKGKFFCOGEDTRNITNKSDCAEASYRWVRHKNYFNQNLGOALMSL 1490
Db 1279 CAFFIIEGILGVOLFCKGKFHCLGVDRNITNRSDCMAANYRWVRHKNYFNQNLGOALMSL 1338
Qy 1491 FVLAKDGDWYDIYDGLDVAVGDOQPIIMNHPMMLLYFISFLLAFFVLNMFVGVVVEN 1550
Db 1339 FVLAKDGDWYIMYDGLDVAVGDOQPTNHPMMLLYFISFLLIIVSFVLNMFVGVVVEN 1398
Qy 1551 FHKCRQOBEERREKRLRLKRSKEKQMAEACKPYSDYSRFLVHLHCTS 1610
Db 1399 FHKCRQOBEERREKRLRLKRR-----KAQRLPYATYCHTRLTHSCTS 1451
Qy 1611 HYLDLFTVIGLVNVTMAHEYOQPOLDEALKICNYIFTVIFVPSVFKLVAFAFRF 1670
Db 1452 HYLDLFTVIFLNVVMTSLHYNQPTSLTALKYCNMFTVFLVAVLKLVAFLRRP 1511
Qy 1671 FQDRWNQDLAIVLLSIMGITLIEIEVNLSPINPTIIRIMVRLRIARVLKLMVGM 1730
Db 1512 FQDRWNQDLAIVLLSVMGITLIEIEINAALPINPTIIRIMVRLRIARVLKLMVGM 1571
Qy 1731 ALLHTVQALPOVGNLGLLFWLFFIIPALGVLELFGDCEHPCBGLGRHATFRNFM 1790
Db 1572 ALLHTVQALPOVGNLGLLFWLFFIYAALGVLELFGKLVNDENPCBGRHATFRNFM 1631
Qy 1791 AFLTLPRVSTGDNWGLMKDPSRDC-DQESTCYNTV--ISPIYFVSFLTAQFVLNVVI 1847
Db 1632 AFLTLFVSTGDNWGLMKDTRDCTHDSRCSLSSQFVSPFLYFVFLTAQFVLNVV 1691
Qy 1848 AVLKMLHESNKAEAEAEAEAELEEM-KTSLSPQHSPLGSPPLWPG-----1894
Db 1692 AVLKMLHDSNKAEQAEAEAEAELEMAHGLGPGPLPTGPGA-FGRGGGAGGGDT 1750
Qy 1895 -----VGG-VNSTDSPKPGAPHTTAHGAASG-----1920
Db 1751 EGGLECRCYSPAQDSLEGELTIIDNLSSGIFH---HYSSPAGCKKHDKQEVQLAETEA 1807
Qy 1921 -----FSLHPTMPV-----HPEVPV-PLGPDLLTVRKSGVS 1952
Db 1808 FSLNSDRSSILGDDLSLSDPTACPPGRKDSKGLDPPPMRVGDDJGCEFFPLSSTAVS 1867
Qy 1953 RTHSLPN-DSYMCNRSSTABSLHGRGWLPKAQSGILSVHSOPADTSCILQPKDVHY 2011
Db 1868 -----PDPENFLCEMEIIPNPV--RSM--LKHDSSQAPSPSPDPASSPLLPWAEFFH 1918
Qy 2012 -----LLQHPGAPTWGAIPKLPPPG-----RSLPAORPLRQAAIHTSDLSVOGLSRE 2060
Db 1919 PAVSASQKPEKGTGTGLPKIALQGSWASLRSPVNCVTLRQATGSDTSLDAS-----1972
Qy 2061 DLLSEVSGPCPLTRSSSFWGSSIQVQKSGISQVSKHRLPAPCPGLEPSWAKDPPE 2120

Db 1973 -----PSSAGSLQTTLEDLSLSDSPRRALGPPAPAG-----2006
Qy 2121 TRSLELDTELWSIGDILLFSSQEEPLFPRLDKKCYVETQSCRRRCFGWLDORRHISIA 2180
Db 2007 -----PRAGLSPAARRL-----SLRGRGLFSLRGLRAHQRS 2038
Qy 2181 VSCLDGSGQRLCPSPSSL-----GGQPLGSGSRPKKCLSPSSIS---IDPPESQG 2229
Db 2039 HS---SGSTSPGCTHDSMDPSDEBGRGAGGAGGAGSEHSETLSLSLTFCCPPP-----2092
Qy 2230 SRPPCPGVCLLR-----RAP---ASDSKDPSSVSPPLDSTA 2262
Db 2093 --PPAPGLTPARKFESTSLAAPGRPHAAALAHGLARSFSAADRKDPGRAPLPNGL 2150
Qy 2263 ASRSPKDTLSLGLSDPTDMDP 2286
Db 2151 GPLAPPPQPL-----PGELEP 2166

RESULT 9
US-09-935-541-4
; Sequence 4, Application US/09935541
; Patent No. US20020150911A1
; GENERAL INFORMATION:
; APPLICANT: Dietrich, Paul S.
; APPLICANT: McGivern, Joseph G.
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
; FILE OF INVENTION: AND USES
; FILE REFERENCE: R0043B-REG sequence listing
; CURRENT APPLICATION NUMBER: US/09/935,541
; CURRENT FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: 09/404,650
; PRIOR FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 2188
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-935-541-4

Query Match 44.9%; Score 5405.5; DB 9; Length 2188;
Best Local Similarity 50.3%; Pred. No. 0;
Matches 1225; Conservative 236; Mismatches 514; Indels 461; Gaps 64;

Qy 51 ASRSSTTCGPGGAAGAGSTEKDFG--SADSEAEGL-----PYPALAPVVFYLS 97
Db 5 ASPPSSAARAP-AAEPGVTTTEQFGPRSPSSPPGLEBPLDGAOPHVPDLPATFAFLR 63
Qy 98 QDSRPSRWCLRTVCNPFVRSVLMVILLNCVTGMPFRPCSDIACDSORCILQAFDFP 157
Db 64 QTTSPRNWCICKMVCNPFVRSVLMVILLNCVTGMPFRPCSDIACDSORCILQAFDFP 123
Qy 158 APTAVEMVVMKVALGIFGKCYLGDPTWNRLDPTFIVTAGMLEYSIDLQNVFSFVTRVRL 217
Db 124 IFPAMEVLMKVALGIFGKCYLGDPTWNRLDPTFIVTAGMLEYSIDLQNVFSFVTRVRL 183
Qy 218 RPLRANRVPSEMRILVTLTLLDTPMLGNVLLLCFFVFFIFGIVGVQVWAGLNRNRCFLPE 277
Db 184 RPLKAINRVPSEMRILVTLTLLDTPMLGNVLLLCFFVFFIFGIVGVQVWAGLNRNRCFLPE 243
Qy 278 NPSLPLSVDLPEYVQYQTEENEDSPICSPQRENMRSCRSVPTLRGEGGGGPPCSL-----332
Db 244 NPTIQDVALPYQYQTEENEDSPICSLSGDNGIMGCHIEIPPLKBEQ---GRECCLSKDDV 300
Qy 333 -DYETYNSSNTT--CVNWNQYTNCSAGEHNPKGAINFDNIGYAWIAIIFOVITLSEGW 389
Db 301 YDFGAGRQDNLASGLCVNMNRYNCRVTSANPHKGAINFDNIGYAWIAIIFOVITLSEGW 360
Qy 390 DIMYFVMDAHSFYNYFIYILLIIVGFSFMNLCVIAVATQFSETKQRESOLMRQVRFL 449
Db 361 EIMYVMDAHSFYNYFIYILLIIVGFSFMNLCVIAVATQFSETKQRESOLMRQVRFL 420

FILE REFERENCE: R00438-BEG sequence listing
CURRENT APPLICATION NUMBER: US/10/425,800
CURRENT FILING DATE: 2003-04-29
PRIOR APPLICATION NUMBER: US/09/404,650
PRIOR FILING DATE: 1999-09-23
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4
LENGTH: 2188
TYPE: PR1
ORGANISM: Homo sapiens
US-10-425-800-4

Query Match 44.98; Score 5405.5; DB 14; Length 2188;
Best Local Similarity 50.34; Pred. No. 0;
Matches 1225; Conservative 236; Mismatches 514; Indels 461; Gaps 64;

QY 51 ASRSSTTCPCGGAAGAGCTEKDPC--SADSEAEGL-----PYPALAPVVPFYL 97
DB 5 ASPSSAAAP-AAEPGVTTQCPGPRSPSPGEEPLDGDADPHVPHDLAPFAFLR 63
QY 98 QDSRPRSWCLRTVCNPFVSMVLVLLNCVTGLMFCPCEDIAQCSQRCILQAFDDFIF 157
DB 64 QTSRPNWCICKWCPNPFECVSMVLVLLNCVTGLMFCPCEDMDCLSDRCKILQVDFDIF 123
QY 158 AFAVENVMKVALGICGKCYLGDWNRLDFFVIAGMLEYSLDLQNVFSAVRTVRVL 217
DB 124 IFPAMVNLKVALGICGKCYLGDWNRLDFFVIAGMLEYSLDLQNVFSAVRTVRVL 183
QY 218 RPLKAINRVSMRLVTLTDLTLMGLNVLVLLCFFVFIQVGVQVWAGLLNRCPLE 277
DB 184 RPLKAINRVSMRLVTLTDLTLMGLNVLVLLCFFVFIQVGVQVWAGLLNRCPLEE 243
QY 278 NPSLPLSDLEPYQTEDESPFICSPQRENGMRSCSVPTLRGEGGGPPCSL----- 332
DB 244 NFIQGVVALPPYQPEEDDEMPFICSLSDNGIMGCHIEPLKEQ---GRECCLSKDDV 300
QY 333 -DIETYNSSNTT--CUNWQYNTNCAGENPKGAINFDNIGYAWIAFOVITLEGWV 389
DB 301 YDFGAGQDLNAGLCVNNRYNVCRTGSANPHKGAINFDNIGYAWIVFOVITLEGWV 360
QY 390 DIMYFVMDASHFYNYFIILLIIVGSPFMNLCVVIATOFSETKQRESOLMRQVRFL 449
DB 361 EIMYFVMDASHFYNYFIILLIIVGSPFMNLCVVIATOFSETKQREHLMLEQORYL 420
QY 450 SNASTLASFSPGSCYBELLYLYILRKAARLAQVSRAIGVRAGLSSPVARSQEPQ 509
DB 421 S-SSTVASYAEPCDCEIEIFQYVCHILRKA-----RALGLYQALQS----- 462
QY 510 PSGSCTRSHRLSVHHLVHHHHHHHHHNGTLVRPASPEIQDRDANGSRRLMLPPP 569
DB 463 -----BQAL-----GPE-----APAP 474
QY 570 STPTSPGGPRGAEVHSFYHADCHLPRVRCQAPPPPCSEASRTVSGKVPVHTSP 629
DB 475 AKQGP-----HAK-----BPRHVQLCPQSPDPA-----TPHT-- 502
QY 630 PPEILKDKALVEAPSPGPTLTSTFNIPGPFSSMHKLLTQSTGAC--HSSCKTSSPCSK 688
DB 503 -----LVQ-----PIPATLAS-----DPASCPCCOHEGRRPSGLGS 534
QY 689 ADSGACPDSPCYCARTGAGEPESADHMPDSDSEAVYFTQDAQHSDLRDPHSRRQRS 748
DB 535 TDSQEGSGS-----GSSAGGEDEA-----DGDGA-----RSEDCASSSELGKEEBEERQ-- 579
QY 749 LGPDAEPSSVLA--FWRLICDTRKIVDSKYVGRGIMAILVNTLSMGIEVHPOPELTN 806
DB 580 -----ADGAVMLCGDVWRETRAKRGIVDSKYFNFGIMAILVNTVSKGIEHPOPELTN 635
QY 807 ALEISNTVFTSLFALEMLKLLVVGPGYIKNPNYINFDGVTWISVWEIVQOQGGGLSVL 866
DB 636 ILEICNVVFTSMFALEMILKLAAGLEFDYLRNPNYINFDISIVIISWEIVQADGGGLSVL 695

QY 867 RTFLRLRVLKLVRFLPALOROLVLMKTMNDVATFCMLLMFLTIFISILGWHFLGCKFAS 926
DB 696 RTFLRLRVLKLVRFLPALOROLVLMKTMNDVATFCMLLMFLTIFISILGWHFLGCKFAS 755
QY 927 ERD-GOTLPDRKNFDSLLMAIVTVFQILTOEDWNKVLVNGMASTSSWAALYFIALMTFGN 985
DB 756 RTDTGDTVPDRKNFDSLLMAIVTVFQILTOEDWNKVLVNGMASTSSWAALYFIALMTFGN 815
QY 986 YVLFNLLVAILVVGPOAGQATKSESEPDFFSPSV-----DGDGRKQGLALVAL 1035
DB 816 YVLFNLLVAILVVGPOAGQATKSESEPDFFSPSV-----DGDGRKQGLALVAL 873
QY 1036 GEHAEALRKLPLLIHT-----AATPMSHPKSSSTGVGEALGSGSRTSSSGSAEPGAH 1091
DB 874 TPNGLHLDPSL--PLGHLGAGAGPA--PRLSLQDPMLVALGSRKSSVMSL---GRMS 926
QY 1092 HEMKCPSPSARSSPHSPMSAASWTSRRSSNSLGRAPSLKRRSPSGRRSLLSGE-QGES 1150
DB 927 YDQSLSSSRSSYYGPMGRSAANASRRSSWN-----SLXKPPSAEHSLLSAERGGGA 980
QY 1151 QDEESSEEE--DRASPAAGSDH-----RHRGSLEREAKSSFDLPDQLQVPG 1193
DB 981 RVCEVAADGPPRAAPLHTPHAHIIHGHPLAHRRHRRHRTLSLONRDSVDLAELVPAVG 1040
QY 1194 LHRTASGRSS--ASEHODCNGKSASGLARTLTD-DPOLDGDGDDNDDEGLSKGERIQAM 1250
DB 1041 AHPRARAWAGAPAGPHEDCNGRMPSS--IAKDVFTKMGDRGDRGEDEEIDTLCFRVRKM 1098
QY 1251 VRSRLPACCRERDSWASAYIPPPQSRFLCHRIITHKMFVHVVLVIFLNCITTIAMERP 1310
DB 1099 IDVYKPDWCVEEDNSVYLPSPENFRVLCOTIAHKLFDYVVLAFILNCITTIAMERP 1158
QY 1311 IDPHSAERIFLTISNIFTAVFLAEMTVKVALGMCQGEQAYLRSSNVLDGLLVLSVI 1370
DB 1159 IEAGSTERIFLTISNIFTAVFLAEMTVKVALGMCQGEQAYLRSSNVLDGLLVLSVI 1218
QY 1371 DILVSMVSDSGTKILGMLRVLRLLRTPLRVLSRAQGLKLVVETLMSLKPIGNIVVIC 1430
DB 1219 DIVVLSAGGAKILGMLRVLRLLRTPLRVLSRAQGLKLVVETLMSLKPIGNIVVIC 1278
QY 1431 CAPFIIFGILGVQLFKGKFFVCOGEDTRNITNSDCAEASRYRWHKYNFNDLQALMSL 1490
DB 1279 CAPFIIFGILGVQLFKGKFFVCOGEDTRNITNSDCAEASRYRWHKYNFNDLQALMSL 1338
QY 1491 FVLASKDQWVDIMYDGLDVGVDQOQIPMNNPNWLLYFISFLLIYAFVLMFMVGVVVEN 1550
DB 1339 FVLASKDQWVDIMYDGLDVGVDQOQIPMNNPNWLLYFISFLLIYAFVLMFMVGVVVEN 1398
QY 1551 FHKCRQHOEBEERARRRREKRLRELEKRSKEKQMAEAOCKPYYSYRSRFLLVHLCST 1610
DB 1399 FHKCRQHOEBEERARRRREKRLRELEKRSKEKQMAEAOCKPYYSYRSRFLLVHLCST 1451
QY 1611 HYLDLFTITGVIGLVNVTMAHEHYQQPOILDEALKICNYITVIFVFSFVKLAFAPRRF 1670
DB 1452 HYLDLFTITGVIGLVNVTMAHEHYQQPOILDEALKICNYITVIFVFSFVKLAFAPRRF 1511
QY 1671 FQDRWNQDLAIYLLSIMGITLBEIEVNLSELNPTIIRMRVLRIRARVLRKLLQWAGMR 1730
DB 1512 FQDRWNQDLAIYLLSIMGITLBEIEVNLSELNPTIIRMRVLRIRARVLRKLLQWAGMR 1571
QY 1731 ALLHTYMQALPOVGNIGLLEFLLFFIYALGVELFGDCEDETHPCGELGRHATFRFGM 1790
DB 1572 ALLHTYMQALPOVGNIGLLEFLLFFIYALGVELFGDCEDETHPCGELGRHATFRFGM 1631
QY 1791 AFLTLFRVSTGDNWNGIMKDPDRDC-DOESTCYNTV--ISPIYFVSFVLTAQFVLVNVVI 1847
DB 1632 AFLTLFRVSTGDNWNGIMKDPDRDC-DOESTCYNTV--ISPIYFVSFVLTAQFVLVNVVI 1691
QY 1848 AVLKMLHEENKEAKEAEAELEAELEEM-KTLSPQPHSPGLGSP----- 1889
DB 1692 AVLKMLHEENKEAKEAEAELEAELEEM-KTLSPQPHSPGLGSP----- 1751
QY 1890 -----FLW-----PCVEG-VNSTDSPKPGAPHTTAHGAASG----- 1920

Db 1752 GGLCRRCYSPAQENLWLDVSLIIDSLEGELTIIDNLSSGSIH---HYSSPAGCKKCHH 1808
QY 1921 -----FSLEHPTMVP-----HPEVPV-PLG 1940
Db 1809 DKEVQLAETAEASLNSDRSSILLGDDLSLEDTACPPCRKDSKGELDPPEPMRVGDLG 1868
QY 1941 PDLLTVRKSGVSRTHSLPN-DSYMCNRNGSTAERSLGRWGGLPKAQSGLISVHSOPADT 1999
Db 1869 ECFPLSSTAVS-----PDENFLCEMEEIIPFNV--RSW--LKHDSSOAPPSPFPDAS 1919
QY 2000 SCILQLPKDHY-----LLOHPCAPTWGAIPKLPPPG-----RSLPAQRLERQAART 2048
Db 1920 SPLLPMPAEFHPFAVSAQKPEKGTGTLPKIALOGSWASURSPRVNCTLLRQATGSD 1979
QY 2049 DSDLVQGLSREDLLSEVSGFSCPLTRSSSFWMGSSSIQVQORSGIOSKVKSHIRLPAPCP 2108
Db 1980 TSLDAS-----PSSSAGSLQTTLEDLSLSDSPRALGPPAPAP 2018
QY 2109 GLEPSWAKDPETRSSLELDELTELWSIGDILLPSQREPLFPRLKKCYSETQSCRRPG 2168
Db 2019 G-----PRAGLSPAARRL-----SLRGRGL 2039
QY 2169 FWLDEQRHHSIAVCLDSGQPRCLCPSPSL-----GQOPLGGPGSRPKKLSPPSI 2220
Db 2040 FSLRGLRAHQRHS--SGGSTSPCTHDSMDPSDEGRGAGGGAGSEHSETLSLSL 2097
QY 2221 S---IDPPESQGSPPCSPGVCLAR-----RAP---ASDSK 2250
Db 2098 TSLFCPPP-----PPAPGLTPARKFSTSSLAAPGRPHAAALAHGLARSPSWAADRSK 2151
QY 2251 DPSVSSPLDSTAASPSPKOTLSLSGLSSDPTMDP 2286
Db 2152 DPPGRAPLMGLPLAPPQPL-----PGELEP 2179

RESULT 11
US-09-935-541-5
; Sequence 5, Application US/09935541
; Patent No. US20020150911A1
; GENERAL INFORMATION:
; APPLICANT: Dietrich, Paul S.
; APPLICANT: McGivern, Joseph G.
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
; TITLE OF INVENTION: AND USES
; FILE REFERENCE: R0043B-REG sequence listing
; CURRENT APPLICATION NUMBER: US/09/935,541
; CURRENT FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: 09/404,650
; PRIOR FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 5
; LENGTH: 1835
; TYPE: PRT
; ORGANISM: Rattus sp.
US-09-935-541-5

Query Match 44.4%; Score 5345; DB 9; Length 1835;
Best Local Similarity 55.4%; Pred. No. 0;
Matches 1138; Conservative 216; Mismatches 375; Indels 324; Gaps 45;

QY 43 PRSRSPVNASRSTTCPGFGAAGAGSTBKDPGSADSEAE-----LPYPALAPVVFVYLSQ 98
Db 8 PSSAAPAPEGITEQGP-----RSPPPSPGLEELEGITNPDPVHPDLAPVAFVCLRQ 62
QY 99 DSRPSRWCLRTVCNPFWRVSRVSMVLILNCVILGMPRPEDTACDSORCIIILQAFDTEFA 158
Db 63 TTSRPNWCICMVCNPFECVSMVLILNCVILGMPRPEDTACDSORCIIILQAFDTEFA 122
QY 159 FFAVEMVVKWALGIFGKKCYLGDWNRLLDFVILAGMLEYSLDLQNVFSFAVRVRLR 218
Db 123 FFAMENVLKQWALGIFGKKCYLGDWNRLLDFVILAGMLEYSLDLQNVFSFAVRVRLR 182

QY 219 PLRAINRVPSMRILVTLLDTPMLGNVLLICFFVFFIFGIVGVQVLWAGLLNRCLFLEN 278
Db 183 PLKALNRVPSMRILVNLLDTPMLGNVLLICFFVFFIFGIVGVQVLWAGLLNRCLFLEN 242
QY 279 FSLPLSVLDLEPYQOTENEDESPFICSPRENGMSRCSVPLRGEGGGGPPCSL-----332
Db 243 FTIQGDVALPFYQPEEDEMPFICSLTGDNGIMGCHIEIPLKQ-----GRECCLSKDDVY 299
QY 333 DYETVNSSNTT--CVNWNQYVWCSAGEHNPFGAINFNDNIGYAWTAIFOVITLEGWVD 390
Db 300 DFGAGRODLNAGSLCVNWNRYNVCRTGNANPHKGAINFNDNIGYAWTAIFOVITLEGWVE 359
QY 391 IMYFMDAHSFYNTFYFILLIIVGSFFMINCLVVIATQFSETKQRESQLMREQVRELS 450
Db 360 IMYVMDAHSFYNTFYFILLIIVGSFFMINCLVVIATQFSETKQREHRLMLEQRVYLS 419
QY 451 NASTLASPEGSCYEELLYLVILYLRKAARLQAQVRAIGVRAGLLSSPVARSQEQEPQ 510
Db 420 -SSTVASVAEPGDCYEEIFQYVCHILRKAKR-----RALGLYQAL-----458
QY 511 SGSCSTRSHRRLSVHHLVHHHHHHHHHGLGNTLRVPRAPEIQORDANGSRRLMLPPPS 570
Db 459 -----QNRQRA-----MGPGT-----PAPA 473
QY 571 TPTPSGGPPRGAEVSHSFYHADCHLEPVRCQAPPCCPSEASGRVTGSKVYPTVHTSPP 630
Db 474 KFGP-----HAK-----EPHCKLCPRHSPLD-----PTPHT-----500
QY 631 PEILKDXALVEVAPSPGPPTLTSTFNIIPGPFSMHKLLTQSTGTGACHSCKISSPCSKAD 690
Db 501 -----LVQ-----PISAIL-----509
QY 691 SGACGPDSCPYC-----ARTGAGEPEADHVMPSDSSEAVYFTQDAQH 734
Db 510 ---ASDPSSCPHCQHEAGRRPGLGSTDGSEGGSGSAE---AEANGDGL-QSDEGVS 563
QY 735 SLDLPHSRRRORSIGPDABPSVLA-----FWRLICDTFRKIVDSKYFGRGIMAILVN 789
Db 564 SD-----LGKEBEEQDGAARLCGDVYMRTRKRLGIVDSKYFNRGIMAILVN 611
QY 790 TLSMGLEYHEQPEELTNALEISNIVFTSLFALEMLKLLIVYGPFGYKINPNYIFGVIVV 849
Db 612 TVSMGLEHEQPEELTNALEISNIVFTSMFALEMLKLAAGFDYLRPNYIFDSIIVI 671
QY 850 ISVWEIVGQGGGLSVLRTFRLMRVLKVRPALQORQLVLMKTMNDVATFCMLLMLEFI 909
Db 672 ISIWEIVGQADGGLSVLRTFRLMRVLKVRPALQORQLVLMKTMNDVATFCMLLMLEFI 731
QY 910 FIFSILGMHIFGCKFASERD-GDTLPDRKNFDSLLMAIIVTVFQILTQEDWNKVLVNGMAS 968
Db 732 FIFSILGMHIFGCKFASERD-GDTLPDRKNFDSLLMAIIVTVFQILTQEDWNKVLVNGMAS 791
QY 969 TSSWAALYFIATMTFGNYVLFNLLVAILVEGFOAEGDATKSESEPDFFSPSVDG-----1022
Db 792 TTPWASLYFVALMTFGNYVLFNLLVAILVEGFOAEGDANRSCDESDQSSNLEBPKLPE 851
QY 1023 --DGRKRLIALVALGEHAEELKSLPLLIH--TAATPMSPKSSSTGVGEALGSGSR 1078
Db 852 GLDNRDLKLCIPMTFNGHLDPSL--PLGAHLGPAGTGTAPRLSLQPDVVLVALDSRK 909
QY 1079 TSSSGSNAEPGAAHEMKCPSPARSPPHSPWASASMTSRSSRNSLGRAPSLKRRSPSGE 1138
Db 910 SSVMSL---GRMSYDQRSLSRSSSYYPGWRSGTWARSSWN-----SLKHKFPSPAE 960
QY 1139 RRSILSGEQES--QDEEESSE--DRASPAGSDH-----RHGSLEREA 1179
Db 961 HESILSGEQESVCRACEGAREEAPTAPLHAPHAAHGHGPHLAHRHRRHRTLSLDT 1020
QY 1180 KSPFDLPDTLOVGLHRTAS--GSSASHEQDCNGKSASGLARTLTD-DPOLDGDGDDN 1236
Db 1021 RDSVDLGELVFWGAHSRAAWGAGQAPGHEDCNGRMPN--IAKDVFTKMDRRDRGEDE 1078

Qy	1237	DEGNLSKGERIQAWVRGRSLPACCRERDSWSAYIPPPQSRFRLLCHR.IITHKMDHVVVLVI	1296
Db	1079	EEIDYTLTCLFRVKMIDVYKPDWCVEWDWSYLFSPENKFRILCQTTIAHKLFDYVVYLA	1138
Qy	1297	IFLNCITIAMERPKIDPHSAERIFLTLNSNIYFATAVFLAEMTKVVALGWCFCGQAYLRSS	1356
Db	1139	IFLNCITIALERPOJEAQSTERIFLTVSNYIFTAIFVGEWTLKVSLUGLFGQAYLRSS	1198
Qy	1357	WNVLGGLLVISVIDILVMSVDSGTKILGMLRLVRLRLTLRLPLVRSRQGLKLVVETL	1416
Db	1199	WNVLGGLFVFSIIDIVVSASAGAKILGVLRVLRLLRLTLRLPLVRSRQGLKLVVETL	1258
Qy	1417	MSSLKPTIGNIVVICCAEFILFGLIGVOLFKGKFPVCOGETRATITNKSDCBAESAYRWVRH	1476
Db	1259	ISSLKPIGNIVLICCAEFILFGLIGVOLFKGKFVHCLGVDVTRNITNRSDCVAANYRWVHH	1318
Qy	1477	KYNFDNLGQALMSLVFLASDKGDWIDIMYDGLDAVGVDOQPIMNHNPMMLLYFISFLLI	1536
Db	1319	KYNFDNLGQALMSLVFLASDKGWNIMYNGLDVAVDVDOQPVTHNPMMLLYFISFLLI	1378
Qy	1537	FFVLNMFGVVVENFHKCRHQHBEERREKRLRLEKKRSKEKQMAEACKPYSD	1596
Db	1379	FFVLNMFGVVVENFHKCRHQEAEAEARRBEERKRLRLEKKR-----KAORLPYYAT	1431
Qy	1597	YSRFLVAVHLCTSHYLDLFTGVIGLVNVTWAMEHYQOPOILDEALKICNYLFTVIFVF	1656
Db	1432	YCPTRLIHSWCTSHYLDLFTFIICLVNVMTSLHYNQPTSLTETALUKYCNMYFTTVFVL	1491
Qy	1657	ESVPKLVAFAPRFPQDQRWQOLDIAIVLLSGIMGTLEEBEIVNLSLPINPTIIRIMRVLRI	1716
Db	1492	EAVLKLVAFLGRFPFKDRWQOLDIAIVLLSVMGITLSEIEIINAALPINPTIIRIMRVLRI	1551
Qy	1717	ARVLKLLKMAVGRALLHTWQALPOVGNIGLIFMLLFPPIPAALGVBELFGDLSCDETHPC	1776
Db	1552	ARVLKLLKMATGRALLDTVQALPOVGNIGLFLMLLFFTYAALGVBELFGKLVCDENPC	1611
Qy	1777	EGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMKDPDRDC--DQBSTCYNTV--ISPIYFVS	1833
Db	1612	EGMSRHATFRNFGMAFLTLFQVSTGDNWNGIMKDTLDCDTHDERTCLUSSIQFVSPILYFVS	1671
Qy	1834	FVLTAQFVLNVVVIAMVKHLESNKBEAELEAELEMLKTLSPQHSPLGSPFLWP	1893
Db	1672	FVLTAQFVLNVVVIAMVKHLLDSDNSKEAQBDAAEMDABIELEM-----	1713
Qy	1894	GVSEGVNSTDSPKCAPHTTHAHGAASGFSLEHPTWPHPEVPVP-LGPDLLTV-----	1946
Db	1714	-AHGLGPCPCPG-----PCPCPCPCPCAGPLRPTSSFCAPG	1750
Qy	1947	RKSGVSRTHSLPNDYSVMCRN-GSTAERSLGHGWGLPKAGSGSILTSVHSQPATDSCILQ	2005
Db	1751	RGSGGAGAGG-DYESHLRCRYCSPAQFTL-----W-----LDSVSLIKDSLEGELTIDNL	1801
Qy	2006	PKDV-HYLLQPHG 2017	
Db	1802	SGSVFHHYASPDG 1814	

RESULT 12

US-10-425-800-5
; Sequence 5, Application US/10425800
; Publication No. US20030180886A1
; GENERAL INFORMATION:
; APPLICANT: Dietrich, Paul S.
; APPLICANT: McGivern, Joseph G.
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
; FILE REFERENCE: R0043B-REG sequence listing
; CURRENT APPLICATION NUMBER: US/10/425,800
; CURRENT FILING DATE: 2003-04-29
; PRIOR APPLICATION NUMBER: US/09/404,650
; PRIOR FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0

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; SEQ ID NO 5
; LENGTH: 1835
; TYPE: PRT
; ORGANISM: Rattus sp.
US-10-425-800-5

Query Match      44.4%; Score 5345; DB 14; Length 1835;
Best Local Similarity 55.4%; Pred. No. 0;
Matches 1138; Conservative 216; Mismatches 375; Indels 324; Gaps 45;

Qy 43 PRSRDPSVASRSSTTCGPGCAAGAGSTGTXDPSGADSEAE-----LPYPALAPVVPFYLQ 98
Db 8 PSAAAPAPPEGTQPGP-----RSPPPSPGLEPTEGTPDVPHPDOLAPVAFCLQ 62

Qy 99 DSRPSGWLRTVGNPFERFVSMVLVLLNCVTGLMFPCCBEDIACDSCRILQAFDDFIEA 158
Db 63 TTSFRNWCIKWCPNPFCECVSMVLVLLNCVTGLMGTQPCDDMECLSDRCKILQVDFDIFI 122

Qy 159 FFAVEMVVKVAILGIFGKKCYLGDWTNRLLDFFIVITAGMLEYSLDLQNVSFSAVRTVRVL 218
Db 123 FFAMENVLKNVALGIFGKKCYLGDWTNRLLDFFIVMAGVVEYSLDLQNINLSAIRTVRVL 182

Qy 219 PLPAINRPSMRILVTLTLLDTPMLGNVLLCFEFPPIFGIVGVQLWAGLNRNRCFLPN 278
Db 183 PLKAINRPSMRILVNLNLTTPMLGNVLLCFEFPPIFGIVGVQLWAGLNRNRCFLEN 242

Qy 279 FSLPLSVDLPEYYOTENEDESPFIQCSOPRENGWRSRVSPTLRGEGGGPPCSL----- 332
Db 243 FTTQGVVALPYYPQPEDDEMFPICSLTDGNGIMGCHIEIPPIKEQ---GRECLSKDDVY 299

Qy 333 DYETYNSSNTT--CVNNQYYTNCAGBNPKGAINPDNIGYAWIAIFQVITLEGWVD 390
Db 300 DFCAGRQDLNAGSLCVNNRNYNVCRTGNANPHKGAINPDNIGYAGIVIFQVITLEGWVE 359

Qy 391 IMYFVMDASHFYNYFIYFILLIIVGSFMINCLVJVIATOFSETKQRESQMLEQRVPLS 450
Db 360 IMYVNDASHFYNYFIYFILLIIVGSFMINCLVJVIATOFSETKQREHLMLEQRQYLS 419

Qy 451 NASTLASFSEPGSCYBELKLYVILRKAARLQAVSRAIGVRAGLSSPVARSQGPQP 510
Db 420 -STVASYAEPGDYEEIYQYVCHILRKAR-----RALGIYQAL----- 458

Qy 511 SGSCSTRSHRRLSVHHLVHHHHHHHHHNGTLVRPRASPEIQORDANGSRRLMLPPPS 570
Db 459 -----QNRROA-----MGPGT-----PAPA 473

Qy 571 TPTPSGPPRGAEVSHSFYHADCHLEPVRCQAPPRCPSEASGRVTGSKYVPTVHTSP 630
Db 474 KPQP-----HAK-----EPSCKLCPRHSPLD-----PTHT----- 500

Qy 631 PEILKDKALVEVAPSPGPTLTSFNIPPGPFSSMHKLLETQSTGACHSSCKISSPCSKAD 690
Db 501 -----LVQ-----PIGAIL----- 509

Qy 691 SGACGPDSPYC-----ARTGAGEPESADHWMPDSDEAVYEFTQDAQH 734
Db 510 --ASDPSSCPHCOHEAGRPSPGLGSTDQSGSGSGSAE---AEANGDGL-QSSEGGVS 563

Qy 735 SLDURPHSRRRORSIGPDAPSPSULA-----FWRLICDTFRKIVDSKYFGRGIMTALVN 789
Db 564 SD-----LGKBEQBDGAARLCGDVWRETRKRLGIVDSKYFNRRGIMMAILVN 611

Qy 790 TLSMGIEYHEQPEELTNALIEISNIYFTSLFALEMILLKLLVYGPFGYIKNPYNI FGVIVV 849
Db 612 TVSMGIEHHEQPEELTNILIEICNNVFTSPFALEMILKLAAGFLDYLRNPYNI FDSIIVI 671

Qy 850 ISVWEIVGQGGGLSVLRTFRMLRVLKLVRFPLALQRLVLMKTMNDNVATFCMLLMFI 909
Db 672 ISIWEIVGQADGLSVLRTFRLLRVLKLVRFPALRRQLVLMKTMNDVATFCMLLMFI 731

Qy 910 FIPSILGMHLFGCKFASERD-GDTLPDRKNFOSLWAIIVTFQILITQEDWNKVLNGMAS 968
Db 732 FIPSILGMHIFGCKFSRLTDTGTVDRKNFOSLWAIIVTFQILITQEDWNVVLNGMAS 791

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Db 639 -----KPGHAKPRH 649
Qy 577 GPPRGASVSHFYHADCHLBPVRQAPPCPSEASGRVTGSGKYVTVHTSPPEILKD 636
Db 650 YPLTVMSILGRQAECLT---RAAHP-----SSGASHPGVGSSEAPCLCPQ 694
Qy 637 KALVEVAP---SPGPPLTSFNIPPGPSSMHKLLETQSTGAC-HSSCKTSSPCSKADS 691
Db 695 HSPLDATPHLVQIPATLAS-----DPASCPCCQHDGRRRPSGLGSTD 739
Qy 692 GACCPDSCPCYARTGAGEPESADHVMPDSSEAYVEFTQDAHSDLDLPHSRRRQSLGP 751
Db 740 GQEGSGS---GSSAGGEDA-----DGDGA---RSEDCASSELKKEEBEQ-----781
Qy 752 DABPSSVLA---FWRLICDTRFKIVDSKYFGRGIMAILNLTSMGIYHEQPE-----802
Db 782 -ADGAVLCGDVWRETRAKLRGIVDSKYFNRGINMAILVNTVSMGIEBHHEQASAAQPGRA 840
Qy 803 -----ELTNALB-----ISNIV-----814
Db 841 CGRQNDLCLWTLKAPCLCHNVPSPGQGVLSHPVTPPHPTAPRMETKQGHGCEEGPQR 900
Qy 815 FTSIFALEMLKLIVYGPFGYIKPNYINIFDGIIVISWEIVGQGGGLSVLRTFRMLRV 874
Db 901 SSDMALEMLKLAAGFLDYLRPNYINIFDSIIVISWEIVGQADGGLSVLRTFRLLRV 960
Qy 875 LKLVFLPALQRLVLMKTMNDNVATFCMLLMLEFIFISILGMHLFOCKFASERD-GDTL 933
Db 961 LKLVFMPALRRQLVLMKTMNDNVATFCMLLMLEFIFISILGMHLFOCKFASERD-GDTL 1020
Qy 934 PDRKNPSLLWAIIVTFQILTOEDNKNVLYNGMASTSSMAALYFIALMTGNVYLFNLLV 993
Db 1021 PDRKNPSLLWAIIVTFQILTOEDNKNVLYNGMASTSSMAALYFIALMTGNVYLFNLLV 1080
Qy 994 AILVEGFOAE-----MSHPKSSSTGVG-----EALGSSRTSSSGSA-----1085
Db 1081 AILVEGFOAEVTVVLAEEAPQGLRTGRGGGLDGGLOKLLAGNLSLKEGVADEVD 1140
Qy 1006 ATKSESPDPFSPSV-----DGDGRKKGLALVALGHEAELRKSLLPLLIHT-- 1053
Db 1141 ANRSYDEQSSNIEBFQKLEGLDSSGDPK--LCPIPTPNHGLDPSL--PLUGHLGP 1196
Qy 1054 --AATP-----MSHPKSSSTGVG-----EALGSSRTSSSGSA-----1085
Db 1197 AGAAGAPRILSLQDPMVLVALGSKSSVMSLGRMSYDQSLVGLGRATAGVQAAGHLVP 1256
Qy 1086 EP-----GAAHMKCPSPARSSPHSPWASSTSRSSNSLGRAPSLKRRSPSGERR 1140
Db 1257 QPWVCLGADPNGNSFOSSSRSSSYGPWGRSAAMASRRSWN-----SLKHKPPSAHE 1310
Qy 1141 SLLSGE--QGESQDEESSEE--DRASPAGSDH-----RHRGSLBREAKSS 1182
Db 1311 SLLSAERGGGARVEVAADGPPRAAPLHTPHAHVHHGPHLAHRHRHRTLSLNDKRS 1370
Qy 1183 FDLPTLVQPLHRTASGRSS--ASEHQDCNGKASGRLEARTLT--DDQLDQDDND-- 1237
Db 1371 VDLAELVPAGAHPRAAWRAAGAPAGHEDCNGRMS--IAKDVFTKMGDRDGEDEEEI 1428
Qy 1238 -----EGNLSKGERIOAWVRSLPACCRERDSWAGYIPPPSPRFR-----LLC---1280
Db 1429 DYVSGGAEGDLTLCFRVKMIDVYKPDWCVEVDWMSVYLSPNRLRDLGWVSELCQG 1488
Qy 1281 -----HRIITHKMFHDVVLVIFLNCITIAMERPKIDPHSAERIFLTLSN 1325
Db 1489 VGDLVWVYVYQRRQRTIAHKLFDYVVLAFILNCITIALERQIEAGSTERIFLTVSN 1548
Qy 1326 YIFTAFLAEMTVKVALGWCFGQOAYLRSWNVLDGLLVLSVIDILVMSVDSGKIL 1385
Db 1549 YIFTAIFVGMTLKVYSLGLYFGEQAYLRSWNVLDGLVFNVSIDIVVSLASAGAKIL 1608
Qy 1386 GMLVRLRLRLRLPLRVISRAQGLKLVVETLWSSIKPTGNIWVLCACCAFFIIFGLIGVOLF 1445
Db 1609 GVLVRLRLRLRLPLRVISRAQGLKLVVETLWSSIKPTGNIWVLCACCAFFIIFGLIGVOLF 1668

RESULT 14

US-10-369-493-6836
; Sequence 6836, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:

; APPLICANT: Cao, Yongwei

; APPLICANT: Hinkle, Gregory J.

; APPLICANT: Slater, Steven C.

; APPLICANT: Goldman, Barry S.

; APPLICANT: Chen, Xianfeng

; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B

; CURRENT APPLICATION NUMBER: US/10/369,493

; PRIOR FILING DATE: 2003-02-28

; PRIOR FILING DATE: 2002-02-21

; NUMBER OF SEQ ID NOS: 47374

; SEQ ID NO 6836

; TYPE: PRT

; ORGANISM: Caenorhabditis elegans

; US-10-369-493-6836

Query Match 29.5%; Score 3553; DB 15; Length 1657;

Best Local Similarity 42.2%; Pred. No. 2.7e-226;

Matches 800; Conservative 234; Mismatches 436; Indels 426; Gaps 42;

Qy 66 AGSTKDPG-----SADSEAGLPLPALPVVFFYLSQSPRPSMCLRTVCN 112

Db 88 ASSEASPSRWEGROIEMNGEEQIEESE-LPYGPAEPALRCFYQARPPKQWALQWMS 146

Qy 113 PWFERSMLVILNCVTLGMFRPCED-IACDSORCRILQAPDDFIFAFFAVEMVVMQVAL 171

Db 147 PWFDRITMAVIMINCVTLMYRCPEDGDCDTCYRCQILDIIDNCIFVYFAPFEMVIMKAL 206

Qy 172 GIEGKKCYLGDWNRLDGDFIVIAQMLEYSYLDLQ---NVSPSAVTRVLRPLRAINRPS 228

Db 207 GFYGPAAVNSDTRNLRDFFIVMAGIAEFVLEHLYGGNINLTARTVLRPLRAVNRIPS 266

Qy 229 MRILVTLTLLDTLPMGLGNVLLCFVFFIFGIVGVLWAGLLNRRCF--LPENFS-----L 281

Db 267 MRILVTLTLLDTLPMGLGNVLLCFVFFIFGIVGVLWAGLLNRRCVNLPKTISENSQAL 326

Qy 282 PLSVDLBPYYOTENEDSPFCSPQRENGMRSCSVPTLRGEGGGGPPCSLDYETYNSSS 341

Db 327 FNNVKLFRFYPE-DTSLEVICSPDANGLHTCSNLPPTVD---GVKCNLTLDYDKVT 382

Qy 342 NTTCVWNYQYTNCSAG-----EHNPFKGAINFEDNIGYAWIAIFQVIT 384

Db 383 NDCSINNIIYNEECQVNIYPSLMTIAISCFIKVMQRPFGQSVSFDNIGFAWIAIFLVIS 442

Qy 385 LEGWVDIMYFMDAHSFYNFIYFILLIVGSGFFMINCLVVIATQFSETKQESQLMREQ 444

Db 443 LEGWTDIMYFQDAHSFNNWIIYFVLLIVIGAFFMINCLVVIATQFSETKQESQLMREQ 502

343 QY TTCVNNNOYTCNSAGBNPKGAINEDNIGYAMIAIPOVITLGGWYDMMYFVMD-AHSP 401
281 Db TEC-----REYNP-----GNFGITNFDNLIFALTVOCTITMEGWTIDILYNTNDAAGT 330
402 QY YNFIYFILLIIVGFFMINCLVIAVIAQFSETKQES-----OLMREQRVRFLSNASTL 455
331 Db WMLYFPIPIIIGSFFMLNLVLGVLSEFAKERERVENRAFLKLRQOQIE-----382
456 QY ASFSEPGSCYELLKYLVIILKARRLAQRVRAIGVLAGLLSPVARSQOEPQPSGCT 515
383 Db -----RELNGYLEWIFKAEVMLABED-----RNAEKSPLDLVK 417
516 QY RSHRLSVHHLVHHHHHHHHHGLNGTLRVPRASPEIQDRDANGSRRLMPPSTTPS 575
418 Db RAATKSRNDLIH-----AEEGBDRFAD-----440
576 QY GPPRGAESVHSFYHADCHLEPVRCQAPPPRCPSEASGRITVSGKVYPTVHTSPPPBLK 635
441 Db -----440
636 QY DKALVEVAPSGPPTLTSTNIPGPPFSMMKLLTQSTGACHSCHSKISPCSKADSGACG 695
441 Db -----LCAVGSPPFARAS-----452
696 QY PDCPCYARTCAGEPESADHWPDSDEAYVEFTQDAHQSDLRDPHRSRQRSLGPDAP 755
453 Db -----LKSGKTESSYF-----RRKEK-----469
756 QY SSVLAFWRLICDTPRKIVDSYKFGIGIMAILVNTLSMGIEYHQBELTNALEISNIF 815
470 Db --MERFF-----IRRMVKAQSFVVVLCVVALNTLCVAMVHYNQPRLLTLYFAEFV 521
816 QY TSUFALEMLKLVYGPFGYKPNYNIPDGVIVVISWEIVGO-----OQGGSLVLTFR 870
522 Db LGLFLTEMSLMYGLGPRSYFRSFCNFDFGVIVGSFVFWMAAKPGSSFGISVLRALR 581
871 QY LMRVLKLVRLPALQOROLVLMKMDNVATFCMLMLFIPTSLTGMHLFGCKFASERDG 930
582 Db LLKRFKVTYKWSLURNVLVLSLMSKSIISLLFLFLFVVFALLGMLFGGQFNODET 641
931 QY DTLPRDNFDSLMAIYVTFQILTQEDWNKVLNGM-----ASTSSWAALYFALMTFGN 985
642 Db PT-----TNFTFPAALITVQILTEDNVAHYGIESQGVSKGMPSFFYVILTLFGN 697
986 QY YVILNLVAILVEGFAEQBATSESEPDPFSPVSDGDRKRLALVALGEHABRLKSL 1045
698 Db YTLNLVFLAIVONLANAQLTKDEEWEBA-----NOKLALQAKEVAEV--SP 746
1046 QY LPPLIHTAATPMKSPKSSSTGVGEA-----1071
747 Db MSAANTISIAARQONSAKARSVWEORASQLRLQNLRSCEALYSEMDPEERLRFATTHLR 806
1072 QY -----LGSGSRRTSSGSAEPGAA-----HH-----EMKCP-----1097
807 Db PMKTHLDRPLVLVGLGRDARGPVGGKARPEABAPSGVDPDRHHHRDKDXTPAAGDQ 866
1098 QY -----PSARSS-----PHSPWGAASWTSSRRSRLNAGPLSKRRSPGERSRL 1142
867 Db DRAEAPKAESGEPGARBERPRPHRSKSEA--GPPEARSERGRGP-----GPEGGRHH 919
1143 QY LSCGQESQDEE-----ESSEEDRASPAGSDHHRGSLB---REAKSFDLPDIL 1189
920 Db RRGSPEEAAREPRRHRHQDPQSKCAGARRARRHRRGPRAGPREAESG-----972
1190 QY QVPG-LHRTASGRSSASE--HQDCNGKSAAGRLA-----RTLRTDDPOLQDDDDNDE 1238
973 Db EEPARRHARHQAQPAHEAVEKETTEKEATEKEAIVEADKEKELRNHQPREHCDLETS 1032
1239 QY GNLSKGBRIQAWRSRLPACCRER-----DSW-----1265
1033 Db GTTVGP-----MHTLFTSLQKVEQEPEDADNRQNVTRMGSPDPDNTIVHIVMLTG 1086
1266 QY -----SAYIFPPQSRFLLCHRI 1283

1087 Db PLGEATVVPSCNVDSLQAEKKKEVEADDVWRSGPRDIVPYSMFCSPNLLRRFCHYI 1146
1284 QY ITHKMFHDVVLVVIIFLNCITITAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTVKVVAL 1343
1147 Db VTKRYFEVWLVVIALSSIALAAEDP--VRTDSPPNNALKVLDYFTGVTFFEMWIKMIDL 1205
1344 QY GWCFGQAYLRSSWVLDGLLVLSVIDILSVW--SDSGTKILGLMLRVLRLRLRLRV 1402
1206 Db GLLLHPGAYPRDLWNILD-----FIVVSGALVAFAGSGKGDKINTIKSLRVLRLRPLKT 1261
1403 QY ISRAOGLKLVETLMSLKPIGNIVVICCAFFIIFGILGVQLPKGKFFVCOGE-----D 1456
1262 Db IKLPLKLVKAVDCVNSLKNVNLIVMLFMFIFAVIAVQLPAGKFFYCTDESKELERD 1321
1457 QY TRN--ITNKSDCABASYR--WVRHKYNFNDNLGQALMSLFLVLASKDGVWDIMYDGLDVGVD 1513
1322 Db CRGOYLDYEKEVEAQRQWKYDFHYDNVLWALLTLFTVSTGEGWPMVLKHSVDATYEE 1381
1514 QY QPIMHNPMLLYFISFLIIVAFVFLNMFVGVVVENFHKCRQHOHEEARRRBEKLLR 1573
1382 Db QGSPGGRMELSIIFYVYVYFVVPFFVFVIFVALIITF-----QEQDKVMBE-----CS 1431
1574 QY LEKRSKKEQMAEAOCKPVYSYR--PRLLVHLLCTSHYLDLFTIGVIGLNVVTWAME 1631
1432 Db LEKNERACIDFAISAKPLTRYMPONRQSPQYKTTWTVSPFPFVFINAMIALNTVLMMK 1491
1632 QY HYQOQIILBALICNYIFTVIFVFSFVKLVAFAPAFRRFFQDRWNQDLDAIALLSIMGIT 1691
1492 Db FYDAPYEYELMLKCLNVFTSMFMECVLIIAAGVLNPRDAWNVDFVTLGSDITIL 1551
1692 QY LESIE-----VNLSLPINPIIIRMLVRLARVLKLVKMAVGRALLHTVQALPQVGNL 1746
1552 Db VTEIAETNFINLS-----FLRLFRAARLIKLRQGYTIRILLMTVQVSKALPY 1602
1747 QY GLLPMLFFIIFAAALGVELFGDLSCDETHPCEGLGRHATPRFGMAFTLFRVSTGDNWNG 1806
1603 Db CLLIAMLFFIYALIGHQVFGNIALDDD---TSNRHNNFTFLQALMLLFRSATGEAWHE 1659
1807 QY IMKD--PSRCDQES--STCVNTVISPIYFSVLTAFV-----LVNV 1845
1660 Db IMLSCLSNQACDQANATECGSDFAVYFVFSFCLSFRLVRNMMPISNEDMTVHTST 1719
1846 QY VIAVLKHL-----ESNKEAKEAELEAL-----ELENKTLIS--POHSP-----LGSP 1889
1720 Db LMAIIRTALEIKLAPAGTKHQHQDAELRKEISVYVWANLPQKTLDLLVPHPKPDEMTYGV 1779
1890 QY F----LWPGVEGVNSTSPKPGAPHTTAHIGAASGFSLEHPTMVPHPEEVVPL-GPDLL 1944
1780 Db YAALMIFDFYKQKTTTRDQOQAPGGLSQMGPSLFP---HPLKATLEQTPAVLARGARV 1836
1945 QY TVRKGVSRTSLPNDSYMCNRNGSTABRSLSHGRWGLPKAQSGLSLSVHSQPADTSCILQ 2004
1837 Db LRQKST--SLSNGAIGNQESSIKESV---SWGTRQTD-----1872
2005 QY LPKDVHYLQPHCAPTGAIPKLPPGCRSLPAORPLRQAAIRTD-----2049
1873 Db -----PHEA-----RPLERGHSTPIVGRSGALAVDQVOMQSIITRRGPDGP 1914
2050 QY --SLDVQGLGSRDLLEVSGPCPLTRSSSFWGSSIOVQORSIGISKVSKHRLPAPC 2107
1915 Db QPLESGQ---RAASHPRLAETQPTVDASPMKRSISTLAQRPRG-----THLCSTTP- 1964
2108 QY PGLEPSWAKDPPETRS-----SLELDTLSWISGDLPLSSQEPFLP- 2149
1965 Db -----DRPPQASHHHHHCHRRRRDRKQSRLEKGPSLS-ADMDGAFSSAVGPGCLPP 2016
2150 QY -----RDLKKYCVETOSCRRRRFGFWLDEORRHSHIAVCLDSGSGPLCLSPS-----2197
2017 Db GEGPTGCRRRERQRGRSQRRQSSSSSEKQRF---YSCDRFGGRPPKPKPSLSH 2073
2198 QY -----SLGQPL-----GGPSRPPKKLSP--PSISIDPPES 2227

Db	2074	PTGTAQEPGPHPGSGSVNGSPLLSTGASTPGRRQLPQPLTPRPSITYKTANS	2133
Qy	2228	-----QGRPPCSPG-----VCLRRAPAD-----SKOPSVSSPLDSTA	2262
Db	2134	SPIHFAQAOTSLPAFSPGRLSRGLSEHNALLQRPUSQPLAPGSRIGSDPYLGQRLDSEA	2193
Qy	2263	ASPPKKDITLSL-----SGLSS	2279
Db	2194	SVHALPEDTITFEAVATNSGRSS	2217

Search completed: April 13, 2005, 19:30:57
Job time : 243 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 13, 2005, 18:36:39 ; Search time 71 Seconds
(without alignments)
3099.264 Million cell updates/sec

Title: US-09-611-257a-24
Perfect score: 12028
Sequence: 1 MLPHRVRCVTPPLRGSR.....KKDTLSLSGLSSDPTDMDPZ 2287

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: Pir1.*

2: Pir2.*

3: Pir3.*

4: Pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	11657	96.9	2254	2 T09053	low voltage-activa
2	3553	29.5	1657	2 T15838	hypothetical prote
3	1720.5	14.3	1810	2 T31092	probable voltage-g
4	1676	13.9	2339	2 A42566	omega-conotoxin-se
5	1655.5	13.8	2259	2 S29236	calcium channel pr
6	1653.5	13.7	2272	2 C54972	voltage-dependent
7	1652.5	13.7	1891	2 T43262	calcium channel al
8	1652.5	13.7	2178	2 S29237	calcium channel pr
9	1650.5	13.7	2288	2 S41080	calcium channel al
10	1642	13.7	2223	2 A47447	calcium channel pr
11	1640.5	13.6	2237	2 T45115	N-type calcium cha
12	1638	13.6	2251	2 B94972	voltage-dependent
13	1637.5	13.6	2270	2 A54972	voltage-dependent
14	1636	13.6	1993	2 T30902	sodium channel SCA
15	1632.5	13.6	2222	2 A37490	voltage-dependent
16	1632.5	13.6	2326	2 A45386	omega-conotoxin-se
17	1631	13.6	2181	2 A38198	calcium channel al
18	1628	13.5	1873	2 A30063	dihydropyridine re
19	1622	13.5	2161	2 JH0564	calcium channel al
20	1619.5	13.5	1911	2 T43048	calcium channel al
21	1616	13.4	1852	2 A37860	calcium channel pr
22	1614.5	13.4	1977	2 S54771	sodium channel alp
23	1613	13.4	2203	2 T42742	voltage-dependent
24	1610	13.4	2143	2 JH0427	voltage-dependent
25	1603	13.3	1610	2 A46227	voltage-dependent
26	1595.5	13.3	1783	2 T37258	probable voltage-d
27	1595	13.3	2166	2 S11339	calcium channel pr
28	1592.5	13.2	2139	2 A44467	voltage-dependent
29	1587.5	13.2	1646	2 JH0422	voltage-dependent

30	1587.5	13.2	1873	2 A55645	calcium channel, v
31	1585.5	13.2	2016	2 A38195	sodium channel pro
32	1580	13.1	1917	2 C88728	protein C48A7.1 [i
33	1577.5	13.1	1559	2 T30535	calcium channel al
34	1574	13.1	2171	2 S05054	calcium channel al
35	1573	13.1	2108	2 S72458	sodium channel pro
36	1567.5	13.0	1687	2 S41742	calcium channel al
37	1565	13.0	1957	2 S68453	sodium channel pro
38	1557.5	12.9	2220	2 A45290	calcium channel pr
39	1556	12.9	2019	2 A33936	sodium channel pro
40	1551.5	12.9	1840	1 CHRTM1	sodium channel pro
41	1549	12.9	1976	2 I56555	sodium channel pro
42	1546.5	12.9	1983	2 A60054	sodium channel pro
43	1546	12.9	2262	2 T30890	calcium channel al
44	1544.5	12.8	1951	2 S00320	sodium channel pro
45	1544.5	12.8	2005	2 A46269	sodium channel alp

ALIGNMENTS

RESULT 1

T09053

Low voltage-activated, T-type calcium channel alpha chain - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004

C:Accession: T09053

R:Perez-Reyes, E.; Cribbs, L.L.; Daud, A.; Lacerda, A.; Barclay, J.; Williamson, M.; Fox

Nature 391, 896, 1998

A:Title: Molecular characterization of a neuronal low voltage-activated, T-type, calcium

A:Reference number: 216538; MUID:98154730; PMID:9495342

A:Accession: T09053

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-2254 <PER>

A:Cross-references: UNIPROT:O54898; EMBL:AF027984; NID:g3786350; PIDN:AAC67372.1; PID:g3

A:Experimental source: strain Sprague-Dawley; brain

C:Genetics:

A:Map position: 17

A:Note: CACNA1G

C:Superfamily: voltage-dependent calcium channel protein alpha-1 chain

C:Keywords: calcium channel; voltage-gated ion channel

Query Match 96.9%; Score 11657; DB 2; Length 2254;

Best Local Similarity 99.7%; Pred. No. 0;

Matches 2219; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy	62	GAAGAGSTEDKPGSADSEAGLPYPALAPVVFYLSQDSRPSRSLRTVCNPFERSVSL	121
Db	30	GRQPGSTEDKPGSADSEAGLPYPALAPVVFYLSQDSRPSRSLRTVCNPFERSVSL	89
Qy	122	VILLNCVTLGNFRPCEDIACDSQRCLIQAFDDFIFAFVAVMVVQVVALGIFGKKCYLG	181
Db	90	VILLNCVTLGNFRPCEDIACDSQRCLIQAFDDFIFAFVAVMVVQVVALGIFGKKCYLG	149
Qy	182	DTNRLDFFVIAGMLEYSLDLQNVPSAVRTVRLPLRAINRVPNRLVTLTLLDPLP	241
Db	150	DTNRLDFFVIAGMLEYSLDLQNVPSAVRTVRLPLRAINRVPNRLVTLTLLDPLP	209
Qy	242	MLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLPENFSLPLSVLDLEPPYOTENEDESPF	301
Db	210	MLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLPENFSLPLSVLDLEPPYOTENEDESPF	269
Qy	302	ICSPRENGMRSCRSVPTLRGEGGGPPCSLDYETYNSSNTTCVNNQYYTNCASGHN	361
Db	270	ICSPRENGMRSCRSVPTLRGEGGGPPCSLDYETYNSSNTTCVNNQYYTNCASGHN	329
Qy	362	PFKGAINFNIGYAWIAIFQVITLEGWVDIMFYFMDAHSFYNFYIFILLIIVGFFMINL	421
Db	330	PFKGAINFNIGYAWIAIFQVITLEGWVDIMFYFMDAHSFYNFYIFILLIIVGFFMINL	389
Qy	422	CLVVIATQFSETKORESOLRQVRFLSNASTLASPECSCEELLYLAVTLKAAAR	481

Db 390 CLVVIATQFSETKQRESQLMREQVRFLSNASTLASPEPGSCVEELLKYLVLIRKAAR 449
Qy 482 RLAQVSAIGVRAGLISSPVARSQOEPOPSGCTSRSHRLSVHHLVHHHHHHHHVHLGN 541
Db 450 RLAQVSAIGVRAGLISSPVARSQOEPOPSGCTSRSHRLSVHHLVHHHHHHHHVHLGN 509
Qy 542 GTLRVPASPEIQORDANGSRRLMLPPSTPTSGGPPRGAESVHSFYHADCHLEPVRCQ 601
Db 510 GTLRVPASPEIQORDANGSRRLMLPPSTPTSGGPPRGAESVHSFYHADCHLEPVRCQ 569
Qy 602 APPRCPSASGRTVGSGKYVPTVHTSPPEILKDKALVEVASPPGPTTTSNIPPGPF 661
Db 570 APPRCPSASGRTVGSGKYVPTVHTSPPEILKDKALVEVASPPGPTTTSNIPPGPF 629
Qy 662 SSMHKLLETOSTGACHESCKISSPCSKADGACPDSCPYCARTGAGEPESADHVPDSD 721
Db 630 SSMHKLLETOSTGACHESCKISSPCSKADGACPDSCPYCARTGAGEPESADHVPDSD 689
Qy 722 SEAVYEFTQDAQHSDLRDPHSRRRQSLGPDAPSSVLAFWRLICDTFRKIVDSKYFGRG 781
Db 690 SEAVYEFTQDAQHSDLRDPHSRRRQSLGPDAPSSVLAFWRLICDTFRKIVDSKYFGRG 749
Qy 782 IMIAILVNTLSMGTEYHEQPELTNALEISNIVFTSLFALEMLLKLLVYGPFGYIKNPYN 841
Db 750 IMIAILVNTLSMGTEYHEQPELTNALEISNIVFTSLFALEMLLKLLVYGPFGYIKNPYN 809
Qy 842 IFDGVIVVISWEIVGQGGSLVLRTRFLMRVLKLVRFPLALORQLVLMKTMNDVATF 901
Db 810 IFDGVIVVISWEIVGQGGSLVLRTRFLMRVLKLVRFPLALORQLVLMKTMNDVATF 869
Qy 902 CMLLMLEFIFISILGMHLFGCKFASERDGDTPDRKNFDSLLMAIVTVFOILTQEDWNKY 961
Db 870 CMLLMLEFIFISILGMHLFGCKFASERDGDTPDRKNFDSLLMAIVTVFOILTQEDWNKY 929
Qy 962 LYNMGASTSSWAALFYFALMTFGNYVLNLLVAILVEGFOAEGDATKSESEDPFSPSVD 1021
Db 930 LYNMGASTSSWAALFYFALMTFGNYVLNLLVAILVEGFOAEGDATKSESEDPFSPSVD 989
Qy 1022 GDGRKKRLALVALGEHAELRKSLLPPLIITHAATPMHSPKSSSTGVGEALGSGSRRTSS 1081
Db 990 GDGRKKRLALVALGEHAELRKSLLPPLIITHAATPMHSPKSSSTGVGEALGSGSRRTSS 1049
Qy 1082 SGSAEPGAAHMKCPSARSPPHSAASSTWTSRRSRNSLGRAPSLKRSPPSGRRS 1141
Db 1050 SGSAEPGAAHMKCPSARSPPHSAASSTWTSRRSRNSLGRAPSLKRSPPSGRRS 1109
Qy 1142 LLSGEGQESQDEESSBEDRASPGSDHRRHGSLEAKSSFDLPDITLQVPLHRTASGR 1201
Db 1110 LLSGEGQESQDEESSBEDRASPGSDHRRHGSLEAKSSFDLPDITLQVPLHRTASGR 1169
Qy 1202 SSASEHQCNGKSGASGLARTLRTDDPQLDGGDDNDDEGNLSKGERIQAWVRSRLPACCRE 1261
Db 1170 SSASEHQCNGKSGASGLARTLRTDDPQLDGGDDNDDEGNLSKGERIQAWVRSRLPACCRE 1229
Qy 1262 RDSWSAYTFPPQSRPRLIICHRITTHKMDPHVVLIIIFLNCITIAMERPKIDPHSAERIFL 1321
Db 1230 RDSWSAYTFPPQSRPRLIICHRITTHKMDPHVVLIIIFLNCITIAMERPKIDPHSAERIFL 1289
Qy 1322 TLSNVIPTAVFLAETWVKVVALGWCFCQAYLRSSNNVLDGLLVLSIVDILVSNVSDSG 1381
Db 1290 TLSNVIPTAVFLAETWVKVVALGWCFCQAYLRSSNNVLDGLLVLSIVDILVSNVSDSG 1349
Qy 1382 TKILGMLRVLLRLTLRLVRSIAQGLKVETLMSSLKPIGNIWVICCAFFIIFGLG 1441
Db 1350 TKILGMLRVLLRLTLRLVRSIAQGLKVETLMSSLKPIGNIWVICCAFFIIFGLG 1409
Qy 1442 VOLFKGKFFVCGEETRNITNKSDCAEASYRWVRHKNYFNLMGQALMSLFLVLSKDGWVD 1501
Db 1410 VOLFKGKFFVCGEETRNITNKSDCAEASYRWVRHKNYFNLMGQALMSLFLVLSKDGWVD 1469
Qy 1502 IMYDGLDVGVDQOQPMHNPWMLLYFISFLIIVAFFVNNFVGVVNFHFKCRHQBE 1561
Db 1470 IMYDGLDVGVDQOQPMHNPWMLLYFISFLIIVAFFVNNFVGVVNFHFKCRHQBE 1529

Qy 1562 EARRREEKRLRELEKKRRSKEKQMAEAQCKPYYSRFRLLVHHLCTSHYLDLFTTGYI 1621
Db 1530 EARRREEKRLRELEKKRRSKEKQMAEAQCKPYYSRFRLLVHHLCTSHYLDLFTTGYI 1589
Qy 1622 GLNVVTMAHEHYQQOQILDEALKICNYITPTVIFVESVFKLVAFAFRFRFQDRWNOLDLA 1681
Db 1590 GLNVVTMAHEHYQQOQILDEALKICNYITPTVIFVESVFKLVAFAFRFRFQDRWNOLDLA 1649
Qy 1682 IVLLSTWGTITLBEIEVNLSPINPTIIRIMRVLRARVLKLLKMAVGMALLHTVMQALP 1741
Db 1650 IVLLSTWGTITLBEIEVNLSPINPTIIRIMRVLRARVLKLLKMAVGMALLHTVMQALP 1709
Qy 1742 QVGNLGLLFWMLFFIFPAALGVLELFGDCEDETHPCEGLGRHATFRNFGMAFLTFRVSTG 1801
Db 1710 QVGNLGLLFWMLFFIFPAALGVLELFGDCEDETHPCEGLGRHATFRNFGMAFLTFRVSTG 1769
Qy 1802 DNWNGIMKDPDRCDQESTCYNTVISPITYFVSFVLTAQFVLNVNVTAVLMLKHEESNKEA 1861
Db 1770 DNWNGIMKDPDRCDQESTCYNTVISPITYFVSFVLTAQFVLNVNVTAVLMLKHEESNKEA 1829
Qy 1862 KEBAEAEAELEEMKTLSPQHPSPGLSPFLWPGVEGVNSTDSPKPGAPHTTAHIGAASGF 1921
Db 1830 KEBAEAEAELEEMKTLSPQHPSPGLSPFLWPGVEGVNSTDSPKPGAPHTTAHIGAASGF 1889
Qy 1922 SLEHPTMVPHPPEVPVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAEBSLGHGWL 1981
Db 1890 SLEHPTMVPHPPEVPVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAEBSLGHGWL 1949
Qy 1982 PKAQSIIISVHSOPADTSCILQPKDVHLLQPHGAPTGAIPKLPPGRSPLAORPLR 2041
Db 1950 PKAQSIIISVHSOPADTSCILQPKDVHLLQPHGAPTGAIPKLPPGRSPLAORPLR 2009
Qy 2042 RQAAIRTDLSLDVQGLSREDLLSEVSGPCLTRSSSFWGGSSIQVQORSIGQSKVSKHI 2101
Db 2010 RQAAIRTDLSLDVQGLSREDLLSEVSGPCLTRSSSFWGGSSIQVQORSIGQSKVSKHI 2069
Qy 2102 RLPAPCGLEPWSWAKDPPETRSLSLELDTLSWISGDLPLSSQEEPLFPDRLKKCYSVETQ 2161
Db 2070 RLPAPCGLEPWSWAKDPPETRSLSLELDTLSWISGDLPLSSQEEPLFPDRLKKCYSVETQ 2129
Qy 2162 SCRRRPFGLWDEORRHSIAVSCLDSDGSPRLCPSPSLGQPLGGPGSPKPKLSPPSIS 2221
Db 2130 SCRRRPFGLWDEORRHSIAVSCLDSDGSPRLCPSPSLGQPLGGPGSPKPKLSPPSIS 2189
Qy 2222 IDPPESQGSRRPPCPGVCLRRRAPASDKDPSVSPDLSTAAASPKKOTLSLSGLSSDP 2281
Db 2190 IDPPESQGSRRPPCPGVCLRRRAPASDKDPSVSPDLSTAAASPKKOTLSLSGLSSDP 2249
Qy 2282 TDMDP 2286
Db 2250 TDMDP 2254

RESULT 2

T15838
hypothetical protein C54D2.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 17-Mar-2000
C;Accession: T15838
R;Minx: P.
submitted to the EMBL Data Library, October 1995
A;Description: The sequence of C. elegans cosmid C54D2.
A;Reference number: Z18415
A;Accession: T15838
A;Status: preliminary; translated from GE/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-1657 <MIN>
A;Cross-references: EMBL:U37548; NID:g1017804; PID:g1017809; PIDN:AAA79201.1; CESP:C54D2.5
C;Genetics:
A;Introns: 40/2; 67/3; 86/3; 121/2; 199/3; 230/2; 308/2; 334/2; 370/2; 439/3; 470/3; 513/3;
C;Superfamily: sodium channel protein

A;Molecule type: mRNA	
A;Residues: 1-1810 <WHI>	
A;Cross-references: UNIPROT:O44930; EMBL:AF041851; NID:g2791840; PID:g2791841; PIDN:AA89	
C;Genetics:	
A;Gene: Na1	
C;Superfamily: sodium channel protein	
Query Match	14.3%; Score 1720.5; DB 2; Length 1810;
Best Local Similarity	25.8%; Pred. No. 6.2e-101;
Matches	509; Conservative 342; Mismatches 694; Indels 429; Gaps 65;
Qy	110 VCNPFERVSMLVILLANLTLGMRPCEDIAQSDQRCLILQAFDDFI-AFFAVENVMVM 168
Db	110 ITNOFFEFFILLITIVNCIFAL-----RDAPEQEVYFAAIYFEMLLKI 155
Qy	169 VALG-IFGKKCYLGDWNRLDFFIVIAQMLEYSLDLQNVFSVAVTVTVLRPIRAINRVP 227
Db	156 IAKGLVMHEYAYLRDPNNWLDVVVILGYVTLVPNVANL--SGIRIPVRLALRTISAVE 213
Qy	228 SMRLVTLTLLDTPMLGNVLLCFVFFIFGIQVQVQVWAGLLRNCRFLPENFSLPLSVDL 287
Db	214 GLKTMVALLKSMKMLSDVLLITFFLCVPAVGQMLFVGSRLNCKVLKPLMTTIDYDS 273
Qy	288 ---EPYOTENEDSPICOPRENGMRSRCSVPTLRGGGGPGPCSLDYETYNSSNT 343
Db	274 FVTNESHYHHPDTPITC-----GNSTAGPCPLNV----- 306
Qy	344 TCVMNYYTNCSEAGEHNPFGKAINFONIGVAMTAIQVITLEGVDIMYFVMDAHSPYN 403
Db	307 TCL-----ANIG-NNPNYGYTNLDFNGWAVITAFQVLTLDYENYVYVLSMSGWY 357
Qy	404 FIYFILLIIVGSFMINLCLVIAVITOPSETKQESQLMREORVRFNLGNASTLASFSPPGS 463
Db	358 IFYFMVIFPGSFYLLNLVLAVALVSY-----QEVIALQDRENYNNLKVASLSYFHG 412
Qy	464 CYEELLKYLVLIRKAARLAQVRAIGVRAGL-LSSPVARSQEPPOPSGCTSHRRLS 522
Db	413 C-----VVPKLLNSKSKTSLASKCMGFCVPCFSGIKQPEHSNG----- 453
Qy	523 VHLVHHHHHHHHYHLNGILRVPRASPE---IQDRDANGSRRLMLPPPTPPSGPP 579
Db	454 ---HASDNESHASTG-GTIRVDSTALEMKMLDKNEVTNGHSLPEPT----- 499
Qy	580 RGAESVHSFYHADCHLEPVRQAPPPRCPSEASGRVTSVGKVPYTVHTSPPEILKOKAL 639
Db	500 ---SSFF-----SVSSDN---SIH-----IRNSS 518
Qy	640 VEVAPSGPPTLTSP--NIPPGFSSMKLLETQSTGACHSCKTSSPCSKADSGACGPD 697
Db	519 TEVMPQ-----TSKFDNIT-----LTKLTDVKS-----SFLKLSAISBOSS----- 555
Qy	698 SCPYCARTGAPESADHVPDSDSEAVVEFTQDAQHSDLRDPHRRRQRSLGPDAPESP 757
Db	556 ---TDGVNDNENINNTQOKSVSFARV-----LTPRGSARQTSTGSAATHKT 601
Qy	758 VL---AFWRLICDTFRKIVDSYFGRGIMAILVNLNGIYHQPQBELTNALBISNIV 814
Db	602 ITKQDTKWRIRRMISKIVLHGVTMTFTFCTVWNTFLSLRYHNMDSNYLMLVIGNKV 661
Qy	815 FTSLFALEMLLKVLPYGPYKIPNIPNIDGVIVLSVWE-----IVGQGGGLSVLRTF 869
Db	662 FTWVFLLEMLKLTAFGFGYKSRWNIIDGFIWISVMVDLMVELLVDDHSDGLSVLRTF 721
Qy	870 RLMRVLKLVRLPALQRLQVLMKMDNVATFCMLMLFIFISILGMHLFOCKFASERD 929
Db	722 RLRLVFKLAGSQWTMMMLSTIARSVQLGNLTLVLGIVYMLAVVGVLFDQYYTKNF 781
Qy	930 GDTLPKRPDLSLLMAIVTVFQILTQEDWNKVLYNGMASTSWAALYFYALMTFGNYLFL 989
Db	782 NGDVP-RWNFTDFWHSFMIFRVLGGE-WIEPLYDCMRASTWATLFFLTIVIGNFLVL 839
Qy	990 NLVAILVEGFGAEG---DATKSESPDFFSPVDGDRKKRLALVALGEHAELRKS-- 1044

RESULT 4
A42566

Db	840 NLFLALLINAFARESLQEAKKTKPKSKFAQGV-----SKLSR-ALRPRSTVSKTKQ 891
Qy	1045 LLPPLLIHTAATPMHPKPSSTGVEALGSGSRRTSSGSAEPGAHHEMKPCPSARSPP 1104
Db	892 VLPIRVHD-----GENATDGD-----APTQNGL 917
Qy	1105 HSPMSAASWTSRRSSNSLGRAPSLKRRSPSGE-----RRSLSGEQESQDEESES 1158
Db	918 ESKTSDSAISTSSNASNAMISAVTAFQGNKKGKLNDRDTFRLSLATE----- 965
Qy	1159 EDRASPACSDHRRGSLEREAKSFDLPTDTQVPLHRTAGSRSSASEHQCNGKASGR 1218
Db	966 -----TANSDSNTSNVLMAASST-----SITGR 989
Qy	1219 LARTLRTDDPQLDGGDDNDENGLSKGERIQAWRSRLPACCREDSMSYAI-FPQSRFR 1277
Db	990 -----QDHGTSDDPPDPMTEVDECCPWCNMKTCGCITR--WKASDGYRSWRLR 1037
Qy	1278 LLCHRIITHKMPDHVVLIIFLNCITIAME-----RPKIDPHSAERIFLTLNVIPTAV 1331
Db	1038 LAVKKEVHEKYPEWTLIAIMASSIALTFEDINLPSRPL-----KEYLQVNLNIFFAVT 1091
Qy	1332 FLAEMTVKVALGCGEAOYLRSWNVLGILLVLSVIDIILVMSVDSGTK--ILGMLR 1389
Db	1092 FSIEFLKVLGL-----GVVSIFRNCNCLDLVLFVPV-----SSVIADSSNQDSSLSLR 1143
Qy	1390 VLRLTLRLPLRVISRAQGLKLVETLMSLKPIGNIVVCCAFFIIFGILGVLPKGF 1449
Db	1144 SLRTLALPLRAISRWEGRVWVNSLLFAIPGIGNVLLVCMVFWLFIISMVGVPFGGRF 1203
Qy	1450 FVCGEDTEN-----ITNKSDEASRYRVRHKYFNFDNLQALMSLFLVLASKDGVWDIMY 1504
Db	1204 FKCVDNKRLPISIVQNRSECIQGYRWNSDINDFSLNGFMALFOVATEGIEWVR 1263
Qy	1505 DGLDVGVDQOPIMNHPWMLLYFISFLIVAFFVLNMPVGVVVENFHKRQHOBE----- 1560
Db	1264 DAVDAREVDOQSDGYNFSAYAFVVFIVGSGFTLNFIVIGIINDFNRLKQYEDFGAL 1323
Qy	1561 -----EABRREKRLRLEKRSKQMAEAQCKPYSDY---SRFLLVHLHCTSHYL 1613
Db	1324 DVLLTQSRAFOTIRKAATKPKKVISRPENSFMWLFVDVHSSRFELI----- 1374
Qy	1614 DLFTIGVIGLVVTVMAHEYQOQIILDEALKICNYIFTVIFVPESVFKLVAFARFPD 1673
Db	1375 -MFF---ICNLILVMMIQHYGQKPAVEQALMIINLVFTGLTLEALIRIWLRL-HYFRE 1429
Qy	1674 RMNQLDLAIVLLSIMGITLEEIEVNLSPINPTIIRIMRVLRIRVLRVLRVLRVLRVLRV 1733
Db	1430 PMNVDFVIVLSTILGILHLEHLELFTPSPF---VARVFRIGRLRFRYKGAIGIRLL 1486
Qy	1734 HTVMQALPOVNGLLFMLLFFIFALGVLELFGDCEDETHPCGELGRHATFRNFGMAFL 1793
Db	1487 FALISLIPALLNIGALLFLIMFIYALIGSSFGYVK-----KTGALDSVNVFETFGNSML 1541
Qy	1794 TLFVSTGDNWNGIMKD---PSRDCQOE-----STCYNTVTSPIYFVSFVLTAQFVLVN 1844
Db	1542 LLFELSTAGNDVLLKLLIKPPCDKLCWICPNGNCSTPWLAVVYFTTLEFLELIIN 1601
Qy	1845 VVIATLMLHEESKEAKEAELEAELEEMKLTSPQPHSPGLSPFLWPCVEGVNSTDSP 1904
Db	1602 MYTALILENLSOAH-EQEEVGVTDLDDMFY-----YHWRFD----- 1638
Qy	1905 KPGAPHTTAHGAASGF-SLEHPTMVPHPEE-----VPVPLGPDLLTVRKSQVSRTH 1955
Db	1639 -PGATQVIPH-SALSDVFDGLDHLRIPQPKFACINLNIPIKQ-----DRVH 1685
Qy	1956 SLPNDSYCNRN--GSTAERSLGHGWLGPQAQSGSILSVHSQPADTSCILQLPK 2007
Db	1686 CFVWQALVRRVLGDIBEDGLG-----SSSVAYTLMKSKMEQHCISTFFPK 1730

Db 1552 VTEIAETNNFINLS-----FLRLFRARLILKLLRQGYTIRILLWTFVQSFKALPVV 1602
Qy 1747 GLLFMLFFIIPALGVNLFGBLDETHPCGEGIGRHAFFNFGMAFLTFPRVSTGNWNG 1806
Db 1603 CLLIAMLFFIYAIIGMVGNIALLDDDD---TSINRHNFFTLQALLMFLFRSATGEAMHE 1659
Qy 1807 IMKD--PSRCDQE--STCYNTVISPIYFVSFVLTAQFVLAVVAVLVMKHLSEESKEAK 1862
Db 1660 IMLSLSNQACDEANATECGSFAYFYFVSFPLCSFLMLNLFVAVIMDNFYLRDSS 1719
Qy 1863 -----EBAELAELE-----LEM-KTILSPQPHSPLG-----SPFLWPGV 1895
Db 1720 ILGPHHLDEFIRVWAEYDPAACGRISYNDMFELKMSPP---PLGLKKCPARVAYKRL 1775
Qy 1896 EGVNSTDSPKGAHTTAHGAAGSFLS-----HPTWVPHPEVPV----- 1937
Db 1776 VRMNPISNEDMTVHFTSTLMALIRTALEIKLAPAOTKQHCDAELKEISVWVANLPQK 1835
Qy 1938 -----PLGDLTLVRSKGVSRTHSLPNDSYMCRNGSTAESLSLGHRCWGLPKAQSIL 1990
Db 1836 TLDLLVPHKDEMTVGKYAA---LMIFDY---KQNTTRDQMOQAPGGL--SQMGVPS 1888
Qy 1991 SVH-----SQPA-----DTSCILQ-----LPKDHYLIQ-----P 2015
Db 1889 LFHPLKATLEQTQPAVLRGARVFLRQKSSTSLNCGAIONOESGIKESVSWQTQDAP 1948
Qy 2016 HGAPTWGAIPKLPPGSRPLAQRPLRQAARTDSLOVQ-----GLGSRE 2060
Db 1949 HEA-----RPFLRGHSTEIPVGRSGAL---AVDVQMSITRRPDQDPQGLSESQ 1997
Qy 2061 DLLS--EVSGPCPLTRSSFWGSSIQVQORSIGQSKVSHIRLPAPCPGLEPFWAKDP 2118
Db 1998 RAASMPRLAETQPTDASPMKRSISTLAQPRG-----THLCSITP-----DRPP 2043
Qy 2119 PETRS-----SLELDELWISGDLPLPSQOEPLFP-----RDL 2152
Db 2044 PSQASSHHHRRCHRRDRKQSLKSGPSLS-ADMDCAPSSAVGGLPFGGEQPTQCRER 2102
Qy 2153 KKYSVETQSCRRPFGWLDQRHSIAVCLDSGQSLCPSPS----- 2197
Db 2103 ERQBRGRSQRRQPSSSSKQRP---YSCDRFGREPPPKPSLSHPTSPAGQEPG 2159
Qy 2198 -----SLGGQPL-----GGPGRS---PKKLSP-PSIS-----IDPESQGS 2230
Db 2160 PHPQSGSVNGSPLLSSTGASTPGRQRRQLPQPLTPRPSITVKTANSSPIHFAQAQTS 2219
Qy 2231 RPPCSFG-----VCLRRAPASD-----SKDPSVSSPLDSTAASPSPKKDTLS 2273
Db 2220 LPAFSGRLSLGSEHNLQRDPLSQPLAPGSRIGSDPYLQORLDSSEAVHALPEDTLT 2279
Qy 2274 L-----SGLSS 2279
Db 2280 FEEAVATNSGRSS 2292

RESULT 5
S29236
Calcium channel protein BII-1, brain - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: S29236
R:Nidome, T.; Kim, M.S.; Friedrich, T.; Mori, Y.
FEB8 Lett. 308, 7-13, 1992
A:Title: Molecular cloning and characterization of a novel calcium channel from rabbit
A:Reference number: S29236, MUID:92354772; PMID:1379552
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-2259 <NIT>
A:Cross-references: UNIPROT:Q02343; EMBL:X67855; NID:g1472; PIDN:CAA48040.1; PID:g1473
C:Superfamily: voltage-dependent calcium channel protein alpha-1 chain
C:Keywords: transmembrane protein

Query Match 13.8%; Score 1665.5; DB 2; Length 2259;
Best Local Similarity 23.8%; Pred. No. 2.6e-97;
Matches 606; Conservative 379; Mismatches 844; Indels 719; Gaps 87;
Qy 62 GAAGAGSTKDPGSADS--EAGLPYPALA-----PV----- 91
Db 5 GEAAAGRAPASBGSDSDQGRNLPGTVPASGSAAYKQSKAQRARTMALYNPIPVQNCFT 64
Qy 92 ---VFYLSQDSRPRSCLRTVCNFWFVRVSMVLVILLNCVLTGMPR--PCEDIAQSORC 146
Db 65 VNRSLFEGEDNIVKYAKKLIDWPFYEMILATIANCIIVLALQHLPEDDKTPMSRR- 123
Qy 147 RILQAFDFIFAFFAVEMVVKWVALG-IFGKCYKLGDTWNRLDFFIVTAGMLEYSLDQ 205
Db 124 --LEKTEPYFIFGCFEAGIKIVALGFIHKGSYLRNGWNVMDFTVVLSGILATAGTHFN 181
Qy 206 --VFSAVRTVAVLPLRAINRVPMSRILVTLTLLDPLMGNVLLLCFFVFFIGVGVQ 263
Db 182 THVDLRTLRAVRLPLKLVSGIPSLQIVLKSIMKAWPLQIGLLFFAILMFAIGLE 241
Qy 264 LWAGLLRNRCLPENFSLPLSDLEPYQTENEDESPFICSQPRENGMRSCRSVPTLRGE 323
Db 242 FYSGKLHRACFVNN-----SGVLEGF-----DPHPHC----- 268
Qy 324 GGGPPCSLDIYETNSSNTTCVNNQYNTNCSEHNPFGKAINFDNIGYAWIAIFOVI 383
Db 269 --GVQCPAGYE-----CKDM-----IGNDGITQFDNLFVAVLTVFCI 306
Qy 384 TLEGVDIMVFMVDA-HSPYNTYFILLIIVGSFFMINLCLVVIATQFSETKQRESQLMR 442
Db 307 TMEGTTVLYNTDNGALGATWNLVYFPLIIIGSFVNLVGLVSGEFAKERERV---- 361
Qy 443 EQRVRFSLNASTLASFSEPGSCYEELLKYLVLAKAARLQAVSRAL-GVAGALLSSPV 501
Db 362 ENERRAFMK-----LRQQOIERELNGYRAWDKABE 392
Qy 502 ARSQGPQSGCTSRHRLSVHLVHHHHHHHHVHLNGTLRVPRASPEIQDRDANGS 561
Db 393 VMLAENKNSGSALEVLRRAT-----IKRSTEAMTRDSS-- 428
Qy 562 RRLMLPPPSTPTPSGGPPRGAESVHSFYHADCHLEPVRCAQPPPCPPCPSEASGRTVSGKV 621
Db 429 ----- 428
Qy 622 YPTVHTSPPPEILKQKALVEVAPSPGPPTLTSFNIPPGFPSSMHKLETTQSTGACHSSCK 681
Db 429 -----DBHCVDIS-----S 437
Qy 682 ISSPCSKADSGACGPDSCPYCARTGAGEPESADHVPDSDSEAVYEFTQDAQHSDLRDPH 741
Db 438 VGTPLARASIKSAKVDGASY-----FRHKE----- 462
Qy 742 SRRRQSLGPDABFSSVLAFAWRLICDTRFKIVDSKYFGRGIMTIALIVNTLSMGIEVHEQP 801
Db 463 -----RLLRISVRHAKVSQVYFVIVLSLVALNTCAVAIVHNQP 501
Qy 802 BELTNALEISNIVFTSLFALEMLLKLLVYGPFCYIKNPYNIFDGVIVVSWIVGQ--- 858
Db 502 QWLTHLYYAEFLFLGLFLEMSLKMVGMPGRIFYHSSFNCFDGVTVGSIFFVWVAIFR 561
Qy 859 --QGGGLSVLRTFLMRVLKLVFLPALQRLVLMKTDNDVATFCMLLMFLFIFSLG 916
Db 562 PGTSFGISVLRALRLRIFKITKYWASLRNLVVSLSMSSMKSIISLLFLFLFVWVALLG 621
Qy 917 MHLFGCKFASERDGTLPDRKRNFDLSLMAIVTVFQILTQEDWNKVLNMG-----ASTSS 971
Db 622 MOLFGGRF-NFNDG---TPSANFDTFPAAITVTFQILTGEDWNEVMVNGIRSQGGVSSGM 677
Qy 972 WAALYPTALMTFGNYLVLLVALLVEGFOAEGDATKSE-SEPDFS----- 1017
Db 678 WSAVYFVILTLFGNYTLNVLAVLAVDNLANAOELTKDEQEESAEAFNQKHALQKAEVSP 737
Qy 1018 -----PSVDGDDGRKKRLAL-----VALGEHAEL 1041

Db 738 MSAPNVPSIERDRRRHHMSWEPSSHLRERRRRHMSVWEQRTSQLRRHMQSSQAL 797
Qy 1042 KSLPLPILIIHTAATPMG--HPKSSSTGV-----GEALGSGSRRTSSGSAEPGAHHE 1093
Db 798 NKEEAPPNNPLNPLNPLNAHPSLRRPRMEGLALGLEKCEBEHVSRRGSLKGA 857
Qy 1094 MKCPS---ARSSPHSPWSA-----ASSWT-----SRSSRNSLGR 1126
Db 858 LDCQSPUSLGRRP--PWLARPCGNCEPALQETAGGETVVTEDRARHQSQRSSHR 915
Qy 1127 APSLKRSPSGERSLLSGEGQESODEEESSEEDRASPAQSDHRRHGS-----LERE 1178
Db 916 RVRTEAKSSASRS-----RSVQSRLDEGASTEGEDHARGSGHCKEPTIHEE 968
Qy 1179 AKSFDPLDPTLOVP-----GLHRTAS-----GRSSAHEQCNKGSASGR-- 1219
Db 969 RAQDLRRTDSLWVPKSGLAGLOEAGTPLVLSPEGVGKEAAPTEQHADGSGEPALLGH 1028
Qy 1220 -----ARTLRDQDQ-----DGDNDDE-----GNLSKGE-- 1245
Db 1029 VOLDVGRASQSEPDLSQVATTDKVTTSTEDTVAIPDAEPLVDSTVVHIGNTKDGEAS 1088
Qy 1246 -----RIQAWRSRLPACCRERDSWSA-YIPPOSRLPCLLCHRIITHKMFHV 1292
Db 1089 PFQEAEMKEAQETEKQKKERPPASGKAWPHSSWFIPSTSNPIRRACHYVNNRYFEMC 1148
Qy 1293 VLVIFILNCITIAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTVKVALGWCFCGEQAY 1352
Db 1149 ILLVIAASSIALAAEDPVLTSERNRV-LRYFDVYFTGVFTFEMVIMQIDQLILQDGSY 1207
Qy 1353 LRSSWNLVDGLLVLSVIDI-LVSWVSDSGTKILGMLRLVLRLLRLPLRVISRAQGLKL 1411
Db 1208 FRDLWNILDFVVVVGALVAFALANALGTNKGDKITIKSLRLVLRPLKTIKRLPKLKA 1267
Qy 1412 VVETLMSLKPIGNIWIWICCAFFIIFGILGVQLFKGFVC--QGEDRN-----INK 1463
Db 1268 VFDCVTSLKNNVNLIVYKLFMFIFAVIAVQLFKGFYFYTDSKDKTEKICIGNYVDHE 1327
Qy 1464 SDCAEASVR-VWRHKYFNPDNIQALMSLFLVLSKGDWVDIMYDGLDVGVDQOQPMHNHP 1522
Db 1328 KMKMEVGKREKREHYDNIWIIWALLTLFTVSTGEGWPQVLQHSVDVTEEDRGSPSRNM 1387
Qy 1523 WMLLYPISFLILVIAFFVLNMFVGVVFNHFKCRHQHQBEEBARREKRLRLKRSKE 1582
Db 1388 EMSIFVYVYVFFVFFVFFVFFVFFVFFVFFVFFVFFVFFVFFVFFVFFVFFVFFVFF 1437
Qy 1583 KOMAEACKPYSDYSR--FRLLVHLLCTSHYLDLFTINGVLGNVMTWAMEHYQOQOILD 1640
Db 1438 DFAISAKPLTRYMPQNRHTFQYRVWHFVVSFETIMATNLTNVLMMKYISAPCTYE 1497
Qy 1641 EALKICYIFTVIFVFESVFKLPAFAFRFPQDRMNQLDLAIVLLSINGITLIEBIEVLS 1700
Db 1498 LALKYLNIAFTMVFSLECVLAVIAGFVFNYPDWTNIFDPTVIGSITEIVLTDKLVNT 1557
Qy 1701 LPINPTIIRNVRUARIARVLKLMVAGMRALLHTVMQALPQVNLGLFLLMFLFFIIFAL 1760
Db 1558 TGFNMSFLKPLRA---ARLIKLRQGYTIRILLTFTVQSPFALPYVCLLIAMLFFIYAI 1614
Qy 1761 GVLEFGDLECD-ETHPCBGLRHRATERFGMAFTLFRVSTGDNWNGIMKD--FSRCD- 1816
Db 1615 GMQVFGNIRLDESH-----INRHNFRSFFGSLMLLFRSAYGEAWQEIJLSCLEKGECEP 1670
Qy 1817 -----QUESTCNTWISPIYFVSFVLTAQFVLNVVVIAMVKHLEESKEAK----- 1862
Db 1671 DTTAPSGQESGCTDLAYVYFVSFFPCFSLMLNLFVAVIMDNFEVLITSDSILGPHH 1730
Qy 1863 --EBAELEAELE-----LEMKTL-SPOHSPGLG-----SPLMPGVEGVNST 1901
Db 1731 LDEFVRVWAEYDRAACGRIHVTEYEMLTMSPL----PLGLGKRCPCSKVAYKRLVLAN-- 1784
Qy 1902 DSPKPGAPHTTAH-----IGAASG-----FSLEHPTMV--PIPEE--- 1934

Db 1785 ---MPVAEDMTVHTSTLMALIRTALDIKIAKGGADROQLDSELOKETLAIWPHLSQKML 1841
Qy 1935 ---VPVPLGPOLLTVRKSGVSRTHSLPNDNSYMCNRNGSTAERSLGHRGWLKPAQSGSILS 1991
Db 1842 DLLVPMPKASD-LTVGKIYAA---MMIMDYKQSKVKQRQL-----EEQKNAPMF 1889
Qy 1992 VHSOPADTSCILQPKOVHYLLQPHGAPTWGAIPKLP-----PGRSPLAQRPLRR 2042
Db 1990 QRMPEPS-----SLPQEI--IANKALP---CLPQPPAGLGGRCGCFAMSPLSQIFQL 1938
Qy 2043 QAAIIRD-----SLDVQGLSREDLLSEVSGPSCPLTRSSSF-----GSS 2084
Db 1939 TCMDPADDDGQFQORSILVVTDPGSMRSTFIRD-----KXSSSWLEEFSEMERSSDNT 1993
Qy 2085 IQVOORSGIQS-KVSKHILRLPAPCPGLEPSPWAKPPETRRSLELDTELTSWISGDLPLPSQ 2143
Db 1994 YKSRRSYHSSRLSLSAH-RL-----NSDSGHKSDTHRSG-GRERGRSKE 2035
Qy 2144 EEPILFPDLKKYVETQSCERRRPFWMDEQRHRSIAVCLDSQSPRLCPSPSLGGQP 2203
Db 2036 REHLLSADVSRCSSE-----RGAQDM-DSPERH-----PSRSPSEGRSQSPS 2078
Qy 2204 LGGPGSPKPKLSPSPSISIDPPESQSGRPPCPSPGVCLRRRAP-----ASDSKDPs-VSSPL 2258
Db 2079 RQGTGSLSESIPIPSVSDTSPRHSRRQLPVPP-----KPRLLSYSLKQQPSNFSPPA 2133
Qy 2259 D-----STAASPPKKDTLSLGLSSDP 2281
Db 2134 DGSQGSLLASPALESQAQVGLPSSSDSP 2161
RESULT 6
C54972
voltage-dependent calcium channel alpha 1E - mouse
C:Species: Mus musculus (house mouse)
C>Date: 12-Apr-1995 #sequence_revision 12-Apr-1995 #text_change 09-Jul-2004
C:Accession: C54972
R:Williams, M.E.; Marubio, L.M.; Deal, C.R.; Hans, M.; Brust, P.F.; Philipson, L.H.; Mil
J. Biol. Chem. 269, 22347-22357, 1994
A:Title: Structure and functional characterization of neuronal alpha-1E calcium channel
A:Reference numbers: A54972; MUID:94350992; PMID:8071363
A:Accession: C54972
A>Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A:Molecule type: mRNA
A:Residues: 1-2272 <WIL>
A:Cross-references: UNIPROT:Q61290; GB:L29346; NID:G522330; PIDN:AAA59206.1; PID:G522331
A:Note: authors translated the codon AGG for residue 788 as Lys, and CCT for residue 886
C:Superfamily: voltage-dependent calcium channel protein alpha-1 chain
Query Match 13.7%; Score 1653.5; DB 2; Length 2272;
Best Local Similarity 23.4%; Pred. No. 1.5e-96;
Matches 596; Conservative 392; Mismatches 835; Indels 721; Gaps 82;
Qy 73 PGSAADSEA-----EGLPYALADPVV-----PFFY 95
Db 13 PGSDGDSDSNRNQGTFVPASGAAAYKOSKQARTMALYNPIPVQNCFVNRSLFI 72
Qy 96 LSQDSRSPRSCLRVTVCNPFVFRVSMVLVILNCVTLGMFR--PCBDIACDSQRCILQAFD 153
Db 73 FGEDNIVRYAKKLIDWPPEYMLATIANCIVLALEQHLPEDDKTPMSRR---LEKTE 129
Qy 154 DFIPAFVAVMVRQVAGL-IFGKCYKGLDPTNRLDFFIVTAGMLEVSLDIQN--VSPSA 210
Db 130 PYFTIGIFCFEAGIKIVAGLGFIFHKGYLRNGWNVMDFTVLVSLGILATAGTHTHVDLRA 189
Qy 211 VRTVRLRLRAINRVSMRLVTLTLLDTPMLGNVLLCFVFFIIGIVQVQWAGLLR 270
Db 190 LRAVRLRLKLVSGIPLSQILVLSIMKAMVPLLIQIGLLFFAILMFAIIGLEFYSGKLH 249
Qy 271 NRCPLPENSPLSVLDLEPYQTENEDESPPICSPQRENGMRSCRSVPTRLAGEGGGGPPC 330
Db 250 RACPMNN-----SGILEGF-----DPPHPC-----GVQGC 274

QY	331	SLDYETVNSSNTTCVNNQYTNCSAGHNPFGAINPDNFCYAMIAIFOVITLGGWD	390
Db	275	PAGYE-----CKDW-----IGPNDGITQFENILFVLTVFQCITMEGWT	314
QY	391	IMFVMDA-HSFNYFIYILLIIVGFFMINCLVVIATOFSETKQESQLMREQRVFL	449
Db	315	VLYNTDALGATWNWLFIFILLIIGFFVLNLVLGVLGSEFAKERERV-----ENRRAFM	369
QY	450	SNASTLASFSEPGSCYBELLKYLYILRKAARLAQVSRAI-GVRAGLLSSPVARGQBP	508
Db	370	K-----LRRQQQIERELNGYRAMIDKAEVMLAEEN	400
QY	509	QPSGCTSRHRLSVHHLVHHHHHHHHLGNTLVRPRASPEIQORDANGSRLMLPP	568
Db	401	KNSGTSALEVLRRAI-----IKRSRTAMTRDSS-----	429
QY	569	PSTPTSGGPRGAESVHSFYHADCHLEPVRCQAPPRCPSEASGRVTGSGKYPTVHTS	628
Db	430	-----	429
QY	629	PPPEILKDXALVEVAPSGPPTLTLSFNIPGPFSSMHKLLTOSTGACHSCKISPCSK	688
Db	430	-----DEHCVDIS-----SVGTPLAR	445
QY	689	ADSGACGSDPCYCARTGAGEPESADHWMPDSDSEAVVEFTQDAQHSDLRDPHSRRQRS	748
Db	446	ASIKSTKVDGASY-----PRHKE-----	463
QY	749	LGPDAEPSSVLAFWRLICDTFRKIYDQSKYFGRGIMIAILNVTLSMGLEYHQEBELTNAL	808
Db	464	-----RLLRISIRHVMKQVFWIIVLSVVALNTACVAIVHNPQOWLTHLL	509
QY	809	EISNIVFTSLFALEMILLKLVYFGPKYKNPNYDFGVIVVISWEIVGQ-----QGGGL	863
Db	510	YYAEFLFGLLELSLMYGMGRPLYPHSSFNCFDFGVTVGSFVFWALFRCTSGFI	569
QY	864	SVLFRFLRMVLKLVRFPLALQORQVAVLMTMDNVATFCMLMLFIFISILGMHLFGCK	923
Db	570	SVLRALRLRIFKITYWASLRNLVLSLMSSKSIISLLFLFLFVIVFALLGMQLFGGR	629
QY	924	PASERDGTLPDRKNFDSLLWAVTVFOILTQEDWNKVLNGM-----ASTSSWAALYFI	978
Db	630	F-NFNDG---TPSANFDTFPAAIMTVFOILTGEDNEMVYNGIRSQGGVSGMMSALYFI	685
QY	979	ALMTGNYVLENLVAILVEGFOAGDATKGE-SEPDFFS-----P	1018
Db	686	VLTLCFNVTLLNVLAIADNLANAQELTKQEBEEAFNQKHALQKAKEYSPMSAPNMP	745
QY	1019	SYDGDGDRKKRLAL-----VALGEHABLRKSLPP	1048
Db	746	STIERDRRRHMSMWEPRSHLRERRRRHHMSVWEQRTSQLRRHMQMSQALANKEEAPP	805
QY	1049	LIHTAATPMS-----HP---KSSSTGVEALGSGSRRTSSGSAEPGAHHEMKCPP	1098
Db	806	MNPLNPLNPLNPLNPLNPLNPLNPLNPLNPLNPLNPLNPLNPLNPLNPLNPLNPLN	865
QY	1099	SARSSPHSPWSAAS---SW-----TSRRSSRNSLGR	1126
Db	866	SALDNQORSPLSLGKREPPMLPRSCHNCNDPIQOEAGGGETVVTTFEDRARHRSQRRSRH	925
QY	1127	APSLKRRSPSGERRSLLSGEGESQDEESSEDASPAGSDHRRHRSGLERAKSFDL-	1185
Db	926	RVRTEGKDSASARS-RSASQERSLDEGVSVGEKEPHEPHSHRSRKEPTIHEERTQDLR	984
QY	1186	-PDTLOVP--GI-----HRTASGRSSASEHQDCNGKSASGRL-----	1219
Db	985	RITNSLWPRGSLVGALDEAETPLVQPOPELEVGRKDAALTEQEAEGSSQALLGDVQLDV	1044
QY	1220	-----ARTLRTD-----DPQLD-----GDDNDENGLSKG	1244
Db	1045	GRGISQSEPDLSCTMNDKATTESTSVTVIAPDVPDVLVDVTWNISNKTIDGEASPLKEA	1104
QY	1245	E--RIQAWRSRLPACCRERDSWA-----YIFPPQSRFLCHRIITHKMFHVILV	1295
Db	1105	ETKEBEEVEKKKKQKKEKRETKAMVPHSSMFIESTTNPIRRACHYIVNLRYEMCILL	1164
QY	1296	IFLNCIITAMERPKIDPHSAERIFLTLISNIFTAVFLAEMTVKVALGCMFGQOAYLRS	1355
Db	1165	VIAASSIALAAEDPVLITNSERNKV-LRYFDVFTVGVTFEVMVKIMDOGLLQDGSYFRD	1223
QY	1356	SNWVLGDLVLISVIDI-LVSNVSDSGTKILGMLRVLRLRLTLRLPLRVISRAQGLKUYVE	1414
Db	1224	LWNILDFVVVVVAVAFALANALGNTKGRDIKTIKSLRVLRLPLTKIKRLPKLKYAFD	1283
QY	1415	TUMSLKIPIGNIVTCCAFFIIFGLGVOLKGFQFVC--QGEDTRN-----INXSDC	1466
Db	1284	CVVTSLKVNFNILIVYKLFMFIFAVIOLKGFQFCTDSKSKOTEKECIGNYVDHEKNK	1343
QY	1467	ASASVYR-WVRHKNFDNLGOALMSLFLVASKDGWVDIMYDGLDVGVDVQDQIPMHNPNWL	1525
Db	1344	MEVKREWKREHFDYDNIWALLTLFTVSTGEGWPQVLQHSVDVTEEDRGPSSNRMEMS	1403
QY	1526	LYFISFLIVAFVFLNMFVGVVFNPHKQHQHQBEEBARRREKRLREKRRSEKQOM	1585
Db	1404	IFVYVVFVVFVFFVNFVFIITF-----QBQDKMMEE---CSLEKNVERACIDFA	1453
QY	1586	AEAQCKPYYSYR--FRLVHHLCTSHYLDLFTIGVLNVVTMAMHYHQOQILDEAL	1643
Db	1454	ISAKPLTRYMPQNRHTFQYRVWHFVVSFETIMAMIALNTVLMVMKYTAPCTVELAL	1513
QY	1644	KICNYIFTVIFVESVFKLAVAFRRFFQDRWNQDLDAIVLSLSIMGITLLEEVNLSLP	1703
Db	1514	KYLNIATVVSLECVLKVIAFGFLNYFRDWNIFDFITVIGSITEIILTDKLVNTSGF	1573
QY	1704	NPTIRIMVRLIARVLKLLKAVGMRALHTVMQALPOVGNLGLLFLMLFFIFIAALGYE	1763
Db	1574	NMSFLKLFRP---ARLIKLRQGYTIRILLTTFVOSFKALPYVCLLIAMLFYIALLGMQ	1630
QY	1764	LEGDLCD-ETHPECEGLGRHATFRNFGMAFLTLFRVSTGDNNGIMKD--PSRDCDQEST	1820
Db	1631	VFGNIKIDESH-----INRHNFRSFFGSLMLLFRSATGEAQEIMLSCLGKEGCEPDTT	1686
QY	1821	C-----YNTVISPIYFVSFVLTAQVUNVNVIAVLMKHELESNKEAK-----E	1863
Db	1687	APSGQNESERCGTDLAYVYFVSIFFCFLMLNLFAVIMDNFNYLTRDSSILGPHLDB	1746
QY	1864	EASLEALE-----LEMKTL-SPQPHSLPG-----SPFLWPGVEGVNSTDSP	1904
Db	1747	FVWVAEYDRAACGRHYHTEMELTMSF---PLGLKRCPSKVAYKRLVLMN-----	1797
QY	1905	KPGAPHTTAH-----IGAAG-----FSLEHPTWV--PHPEE-----	1934
Db	1798	MPVAEDMTVHTSTLMALIRTALDIKAKGADRQQLDSELOKETLAIWPHLSQKMLDLL	1857
QY	1935	VPVPLGPDLLTVKSGVSRTHSLPNDSYMCRNGSTAERSIGHRGWGLPKAQSGSILSVHS	1994
Db	1858	VPMPKASD-LTVGKIYAA--NMIMDYKOSKVYKORQQL-----EQKNAPMFORM	1905
QY	1995	QPADTSCILQPKDV-----HYLQPHGAPTGAIPKLPPCPSPLAQRPRLRQOAIR	2047
Db	1906	EPS-----SLPQEIINANAKALPYLOD---PVSGLSGRSGYSPMSGPLSPQEIFOLACM-	1955
QY	2048	TDSLVDVQGLSREDLSEVSGPSCP-----TRSSSFV-----	2080
Db	1956	-DPADDQFOEQOSLV--VTDPSMRRSFSTIRDKRSNSLWLEEFMSERSENITYKRRR	2012
QY	2081	-GGSIQVQ-----QRSG-----IOSKVSKHRLP--APC-----PGLEPSW-	2114
Db	2013	SYHSLSLRAHRLNSDGHKSDTHSRGREGRSKERKLLSPDVSRNCSEERTGTQADWE	2072
QY	2115	-----AKDPETPRTSSLELDTLSWISGDLPLPSQEEPLFPRLDKKCYVETQSCRPPG	2168
Db	2073	SPERRQSRSPSEGRSQTPNRQGTGSLSESIPTSDTSTPRRRLQPLPPVP---KPRPL	2129
QY	2169	FWLDEQRHSTAVSCLDSGSGPRLCPSPSSILGGOPLGSGRPPKKK-LSPPSIDDPES	2227

Db 2130 LSYSLSMRHTGGISPPDPGSE-----GGSPASQALLESNACLTSSNSLHPQOG 2179

Qy 2228 QGSRPP---CSPGVCLRRRAPSD 2248

Db 2180 QHPSPQHYISBPYLALHEDSHASD 2203

RESULT 7

T43262

calcium channel alpha-1 chain, L-type - Stylophora pistillata

C:Species: Stylophora pistillata

C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004

C:Accession: T43262

R:Zoccola, D.; Tambutte, E.; Senegas-Balas, F.; Michiels, J.P.; Failla, J.P.; Jaubert, J.

Gene 227, 157-167, 1999

A:Title: Cloning of a calcium channel alpha subunit from the reef-building coral, Stylophora pistillata

A:Reference number: 222375; MUID:99148007; PMID:10023047

A:Accession: T43262

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-1891 <ZOC>

A:Cross-references: UNIPROT:O97017; EMBL:U64465; NID:G4204977; PID:G4204978; PIDN:AAD114

C:Gene: CACHL

C:Superfamily: voltage-dependent calcium channel protein alpha-1 chain

Query Match 13.7%; Score 1652.5; DB 2; Length 1891;

Best Local Similarity 24.8%; Pred. No. 1.4e-96;

Matches 523; Conservative 331; Mismatches 623; Indels 633; Gaps 60;

Qy 115 PERVSMVLINLCVTGLMFRCEDIACDSQRILQAFDDFIP-AFAVENWVQWVALG- 172

Db 83 FDMVILITIFANCAALAAFEPLPE--XDSSEINDNLEVAEYVFLAVFTMEAVLKIIAYGF 140

Qy 173 IFGKKCYLGDWNRDLDFIVLAG---MLBYSLDLQNVSPSAVRTVRLRLRAINRVP 228

Db 141 LFHPCALIRGNWILDFVIVVGLATILVKATLSSGDFDVKALRAFVRLRLRVSGVPS 200

Qy 229 MRILVTLTLLPMLGNVLLCPFFVIFGIVGVOLWAGLLRNRCFIPENFSLPSVDLE 288

Db 201 LQVLSNIIKALIFLHIALLVFVFIYIAGIVELFMRLHKTGY--DNVTGAESPE-E 257

Qy 289 PYYOTENEDESPFICSQPRENGMRSRVSPTLRGEGGGPPCSLDYETNSSTTTCVNW 348

Db 258 PH-----PCS-----SGSGGFQCDKA 273

Qy 349 NOYTYNCSAGBNPFKGAINDNIGYAMIAIFQVITLEGWVDIMVFWMDA-HSFYNFIYF 407

Db 274 AGQV--CEGWKGNHGTNFDNIGLACMTVFQICITLEGWTDVLYWINDAVGNSWPVYF 331

Qy 408 ILLIIVGFFMINCLVVIATQFSETKOR-----ESQLMRQR-----VRLPSNAS 453

Db 332 VTLIIWGSFFVLNLVLGVLSEFAKARRKQSGEFQKREKQVQVEDAYNGYLDWITQAE 391

Qy 454 TLASFSPGSCYEELLYLVILKAAARLQAVSRATGVAGLLSSPVARSQGPQSPGS 513

Db 392 DIEGDSSESGDES-----KASKK-----TSSRQSR-----EDIE 423

Qy 514 CTRSHRLSVHVLVHHHHHHHHHNGTLRVPRASPEIQDRDANGSRRLMLPPPSTPT 573

Db 424 IDNRERQDSI-----SQDTHY----- 441

Qy 574 PSGGPRGAESVHSFYHADCHLEPVRCOAPPRCPSEASGRVSGKVPYFTVHTSPPEI 633

Db 442 ----- 441

Qy 634 LKDXALVEVAPSPGPPTLTSENIIPGPSSMHKLELTQSTGACHSSCKISSPCSKADSGA 693

Db 442 -----GWCHNEKKV----- 450

Qy 694 CGDSCPCYARTGAGEPESADHVPDSDSEAVYFTQDAQHSLDRDHSRRQRSLGPD 753

Db 451 -----LKKWHHRQTE----- 461

Qy 754 EPSSVLAFWRLICDTFRKIVDSKYFGRGIMTALIVNTLSMGIEYHEQPEELTNALEISNI 813

Db 462 -----LRKAVKTOAFYIWIIVVVFSLTALHYDQPDWLTKEFDIANK 506

Qy 814 VFTSLFALEMLLKLIVYGPFGYIKNPYNIIPGVIVV-----ISVWEIVGQGGGLSVLRT 868

Db 507 LFLGIFTIEMIVMYCIGFHYGFASLFRNFDCLVVISLLELAITEAKUPPIGISLURC 566

Qy 869 FRLMRVLKLVFLPALQRLVLMKTMNDVATFCMLLMFLFIFISILGMHLFGCKFASER 928

Db 567 IRLRLIFKVTYMSLSNLVASLNSMRSIAGLLLSLFLMLICSLGMLQIFGKFF--NT 624

Qy 929 DGDTPRKPKPDSLLMAIVTVFQILTQEDNKNVLYNGHAS-----TSSVAALYFIAM 981

Db 625 DDDIEP-RSNPDSFWRALITTVFQILTGEDNNAVMDIGIRAWGGIGEGSATAILYFIFLV 683

Qy 982 TFGNYVLNLLVAILVSGFQAEGDATKSESEPDFFSPVDGDKRKLALVALGEHAEL 1041

Db 684 VVGNYILLNVLAVNLADAENLTWESE-----KSKK-----EKARE 724

Qy 1042 RKSLPLPLIITATPMSPKSSSTGVGEALGSGSRRTSSGSAEPGAHHMKCPPSAR 1101

Db 725 KEAL-----KMGKSVDSQ-----RIDQDGAIVPN----- 749

Qy 1102 SSPSPWSAASSWTSRRSRNSLGRAPSLKRSRSPSGERRSLSGEGSESQDESESEDR 1161

Db 750 ---HS-----SASRSNVTLDKSTQSLHSTG----- 771

Qy 1162 ASPAGSDHRRHGSILEREAKSFDLPDQLVPLHRTAGRSSASEHODCNCKSASGLAR 1221

Db 772 -----TLNGNVARTAS-----HDDVEAQS----- 791

Qy 1222 TLRTDDPQLDG-----DDNDDEGNLSKGERIQAVWRSLPACCRERDSWSAYIFPPQSRF 1276

Db 792 ---TDISEIVGSKSAVNNESSASASSDDID---RAPMP-----PESALFISPTNIF 839

Qy 1277 RLCHRIITHKMDHVVLVIIIFLNCITIAMERPDKIDPHSABRIFLTISNYIFTAVFLAM 1336

Db 840 RVVCYKIATNTYFVNFILICLIIVSSILLAAEDP-LNASAKENQVLNYPDYFTSVTFPEI 898

Qy 1337 TVKVVALGMCFGEOAYLRSSWNLVDGLLVLSIVLIVSMVSDSGTKILGMLRVLRLLRT 1396

Db 899 LVRFISYGLILHKGSCFRSAFNLLDLVSVSVSISLR-----TSQFSVRLRLVLRV 952

Qy 1397 LRPLRVISRAQGLKLVVETLMSLKIPIGNIVICAFPIIFGILGVOLFKGKFFVQCGED 1456

Db 953 LRPLRAINRAKGLKVVQSVFVAVKTIIGNIKLVMTLQFLPAVIGVQLFKGTFSCNDE- 1011

Qy 1457 TRNITNKSDCAEASY-----RWVRHYNFNLGOALMSLFLVASKOGWV 1500

Db 1012 --KILTAEEC-QGNYIDFKGGLSNPVYKEREWRHRHDFDNVGNAMLTFLVTMTFEGWP 1068

Qy 1501 DIMYDGLDVGVDQOQPMNHNPMMLLYFISFLLVAFVFLNMVGVVVENFHKCRHQHEE 1560

Db 1069 GILENSIDSTEVDKGNPNRPNWAIYIIIIIAFFWNIFGVIVTF----- 1119

Qy 1561 EEARREKRLRLKREKRSKEQMAEQCKPYYSYDSRFFLLVHLCTSHYLDLFTGV 1620

Db 1120 -QSEGREEFKGCGLDKNQRCIEFALKAKPKRYIPENRLQFHIWVPVTSQAPEVLIFAF 1178

Qy 1621 IGLNVVTMAEHVQOQIOLDEALKICNYITFVIFVFESVFKLVAFARFRFPQDRWNQDL 1680

Db 1179 IVCNVTVMQYQEPKLYTRVLDGFGNIGTAVFLECEILKIAFKPKNYFTDRWNLPDF 1238

Qy 1681 AIVLLSTMGITLBEIEVNLSPINPTIIRIMRVLRIRVLRVLRVLRVLRVLRVLRVLRV 1737

Db 1239 IIVVGSIIIDITMNEVSSESQMFAG-----PFLRLRALRVKLLNKGSGIKTLTWTFFIKSP 1293

Qy 1738 QALPQVGNLGLLMLFFIFAAALGVLFGLDECDETHPCFCEGLGRHATFRNFGMAFLTLFR 1797

Db 1294 QALPYV---ALLIVMEFIVAVIGMQMFGRIANS---TAINNNNFQIFPQSLMVLFR 1347


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QY 1293 VLVIIFLNCITIAMERPKIDPHSABRIPLTUSNIYITFAVLAEMTVKRVVALGWCFCGQAY 1352
Db 1149 ILLVIAASSALAAEDPVLNSEN RV-LRYDFVYFTFEMVIRIMIDQGLTLODGSY 1207
QY 1353 LRSSWNVLDGLLVLSVIDI-LVSMVSDSGTKILGMLRLVRLTTLRPLRVISRAQGLKL 1411
Db 1208 FRDLWNILDVVVVGALVAFALANALGNTKGRDITKISLRVLRLVLPKTKIKLPLKKA 1267
QY 1412 VVETLMSLKPIGNIVVICAFFIIFGILGVLQFKGPFVC--QGEDTRN-----ITNK 1463
Db 1268 VFDCVITSLKNVFNILIVKLFMEIFAVIAVQLFKGFFYCTDSSKOTKEKICIGNYVDHE 1327
QY 1464 SDCAEASR-WRKYNFDNLQGLMSLFLVLSKDGWDIMYDGLDVGVDQDQIMMHP 1522
Db 1328 KNKMEVGRKWEKHEFYDNIWALLTLFTVSTGEGPQVLQHSVDVTEEDRGFSRNRM 1387
QY 1523 WMLLYFISFLILVAFVFNMFVGVVFNHFKRQHQBEEARRRERKRLRLEKRSKE 1582
Db 1388 EMSIFYVYVFPFVFNIFVALIITP-----QEGDKMEE--CSLEKNERACI 1437
QY 1583 KQMAEACKPYISYSR--FRLLVHLCTSHYLDLFTIGVIGLNVVTVMAHEHYQQQLD 1640
Db 1438 DFAISAKPLTRYMQNRHTFYRVWHFVVSFSPPEYTIMAMIALNTVVLMMKYISAPCTYE 1497
QY 1641 EALKICNYITFVIFVFSVKLVAFAPRRFPQDRWNQLDLAIVLLSIMGITLIEIENLS 1700
Db 1498 LALKYLNAFTMVPSECLVKLVIAFGFVNVPRDTWNI FDTFTVTSITEIVLTDSKLVNT 1557
QY 1701 LPINPTIIRMRVLRIARVLKLVKAWGMRALHTVMOALPQVGNLGLFWLLFIPAAL 1760
Db 1558 TGFNMSLQFRA---ARLIKLRQGYTIRILLTFFVQSFKALPYVCLLIAMLFYIYAI 1614
QY 1761 GVLEFGDLECD-ETHPCGELGRHATFRNFGMAFILTFRVSTGDNWNGIMKD--PSRCD- 1816
Db 1615 GMQVFGNIRLDESH---INRHNFRSFGSLMLFRSATGEAWQEIIMLSCLGEKCEP 1670
QY 1817 -----QSTCVNTWISPIYFVSFVLTAQFVLNVVIAVMKHLSESNKAK----- 1862
Db 1671 DTTAPSGQESERCGTDLAYVYFVSFFCFCSFLMLNFVAVIMDNFYLTRDSSILGPHH 1730
QY 1863 --BEAELEAELE-----LEMKTL-SQPHSPLG-----SPFLWPGVEGVNST 1901
Db 1731 LDEFVRVWAEDRAACRIHYTEMYLEMTLMSPLGKGCPCVKVAYKRLVLMN-- 1784
QY 1902 DSPKGPAPHTTAH-----IGAASG-----FSLEHPTMV--PHPEE-- 1934
Db 1785 --MPVAEDMTVHTSTLMALIRTALDIKIAKGADRQQLDSELOKETLAIWPHLSQKML 1841
QY 1935 --VPVPLGPDLLTVRKSGVSRTHSLPNDSTYMCNRNGSTAERSLGHGWLGPXAGSGILS 1991
Db 1842 DLLVPMPKASD-LTVGKIYAA--MMIMDYKQSKVKQRRL-----EEQKNAPMF 1889
QY 1992 VHSOPADTSCILQPKDVHYLQHPGATWGAIPKLPP-----PGRSPLAQRPLRR 2042
Db 1990 QRMFES-----SUQBEI-IANKALP--CLPQGGPAGLGGSGCPAMSPQLFOL 1938
QY 2043 QAAARTD-----SLDVQGLSGREDLLSEVSGPCPLTRSSSFV-----GGSS 2084
Db 1939 TCMDPADDDGQFQORSILVTDPCSMRSSFITRD-----KRSSSWLEEFMSERSDNT 1993
QY 2085 IQVOORSGIOS-KVSKHIRLPAPCGLEPSPWAKDPPETRSLELDTLSLTSGLDLPSSQ 2143
Db 1994 YKSRRSYHSLRLSAH-RL-----NSDSGHKSDTHRS-GRERGRSKE 2035
QY 2144 BEPLFPDLKKCYSVETQSCRRRPGFWLDEORRHSAVCLSDSGSQRLCPSPSLGGQP 2203
Db 2036 REHLLSADVSCSSEE-----RGAQDMSDPERHPSFSEGRSQSPSRQGTGSLSESSIP 2091
QY 2204 LGGPGSRPKKLSPPSISIDPPEQGGRRPPC-----SPGVCLRRRAPASDSKDSVSPL 2258
Db 2092 SVSDTSTFRQWQGEQGVLLHPHGGCGWPCRRRWMPG---RRGWSGEKSHSLPHCGR 2148
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QY 2259 DSTAAS 2264
Db 2149 DSTGA 2154

RESULT 9
S41080
calcium channel alpha-1 chain - mouse
C;Species: Mus musculus (house mouse)
C;Date: 07-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 17-Mar-1999
C;Accession: S41080
R;Coppola, T.; Waldmann, R.; Borsotto, M.; Heurteaux, C.; Romey, G.; Mattel, M.G.; Lazduo
FEBS Lett. 338, 1-5, 1994
A;Title: Molecular cloning of a murine N-type calcium channel alpha-1 subunit. Evidence
A;Reference number: S41080; MUID:94139884; PMID:8307146
A;Accession: S41080
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-2288 <COP>
C;Superfamily: voltage-dependent calcium channel protein alpha-1 chain

Query Match 13.7%; Score 1650.5; DB 2; Length 2288;
Best Local Similarity 23.8%; Pred. No. 2.4e-96;
Matches 632; Conservative 367; Mismatches 783; Indels 875; Gaps 94;

QY 60 GPAGAGAGSTEKPGSADSEAGLP-----YPALAPV----- 91
Db 23 GGGAGGAGG----PGQG-----GLPPGQRVLYKQSIARARTWALYNPI-PVKQCFTVN 72
QY 92 -VFYLSQDSRPRSWCLRTVCNPFERVSMLVILLNCTVILGMPRCPDIACDSORCRLQ 150
Db 73 RSLFVSESDNVNRKIAKRIETWPFYEMILATIANCIVLAL-----EQHLPGDKTPMSE 128
QY 151 AFDD---FIFAFFAVENVVKNVALG-IFGKCYLGDTWNRLDFFIVIAGLMSEYS---LDL 203
Db 129 RLDDTEPYFIGIFCFEAGIKIIALGFVFKGSLRNGWNVDFVVLVTGILATAGTDFDL 188
QY 204 QNVSFSAVRVTVLRPLRINRVPSMRILVTLTDLTLMGLNVLLCLFFVFFIGIVGQV 263
Db 189 R-----TLRAVRVLRPLKLVSGIPSLQVLKSIKMAVPLLIQIGLLFFAILMEIGLE 243
QY 264 LWAGLLNRCLFLENFSLPLSVLEPYVQYQTENEDESPFICSPQRENGMRSCRSVPTLRGE 323
Db 244 FYMGKFHACF-----PNSTDEPV----- 263
QY 324 GGGGPPCSDLYETYNSSNTTCVNNQYNTCSAGEHNPFGAINFDNIGYAMIAIQVI 383
Db 264 --GDFPGKDPAPRQCQDTEC---REYWP-----GPNFGITNFDNIFAILTVFCI 311
QY 384 TLGWDVIMTVMD-AHSFYNFYFILLIIVGSPFMNLCIVVIAIATOPSETKQRES----- 438
Db 312 TMEGWTDILYNTDAAGNTWNWLYFIPLIIGSFPMNLNLVLGVLGSGFAKERERENRRA 371
QY 439 --OLMRQVRVFLSNASTLASFSFSGCYBELLYVILRKAARLAAOVSRRAIGVRAGL 496
Db 372 FLKLRQOQIE-----RELNGYLEWIFKAEVMLABED----- 404
QY 497 LSSPVARAGQEPQPSGSTRSHRRLSVHVLVHHHHHHHHHHLGNGTLRVPRSPASIQDR 556
Db 405 -----KNAEKSPDLVKRAATKSRNDLIH-----AAEGEDR 437
QY 557 DANGSRRLMLPPPTPTPPSGGPPRGABSVHSFYHADCHLEPVRCAQPPRCPSEASGRTV 616
Db 438 -----FVDL----- 437
QY 617 GSGKVVYTVHTSPPEILKDKALVEVAPSPCPPTLTSTFNIPPGPSSMHKLELTQSTGAC 676
Db 438 -----FVDL----- 441
QY 677 HSSCKISSPCKADSGAGCPDSCPYCARTGAGEPESADHVMPSDSDSEAVYFTODAOHSD 736
Db 442 ---CAVGSPPARAS-----LXSGKTESSSYF----- 464
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Db 1714 -PLGLGKKCSKVAYKELVLMNMPVETDKT-VHT-STLMGLINTALQIKLAROGA-----1766
Qy 1928 MYPHEVPVPLGDLTLVRKSGVSRTHSL--PNDSYMCRNGSTABRSLSLGRGWGLPKAQ 1985
Db 1767 ---DKQLDAELRKEINTIWPILSOKTLDLLVPMHTY-----SDLTVG-----KIV 1809
Qy 1986 SGSLSVHSGPADTSCILQIPKDVHYLLQPHGAPTGAIPKLPPOGSPLAQR-----PLR 2041
Db 1810 AAMIMDYKQSKNKYKQLQEE-----QSRTPMFORMEASSLP 1848
Qy 2042 ROAIRTDSDLV--QGLGREDLLSEVSGPCPLTRSSSPWGGSSIQVQORSIGQKSVK 2099
Db 1849 PQIISTSGPLQYLTGTGPDVDSRSEFT-PLVLPFPVWFQOGRYSSGCEIHKORPELK 1907
Qy 2100 HIRLPAP-----CPGLEPSWAKDPPETRSLSLEL-----DTELSWISGDLL 2139
Db 1908 KIKLEYPHYGHVLPENQGRAVSMPLREIESAEDTSPKRSLSLSTFAAHNSNSTWLNEYSL 1967
Qy 2140 PSSQEEPLFPDLKKCYVETQSCRRRPGFWLDEQRHSIAVSCLDGSGQPRLCPSSSL 2199
Db 1968 ---ERAGPBDLYKRWSS---RRP-----LRP-----PKRSSN 1992
Qy 2200 GGQPLGGPGSPKKLSPPSISI-----DPPESQG-----SRPPCGVGLRRRAPAS 2247
Db 1993 AGSRERG-RSRERKHLSPERSVSTGCGAHPGHRGLDQLSHSP-SPGYSHRPREQVN 2050
Qy 2248 DSKDPSVSPDSTAASPSKPKOTLSLGLSSDP 2281
Db 2051 SSVS---ESPVSSTGTPPKQGRQLPQTSPSKP 2081
RESULT 11
T45115
N-type calcium channel alpha-1 chain, omega-conotoxin-sensitive [imported] - human
C:Species: Homo sapiens (man)
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
C:Accession: T45115
R:Williams, M.E.; Brust, P.F.; Feldman, D.H.; Patthi, S.; Simerson, S.; Maroufi, A.; McC
Science 257, 389-395, 1992
A:Title: Structure and functional expression of an omega-conotoxin-sensitive human N-type
A:Reference number: A42566; MUID:92335886; PMID:1321501
A:Accession: T45115
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-2237 <WIL>
A:Cross-references: UNIPROT:Q00975; EMBL:M94173; NID:G179759; PIDN:AAA51898.1; PID:G1797
A:Experimental source: cell line IMR32; neuroblastoma
C:Genetics:
A:Note: CCHLIA2
C:Function:
A:Description: calcium influx
C:Superfamily: voltage-dependent calcium channel protein alpha-1 chain
Query Match 13.6%; Score 1640.5; DB 2; Length 2237;
Best Local Similarity 23.5%; Pred. No. 1e-95;
Matches 614; Conservative 350; Mismatches 815; Indels 839; Gaps 82;
Qy 59 PGGAAGAGSTEKDPGSADEAGLPYPALAV-----VFFVLSQDSRSPSWCLRT 109
Db 32 PGFGGLQPGQORVLYKOSIAQARTWALYNPIPVKQNCFTVNRSLVFFSDNVRVYAKRI 91
Qy 110 VCNWPFERYSMVLINCVTLGMFRPCEDIACDQRCRILOAFDD---FIFAFVAVMV 166
Db 92 TEWPFPEYMLATIIANCIVAL-----EQHLPDGDTPWSERLDTPYFIFIGCFEAGI 147
Qy 167 KWVALG-IFGKKCYLGDTWNRLDFFVIAGMLEYS---LDLQNVFSFAVTVRVLRPLRA 222
Db 148 KIIALGFVFKHGYLNGWNVMDVVVLTGILATAGTDFDLR-----TURAVRVLRPLKL 202
Qy 223 INRVPSMRILVTLTLLDTPMLGNVLLCPFFVFFIFGIVGVQLWAGLNRNRCFLPENFSLP 282
Db 203 VSGIPSLQVVLKSIKMAWVPLLQIGLLLPAILMFAIIGLEFFWKGFKACF-----P 255

Qy 283 LSVDLPEYYQTENEDESPFICSQPRENGMRSCRSVPTLRGEGGGPPCPSLDYETYNSSN 342
Db 256 NSTDAEPV-----GDFPCGKEAPARLCBGD 280
Qy 343 TTCVMNNOYYTNCAGAHNPFGKAINFDNIGYAMIAIPOVITLEGWDIMYFVMD-AHSF 401
Db 281 TEC---REYWP-----GPNFGITNFDNIFALTVPQCITMEGTWTDILYNTNDAAGT 330
Qy 402 YNFIYFILLIIVGSEFMNLCLVVIATOFSETKORES-----OLMRQORVFLSNASTL 455
Db 331 MNWLYFIPILLIIGSFPMNLVLVLSGEFAKEREVENRRAFLKLRRQQOIE-----382
Qy 456 ASFSBPSCYCELLKYLVIILKKAARLAQVRSRAGVRAGLLSVARSAGGEPQPSGCT 515
Db 383 -----RELNGYLEWIFKAEVWLAEBD-----RNAEKSPLDLK 417
Qy 516 RSHRLSVHLVHHHHHHHHHNGTLRVPRASPEIQDRDANGSRRLMLPPPTPTPS 575
Db 418 RAATKSRNDLIH-----AEGEDRPAD-----440
Qy 576 GGPGRGAESVHSFYHADCHLEPVRQAPPPRCPSSEASGRVTGSGKVYPTVHTSPPEILK 635
Db 441 -----LKSGKTESSYF-----RRKEK-----469
Qy 756 SSVLAFWRLICDTFRKIVDSKYFGRGIMIAILVNTLSMGIYHEQPEELTNALEISNIVF 815
Db 470 --MFRF-----IREWKAQSFYVWLCVVALNTLCVAMVHYNQPRRLTTLTYFAEFVF 521
Qy 816 TSLFALEMLKLLIVYQPGYIKPNYIFDGVIVVTSVWEIVGQ-----QGGGLSVLRTPR 870
Db 522 LGLFLTEMLKMYGLPRSYFFSSFCDFGVIVGSVFVFWAAIKPGSSFGISVLRAIR 581
Qy 871 LMEVLKFLPALORQVLVLMKTMNVATFCWMLLMFIFISILGMHLFGCKFASERDG 930
Db 582 LLRFKTKYWSLRLNVLSLNSMKSIIISLLFLFLFVFWALLQWQLFGQGFQDET 641
Qy 931 DTLPRKDNFDSLWAIIVTVFQILTQEDWNKVLNGM-----ASTSSWAALYFIALMTFEN 985
Db 642 PT---TNFTTFAAILTVFQILTGDMVNAVYHGIESQGGVSKGMFSSFYFIVLTLFGN 697
Qy 986 YVLFNLLVAILVEGFOAEGDATKSESEPDFSFSDGDRKRLKRLVALVALGEAEKSL 1045
Db 698 YTLNLFELAIVDNLANAQAELTKDEEMEEAA-----NQKLALQKAKEAEV--SP 746
Qy 1046 LPPLLIHTAATPMHPKSSSTGVGEA-----1071
Db 747 MSAANISIAARQNSAKARSVWEQRASQLRNLQNLASCEALYSEMDPEERLREATTHLR 806
Qy 1072 -----LGSGRRTSSSSGAEPGAA-----HH-----EMKCP-----1097
Db 807 PMKTHLDRLPLVVLGELGDRGARGPVGGKARPEAAEPGVDPRRHHHRDKDXTPAAGDQ 866
Qy 1098 -----PSARSS---PHSPWSAASWTSSRSNLSGRAPSLKRRSPSGERRSL 1142
Db 867 DRAPKAESEGFCAERPRPHRSKKEAA--GPPEARSEGRGP-----GPEGGRHH 919
Qy 1143 LSGSQESQDEE-----SSSEEDRASPGSDHRRGSLE---REAKSFDLDDTL 1189
Db 920 RRGSPPEAAERPRHRAHRHQDPSKACAGKERRAHRGGRAGPREAEG-----972
Qy 1190 QVPG-LHRTASGRSSASE--HODCNKGSASGLA-----RTLRTDDQLQDGGDDNDE 1238
Db 973 BEPARRHARHQAOPAHEAVEKETTEKEATEKEAIVEADKEKELRNHQPREHCDLETS 1032

Qy 569 PSTPTSGPPGARGAESHVSPYHADCHLEPVRCQAPPPCPSEASGRTVSGKVYPTVHTS 628
 Db 429 ----- 428
 Qy 629 PPEILKOKALVEVAPSPGPTLTSTFNIPGPSSMHKLELTQSTGACHSSCKKISPCSK 688
 Db 429 -----DEHCVDIS-----SVGTPLAR 444
 Qy 689 ADSGACPDSCPCYARTGAGEPESADHVPDSDSEAVYEFTQAOHQSDLRDPSRRRORS 748
 Db 445 ASIKSAKVDGSY-----FRUKE----- 462
 Qy 749 LGPDAPSSVLAFWRLCDTFRKIVDSKYFRGIMTALVNTLSMGLEYHEQPEELTNAL 808
 Db 463 -----RLLRISIRHMVKSQVFIWLSLVALNTACVAIVHNNQPOWUHL 508
 Qy 809 EISNIVTSIPALRMLKLLVYGPFGYIKNPYNIFDGVIVVSVWEIVGQ-----QGGGL 863
 Db 509 YYABFLGLLELSLKMVGMPRLYFHSFNCDFGVTVGSIFEVVMAIFRPGTSFGI 568
 Qy 864 SVLRTRMLRVLKLVRFPALQROLVVLMTMDNVATFCMLMLFPIFISILGWHLFCK 923
 Db 569 SVLRALRLRIFKITKYWASLRNLVWSLMSMKSIISLLFLFLFIVVFAALLGQLFGGR 628
 Qy 924 FASERDGTLPDRKNEDSLLWAIIVTFQILTQEDNMNVLYNGM-----ASTSSWAALYFI 978
 Db 629 F-NFNDG---TPSANFDTFPAIMTIVFQILGEDWNEVMYNGIRSQGVSGWMSAIYFI 684
 Qy 979 ALMTFGNVVLNLAIVLVEGFOAGDATKSE-SEPDPFS-----P 1018
 Db 685 VLTLGNTLLNVLAVIADNLANAQELTKDEEEAFNKHQALQAKEVSPMSAPNMP 744
 Qy 1019 SVDGDRKKRLALVALGEHAEHLKSL-----LPPLIHTAATPM-S 1059
 Db 745 STIERERRRHMS-VWEQRTSQLRKHQMOSQEAALNREEAPTNPPLNPLNLSINPLNA 803
 Qy 1060 HP-----KSSGTG-----GEALGSGSRRTS-----SSGSAEPG 1088
 Db 804 HPSLYRRPRAIEGLALGALEKFEERISRGSLKGDGDRSSALDNQRTLSLGOREPP 863
 Qy 1089 --AAHEMKCPSPARSPPHSPMSAASWTSRRSRNSIGRAPSLKRRSPSERSLSLGE 1146
 Db 864 WLAPCHGNCDPTQOEA--GGGEAVVTFEDRARHRSQRRS---RHRVRTEGKESAS 918
 Qy 1147 GQESQDEEESSEDSPAGSDHRRG-----SLEREAKSSFDLPDLOVPLGHRAS 1199
 Db 919 RRSASQERSLDEAMPTGEKDHRLGNHGAKEPTIQEERAQDLRTNSLAVSRGSLAG 978
 Qy 1200 GRSSAS-----BHQCNGKSASGRLAR-----T 1222
 Db 979 GLDEADTPLVLPHELVGHVHLVTEQEPESQALLCNVQDMGRVISQSEPLDSCIT 1038
 Qy 1223 LRFD-----DPOLD-----DDNDGRLSK 1243
 Db 1039 ANTDKATTESTSVTVAIPDVLVDVTVVHISNKTGDEASPLKEAIREDEEVEKKQK 1098
 Qy 1244 GERIQAWVSRPACCRERDSAVIFPQOSFRLLCHRIITHQMFHDVHLVFIIFLNCIT 1303
 Db 1099 KEKRETG-KAMVPHS-----SMFISTNPIRRACHYVNLRYFEMCILLAVIAASSIA 1150
 Qy 1304 IAMERPKIDPHSAERIFLTSNFIYFAVLAEMTVKVALGWCFGEOAYLRSNVLDGL 1363
 Db 1151 LAAEDPVLNTERNKV-LRYFDVFTGVFTFEMVIMQIDQGLIQDGSYFRDLNMLDFV 1209
 Qy 1364 LVLSIVIDI-LVSMVSDSGTKILGMLRLRLTLRPLRVISRAQGLKLVWETLMSLKP 1422
 Db 1210 VVYGALVAFALANALGTNGRDKTKNSLRVLRLVPLTKIKELPKLKAFCVVTSLKN 1269
 Qy 1423 IGNIWVCCAFFIIFGLIGQLFKGFVC--QGEDTRN-----ITNKSQCAEASYSR-W 1473
 Db 1270 VFNLLIVYKLFMFIFAVIAQLFKGFFCYCTDSSKDETEKICIGNYVDHEKNMVKRGW 1329
 Qy 1474 VRHKYNFDNLGOALMSLFLVLASKDGWDIMYDGLDAVGVDQDQPMNHNPMWLLYFISFL 1533

Db 1330 KRHEFYDNIWALLTLFTVSTGEGWPQVLQHSVDVTEEDRGPSRSRNMENSIPIYVYFV 1389
 Qy 1534 IVAFVLMFVGVVVENFHKCRQHQEERREARRRLEKRRKRSKEQMAEAOCKPY 1593
 Db 1390 VFPFFVFNIFALLIITF-----QEGDKWEE---CSLEKERACIDFAISAKPLTR 1439
 Qy 1594 YSDYSR--FRLLVHHLCTSHYLDLFTIGVIGLNVVTWAMEHYQOQILDEAKICNIFT 1651
 Db 1440 YNPQWHTFOYRVHVFVSPSEYTIMAMIALNTVLMKYSAPCTVELAKYLNIAFT 1499
 Qy 1652 VIFVESYFKLVAFARFRFPDRWNQDLALVLLSIMGITLEEIVNLSLPINTIIRIM 1711
 Db 1500 MVFSECVKLVIAFGFLNYFRDTWNIFFITVIGSITEIILTDKSLVNTSGNMSFLKJF 1559
 Qy 1712 RVLRARVLLKLVAGVGRALLHTVMOALPOVGNLGLLFLMLFFIFFAALGVELEGLDCE 1771
 Db 1560 RA---ARLIKLRQYTRILLWTFFVQSFALPVYCLLIAMLFYIYIAGIQQVFNKID 1616
 Qy 1772 -ETHPCEGLGRHATFRNFGMAFLTLFRVSTGNNNGIMKD--PSRDCQESTC----- 1821
 Db 1617 BESH---INRHNFSPFGSLMLLFRSATGEAQEIMLSCLGKGEKCPDPTTAPSGQNE 1672
 Qy 1822 --YNTVISPIYFVFLTAQFVLNVVIAVLMKHLSESNKEAK-----EEAELEAL 1871
 Db 1673 ERCGTDLAYVYFVFPFCSPFLMLNLFVAVIMDNFEYLTRDSSILGPHHLDFFVRWAEY 1732
 Qy 1872 E-----LBNKTL-SPQHPSPLG-----SPFLMPGVEGVNSTDSKPGQAPHTT 1912
 Db 1733 DRAACGRHIHYEMVEMTLMSF---PLGLKRCPSKVAYKRLVLMN---MPVAEDMT 1783
 Qy 1913 AH-----IGAASG-----FSLEHTVW--PHPEE-----VPVPLGPD 1942
 Db 1784 VHTFTMALIRTALDITKAGGADROQLDSELOKETLAIWPHLSQKMLDLLVPMKASD 1843
 Qy 1943 LTVKRSQVSRTHSLPNDSYMCRNGSTABRSLSHRGWLKPAQSGSILSVHSQPADTSCI 2002
 Db 1844 -LTVGKIYAA---MMIMDYKOSKVKQKQOL-----BEQKNAPMFORMEPS----- 1886
 Qy 2003 LQLPKDV-----HYLQPHGAPTGAIPKLPPOGRSPLAORPLRQARITDSDLVQO 2055
 Db 1887 -SLPQEIIANAKALPYLOQD---PVSGLSGRSGYFSPMSPLSPQDIFQLACM--DPADDDQ 1940
 Qy 2056 LGSRELLLEVSPSCPL-----TRSSSFWGSSIOVQORSGIOQSVKSHIRLPAFC 2107
 Db 1941 FQERQSLV--VTDPSSMRRSFSTIRDKRNSW-----LEFSPMERSS----- 1981
 Qy 2108 PGLPQWAKDPPETRSLELDT-ELSWISG---DLLPSSQEPPLFPRDLKKYCVSVETQSC 2163
 Db 1982 ---ENTYKSRRSYHSSLSRLSAHRLNSDSGHKSDTHPSGGRERRRRKERRKLLSPDVSR 2038
 Qy 2164 ---RRRPGFWLDEQRHRSIANSCLDSGSPRLCPSPLSGGOLPGGSPGRPKKLSPPS 2219
 Db 2039 NSEERGTOADWESPERRQS-----RSPSEGRSQTNPQGTGSLSESIPI 2083
 Qy 2220 IS-IDPESOGSRPPCSPG-----VCLRRRA-----PASDSKD--PSVSSPLDSTAA 2263
 Db 2084 VSDTSTPRRRRQLPVPPKPRPLLSYSLIRHAGSISPPADGSESGPLTSALESNNA 2143
 Qy 2264 -----SPSPKK 2269
 Db 2144 WLTESSNPHPOQ 2156

RESULT 13

A54972

voltage-dependent calcium channel alpha 1E-3 - human

C:Species: Homo sapiens (man)

C:Date: 12-Apr-1995 #sequence_revision 12-Apr-1995 #text_change 09-Jul-2004

C:Accession: A54972

R:Williams, M.E.; Marubio, L.M.; Deal, C.R.; Hans, M.; Brust, P.F.; Philipson, L.H.; Mil J. Biol. Chem. 269, 22347-22357, 1994

A:Title: Structure and functional characterization of neuronal alpha-1E calcium channel

A;Reference number: A54972; MUID:94350992; PMID:8071363

A;Accession: A54972

A;Status: preliminary

A; Molecule type: mRNA

A;Molecule type: mRNA
A;Residues: 1-2270 <WIL>

A; Cross-References: UNIPROT:Q15878; GB:L29385; NID:g495869; PIDN:AAA59205.1; PID:g495870
A;Cross-References: UNIPROT:Q15878; GB:L29385; NID:g495869; PIDN:AAA59205.1; PID:g495870
C;Superfamily: voltage-dependent calcium channel protein alpha-1 chain

C;Superfamily: voltage-dependent calcium channel protein alpha-1 chain

Query Match	13.6%	Score 1637.5;	DB 2;	Length 2270;
Best Local Similarity	23.6%	Pred. NO. 1.6e-95;		
Matches 601;	Conservative 394;	Mismatches 815;	Indels 741;	Gaps 87;

Qy	73	PGSADSEA-----EGLPYPALA-----PV-----VFY 95
Db	12	PGSGDSDQSRNRQGTVPVPSGQAAAYKQTKAQRATMALYNPIPVQNCFTVNRSLFI 71
Qy	96	LSQDSRPRSCLRTVCNPFWRFSVSMVLILLACVTLGMPF--PCEDIACDSQRCLIOAPD 153
Db	72	PGENIRVKYAKGIDWPPFYMILATTIANCIVLAEQHLPEDDDKTPMSRR--LEKTE 128
Qy	154	DFIEAFPAVENVMKVVALG-IFGKKCYLGDWNRLDFFVIAGMLEYSLDLQN--VSPSA 210
Db	129	PYFTGICFCEAGIKIIVGFIHKGSYLRNGWNWMDFIVLSGILATAGTHTHVLDLT 188
Qy	211	VRTVRLRLPRAINRVPSMRILVTLTLLDTPMLGNVLLCFPVFFIFGIVGQLWAGLR 270
Db	189	LRAVRLRLPLKSGIPSLQIVLKSIMKAWPFLQIGLLFPAILMFAIIGLEFYSGKLH 248
Qy	271	NRCFLPENFSLPLSDLEPPYQTENEDESPTFCQPRENGMRSRCSVPTLRGEGGGPPC 330
Db	249	RACFMNN-----SGILEGF-----DPPHC-----GVQGC 273
Qy	331	SLDYETYNSSNTTCVNNQYTYNCSAGEHPFKGAINFDNIGYAWIAIFQVITLEGWD 390
Db	274	PAGVE-----CKW-----IGNDGITQDNLFVLTVFQICITWEGWTT 313
Qy	391	IMYFVMDA-HSFYFNPIFYILLIIVGSFFMINCLVVIATQFSETKQRESQLMREQRVFL 449
Db	314	VLYNTNDALGATMNWLYFIPLIIGSFFVLNLVLGVLSGEFAKERERV-----ENRAF 368
Qy	450	SNASTLASFSPGSGYEBLLKYLVYLKKAARLQAQVSRAI-GVRAGLLSSPVARSQGP 508
Db	369	K-----LRRQOQIERELNGYPAWIDKAEVWMLAEN 399
Qy	509	QPSGSTRSHRRLSVHHLVHHHHHHHVLGNGTLRVPRASPEIQDDANGSRRLMLPP 568
Db	400	KNAGTSALEVLRAT-----IKRSTEAMTRDSS-----428
Qy	569	PSTPTSGPPRGAEVSHFYHADCHLEBFRVRCQAPPPRCPSASGRTVSGKVYPTVHTS 628
Db	429	-----428
Qy	629	PPPEILKDKALVUPVAPGPPPTLTSFNTPPGFFSMHKLLTQSTGACHSSCKISSPCK 688
Db	429	-----DEHCVDIS-----SVGTPLAR 444
Qy	689	ADSGACGPDSCPYCARTGAGEPESADHWMPDSDSEAVYEQDAOAHSDLRDPHSRRQRS 748
Db	445	ASIKSAKVDGVS-----FPHKE-----462
Qy	749	LGPDAEPSSVLAFWRLICDTPRKIVDSYKFRGIMAILVNTLSMGIEYHEQPELTNAL 808
Db	463	-----RLLRISIRHMVKSVFYWIVLSLVALNTACVAIVHNPQWMLTHLL 508
Qy	809	EISNIVTSLPALEMLKLIVYGPFGYIKNPNIPDGWIVLISVWEIVGQ-----QGGL 863
Db	509	YYABFLFLGLFLEMSLKWYGMGPRLYPHSHSFCNCFDGTGVTGSIPEVWMAIPRPGTSFGI 568
Qy	864	SVLRTFLRMVLLVRLPALQORQVLVLMKTMNDVATFCLMLMLFIFISILGMLHFGCK 923
Db	569	SVLRLALLRIRFKITKYWASLRNLVSLMSWKSIIISLLFLFLFVIFVALLGMLQFGGR 628
Qy	924	FASERDGGTLPDRKNFDSLLWAIVTVOILTOEDWNKVLXNGM-----ASTSSWAALYFI 978

Db 1674 GEKCEPDTTAPSONENERCGTDLAVVYFSFIFFCSFLMLNLFVAVIMDNFYLTRDS 1733
Qy 1862 K-----BEAELEABLE-----LEMKTL-SQPHSLPG-----SPFLWPG 1894
Db 1734 SILGPHLDEFVRWAEYDRAACGRIRHYTEMELTLMSP-----PLGLKRCPSKVAYKR 1789
Qy 1895 VEGVNSDTPKPGAPHHTAH-----IGAAAG-----FSLEHPTWV--P 1930
Db 1790 LVLWN-----MPVAEDMTVFTSTLMALIRALTALDIKAKGADROQLDSELOKETLAIWP 1844
Qy 1931 HPEE-----VPVPLGPDLLTVKRSVGRTHSLPNDSYNCRNGSTAERSLGRHWGLPKA 1984
Db 1845 HLSQKLDLLVPMKASD-LTVGKIYAA--MMIMDYKQSKVKQKQQL-----EE 1892
Qy 1985 QSGSILSVHSGPATSCILQPKDV-----HYLLQPHGAPTWGAIPKLPGRSPLAQ 2037
Db 1893 QKNAPMFQRMPEPS-----SLPOEIIANAKALPYLOD-----PVSGLSGRSGYFMSMPLSP 1943
Qy 2038 RPLRQAIRTDLSLDVQGLSGREDLLSEVGSPSCPL-----TRSSFWGGSSIOVOQ 2089
Db 1944 QDIFQLACM--DPADDQFQERQSLV--VTDPSMRSSFSITIRDKRNSNW-----LEE 1993
Qy 2090 RSGIQSVKSHIRLPAPCPGLEPWSAKDPPETRSLELDT-ELSWISG-----DLLPSQEE 2145
Db 1994 FMSERSS-----ENTYKRRRSYHSLRLSAHRLNSDSGHKSDTHPSGGR 2039
Qy 2146 PLFRDLKCKSVETQSC-----RRPGFWLDEQRHSAIVSLDGSQPRLCSPSPSLGG 2201
Db 2040 RRSKERKHLSPDVRNCRNSEERTQADWESPERQSS-----RSPSGRS 2084
Qy 2202 QPLGGPSRPPKLLSPSPIS--IDPPESQSGSRPPCSPG-----VCLRRRA-----PAS 2247
Db 2085 QTPNRQGTGSLSESSISFVSVDTSFPRSRRLQFPVPPKPRLLSYSLRHAGSISPPAD 2144
Qy 2248 DSKD--PSVSPDLSTAA-----SPSPKK 2269
Db 2145 GSEEGSPILTSQALSNNAWLTFESSNPHPOQ 2175

RESULT 14
T30902
sodium channel SCAP1 alpha chain - California sea hare
C:Species: Aplysia californica (California sea hare)
C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C:Accession: T30902
R:Dyer, J.R.; Johnston, W.L.; Castellucci, V.F.; Dunn, R.J.
DNA Cell Biol. 16, 347-356, 1997
A:Title: Cloning and tissue distribution of the Aplysia Na+ channel alpha-subunit cDNA.
A:Reference number: 220929; MUID:97238630; PMID:9115644
A:Accession: T30902
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1993 <DYE>
A:Cross-references: UNIPROT:P90670; EMBL:U66915; NID:g1842248; PID:g1842249; PIDN:AAC474
C:Superfamily: sodium channel protein

Query Match 13.6%; Score 1636; DB 2; Length 1993;
Best Local Similarity 25.8%; Pred. No. 1.7e-95;
Matches 518; Conservative 348; Mismatches 702; Indels 442; Gaps 69;

Qy 94 FYLSQDSRPRSWCLTVCNMPFERSVLMVLINCVTLGM--FRPCEDIACDSQRCLQA 151
Db 119 FLLSPFNIRRIAYIYLHPIFSLVMMTLVNCVFAITSYTP-----PA 164
Qy 152 FDDTFE-AFFAVEMVVMVALGIFGK-CYLGDTWNRLDFFIV-IAAGMLEYSLDLQNVSF 208
Db 165 FVEHIFLGLIYVEAVKVLRSRGVFLKPTTYLRDPWNWLDFFVISLAYMTVTKFQNL-- 222
Qy 209 SAVRTVRLRLPRLAIRNPVSRMILVTLTLLDLPMLGNVLLLCFFVFFIFGIVGVLWAGL 268
Db 223 QALRTFRVRLAKTISVIPGLKTIIVGALLEAVRRLDRDWMLTVFLSIFALIGMLQYSGA 282
Qy 269 LNRCLFENFSLPLS-----VDLEPYQOTENEDESFPICSPRENGMRSRCSVPT 319

Db 283 LRQKCVLNPVPELGTNITHDEWMDVNNESHQKDFYDEWQ-VC----- 325
Qy 320 LRGEQGGGPPCSLDYETYNSSNTTCV-NWNQYTYNCASAGEHNPFPKGAINEFNIGAWIA 378
Db 326 --GNGTGACKG--NGTINGTAEWJCLPNIGQ-----NPNHDTFSFDFNGMALLC 371
Qy 379 IFQVITLEGWDMVFMVMDAHSFYNFYIFILLIIVGSPFMINLCLVVIATQFSETKQRES 438
Db 372 AFELMTQDFWESLYHLVRAVGAHCLYFVLVILLGSLVNLILAIVAMSDET-QKOD 430
Qy 439 QLMREQVRFLSNASTLASFSFGSCYBELLVILKAAARLA-QVSRAGIVRAGLL 497
Db 431 QADAEEEA-----AEARQE-----EEARKEALSIMTKSPSNSSWNDFEAGVR-- 472
Qy 498 SSPVASSGQPPGSGCTSRHRLSVHLLVHHHHHHHHLGNGTLRVPRASPEIQDRD 557
Db 473 ---TAGDKAEEKERLSLTSCHSATSAHLKPSRLNQKRH-----SLSLP-GSPYIHRN 521
Qy 558 ANGSRRLMLPPPSTPTPFGGPPRGAESVHSFYHADCHLEFVRCAQPPPRCPSEASGRTVG 617
Db 522 SRGQSVWRKPVPTAKRS-----PCCPDR----- 545
Qy 618 SGKVYETVHTSPPEILKDKALVEVAPSPGPTLTSTF---NIPPG---PFSSMHKLET 670
Db 546 QPLVHTHTLENLPLP-FADDSAAV---TPSSEDLNCFIRNMPNGRRFASFASQRPDGT 600
Qy 671 QSTGACHSSCKTSPSCSKADSGACGPDSCPYCARTGAGE-----PESA-D 714
Db 601 GRSGSRSS--FASNHSRASRTSRG-----SQGDRTKTQTLNFKKGVKVPDWLD 649
Qy 715 HVMPSDSSEAVYEFQDAQHSDLRDPHSRRR---ORSIGPDAEPSVLA----- 760
Db 650 KSKLDDQDSV--SSGSGCHCEPKAKASBNPFLSHSPGPGPNVEMKDMVMDILDKOASG 707
Qy 761 -----FWRLLC-----DPRKI-----VDSKYFGRGIMAILVN 789
Db 708 HRSFVSMTSIHORTWKDINWKYFCWDCHPNFKQLRQLVSLFIMDAFVDLFTICILVN 767
Qy 790 TLSMGIEYHEQPEELTNALEISNIVFTSLFALEMLKLIVYGPFGYIKNPYINFDGVVV 849
Db 768 TAFWAMEHYDMEDDLKAVSNAANLVTAIFAFAVEAFKILALSVPVYFKDGNIFDSIIA 827
Qy 850 ISVWEIVGQGGSLSVLRTFRLMRVLKVLRFALORQLVLMKTMNDVATFCMLLMFI 909
Db 828 LSLMELSMTKLPLGLSVLRAFLRLRVFLAKSWFTLNNLTAIVGRGTWALGNLIIIVLGI 887
Qy 910 FIFSLGMLHFGCKEAS-ERD-----GDTLPDRKNFDSLLMAIVTVFOILTQEDW 958
Db 888 FIFAVMGQQLFSSDYKTYEREIDAAGNVINKDKMP-RWNFNDFLHSFMIVFVLCGE-W 945
Qy 959 NKVLYNGMASTSSWAAL-YFIALMTFGNVYLFNLVAILVEGFOAG-DATKSESEPDFF 1016
Db 946 IESMW-GCYLVSGWACVPFPELLTAVGNLVNLFLALLSSFGSESLQSESDDEPSKI 1004
Qy 1017 SPVVDGDRKKRLA-----LVALGEHAELAKSLPLLIHTAATPMHSHKSSSGVG 1069
Db 1005 AEAI---DRFRFGNWKVKIIVCTIKVLQKQNRWPP-----PTTQOS 1045
Qy 1070 EALGSGSRRTSSGSABPGAAHEMKCPPSARSPPHSPWASAASWTSSRRSRSLGRAPS 1129
Db 1046 EVNG-----KDPVVVDGTVVSNEKTPDDFPDGPCCPAQAIC----- 1082
Qy 1130 LKRSPSGERRSLLSGEGSQDEEESSEEDRASPGSDHRRHGRSLEREAKSSFDLPDL 1189
Db 1083 -----SAKDLKSPSGS-HSNSGS----- 1100
Qy 1190 QVPLHRTASGRSSASEHQDCNGKSGASRLARTLRTDDPOLDDGDDNDDEGNLSKGERIOA 1249
Db 1101 -----SHCSCCSLSESAQTKID---LEADHEINEVEI-----V 1132
Qy 1250 WVR-----SRLPACCRERDS-----WSAYIFPQSRFRLCHRIITHKMFPHV 1293

1087 QY -----PGAHEWKKCPSPARSPPHSPW-----SAASSWTSRS 1119
 814 Db LTVLDNORSPSLGKREPPWLPSPCHG--NCDPTQOETGGTGVTFVTFEDRAHQSORR 871
 1120 QY SRNSLGRAPSLKRSPPGERSLLSGEGOSQDEEBSSEDRASPAGSDHRRHSGSLEREA 1179
 872 Db SRRHRVTEKESASASRSR-----SASQERSLDEGVSDGEKEHEPQSSHRSKEPTIHEE 927
 1180 QY KSFDDL--PPTLOVP---GL-----HRTASGRSSASEHQDCNCKSASGRL 1219
 928 Db ERTQDLRTNSLWVPYRSGGLVGLDEAETPLVQPOPELVGKDAALTEQEAEGSSQALL 987
 1220 QY RLRTRDDPOL-----DG- 1232
 988 Db ADVQDVGRTISQSEPDLSCMTTMDKATTESTSVTVVAIPDVPLVDSTVVISNKTIDGE 1047
 1233 QY -----DDNDSDGNLSKGBRIQAWVRSLPACCRERDSWSAVIFPPQSRFRLLCH 1281
 1048 Db ASPLKEAETKEEEREVEKKQKKEKREG-KAMVPHS-----SMFIPSTTNPIRKACH 1099
 1282 QY RIITHKMFHDVVLVIFLNCITIAMERPDKIDPHSAERIFLTSNYFTAVFLAEMTVKV 1341
 1100 Db YVNLVRFEMCILLVIAASSIALAEDPVLNTSERNKV-LRYFDYVFTGVFTFEMVWKMI 1158
 1342 QY ALGWCFGEOAYLRSSWVLDGLLVLISVIDI-LVSMVSDSTKITGLMLRLVRLRLRL 1400
 1159 Db DQGLTLDGYSYFRDLWNLDVFWVVGALVAFALANALGTNKGRIKTIKSLVRLVRL 1218
 1401 QY RVISRAQGLKLVETLMSLPIGNIVVICAPFIIFGILGVQLFKGKFFVC--QGEDTR 1458
 1219 Db KTIKELPKLKAFCVTVSLKNNVILIVYKLFMFIPIAVIAVQLFKGKFFYCTDSSKDE 1278
 1459 QY N-----ITNKSDDCAEAYR-WVRKYNFDNLGOALMSFLVASKDGVMDIMVGLDAVG 1511
 1279 Db KECIGNYVDHEKMEVKGREWKREHFEYDNI-IWALLTLFTVSTGEGWPQLQHSVDTE 1338
 1512 QY VDOQPIKNNPMLLYFISLLIVAFVNLNMFVGVVENFHKRQHQBEEBAREERKRL 1571
 1339 Db EDGFSRNRNMEMSIFYVYVFWFFVFFVFNIFVALIITF-----QEQGDKWEE--- 1388
 1572 QY RLLEKRRSKEKQMAEACKPYSDYSR--FRLVHLCTSHYLDLFTITGVIGLNVYMA 1629
 1389 Db CSLEKNERACIDFAISAKPLTRYMPQNRHTFQYRVHFWVSPSEYTIMAMIALNTVVL 1448
 1630 QY MEHYQOQLDALKICNVITVIVFESVFKLVAFAFRFPDDRWNOLDLAILVLLSIMG 1689
 1449 Db MKYISAPWYELALKYLNIAFTNVLFSLECVLKVIAFGFLNFRDWNIFDITWIGSITE 1508
 1690 QY ITLEETEVLNLSLPINPTIIRIMRVLRIARVLKLVKMAVGMRAALLHTVMQALPOVGNLGL 1749
 1509 Db IILTDSKLVNTSGFNMSFLKLFR-----ARLJKLQGVTRILLWTFVQSFKALFYVCLL 1565
 1750 QY FMLLPFIIFALGVLELPGDLECD-ETHPCGLGRHATFRNFGMAFLTLFRVSTGDNWNGIM 1808
 1566 Db IAMLFFIYAIIGMVFQGNKLDDESH-----INRHNFRSFFGSLMLLFRSATGEAWQEI 1621
 1809 QY KD--PSRDCDQESTC-----YNTVISPIYFVSFVLTAQFVLNVVVIAYVMKHLEES 1857
 1622 Db LSCLEKGECEPDITAPSGQESERCCTDLAYVYFVSFIFFCSFLMLNLFVAVIMDNFEYL 1681
 1858 QY NKEAK-----EEAELEAELE-----LEMKTL-SPQPHSLG-----SPF 1890
 1682 Db TRDSSILGPHHLDFFVRVWAEYDRAACGRHYTEMYLEMTLMSPL-----ELGLKRCPSKV 1737
 1891 QY LWFGEVGVNSTDPKCAPHTTAH-----ICAASG-----FSLEHPTM 1928
 1738 Db AYKRLVLMN-----MPVAEDMTVHTFTSLMALIRTALDIKAKGADRQOLDSELOKTEL 1792
 1929 QY V--PHDEE-----VPVPLGPDLLTVKSGVSTHSLPNDSYNCRNGSTAEBSLHGRWG 1980
 1793 Db AIWPHLSQKMLDLLVPMFKASD-LTVGKIYAA---NMIMDYKQSKVKRQOOL----- 1842
 1981 QY LPKQSGSILSVHSQPAD-TSCILQLPKDVHLLQPHGAPTWGAI PKLPPGGRSPLAQRP 2039

1843 Db --BEOKNAPMFORMEPSSLPQEIISNAKALPYLOD---PVSGLSGRSGYPSWSPLSPQE 1897
 2040 QY LRRQAAITDSLDVQGLSGREDLLSEVSGPSCPL-----TRSSSFV----- 2080
 1898 Db IFQLACM--DPADGQTOEQOQSIV--VTDPSMERSFSTIRDKESNSWLEEFMSERSSE 1953
 2081 QY -----GGSSIQVQ-----QSG-----TQSKVSKHRLP--APC----- 2107
 1954 Db NTKYSRRSYHSLRLSAHRLNSDGHKSOTHRSGRGRGRKSKHLLSPDVRCNSEE 2013
 2108 QY PGLPSW-----AKDPPETRSLLELDTLSWISGDLPLSSQOEPLFPRLKKCYSVET 2160
 2014 Db RGTQADWESPERROSRSPEGRSOTPNRQGTGSLSESSIPSISTSTPRRERRQLPPVPP 2073
 2161 QY QSCRRRPGFWLDEQRRHSIAVSCLDGSGQPRLCPSPSSGLGQPLGGPGRPKK-LSPPS 2219
 2074 Db ---KRPDLISVSLMNRHTGIGISPPDGSE-----GGSPLASQALESNSACLRESS 2120
 2220 QY ISIDPPESQGRPP---CSPGVCLRRRAPAD 2248
 2121 Db NSLHPQOQGHPSPOHYISEPVIALHEDSHASD 2152

Search completed: April 13, 2005, 19:11:27

Job time : 123 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 13, 2005, 18:58:40 ; Search time 278 Seconds
(without alignments)
4212.680 Million cell updates/sec

Title: US-09-611-257A-24

Perfect score: 12028

Sequence: 1 MLPHRVRPCVTPPLRGSAR.....KKUTLSLSGLSSDPTDMDPZ 2287

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_crembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	11657	96.9	2254	1 CCAH_RAT	O54898 rattus norv
2	11532	95.9	2288	2 Q9WUB8	Q9WUB8 rattus norv
3	11372.5	94.6	2295	2 Q9WUT2	Q9WUT2 mus musculu
4	11263	93.6	2248	2 Q6PFV8	Q6PFV8 mus musculu
5	10732.5	89.2	2377	1 CCAH_HUMAN	O43497 homo sapien
6	6809.5	56.6	1389	2 Q6ZPX4	Q6ZPX4 mus musculu
7	6226	51.8	2359	1 CCAH_RAT	Q9eq60 rattus norv
8	6222	51.7	2353	1 CCAH_HUMAN	O95180 homo sapien
9	6190	51.5	2365	1 CCAH_MOUSE	O88427 mus musculu
10	5418	45.0	2223	1 CCAI_HUMAN	Q9p0x4 homo sapien
11	5354	44.5	1835	1 CCAI_RAT	Q9z0y8 rattus norv
12	4750.5	39.5	1994	2 Q7Z6S8	Q7Z6S8 homo sapien
13	4188.5	34.8	1762	2 Q7PQV4	Q7PQV4 anopheles g
14	4137.5	34.4	2893	2 Q9W433	Q9W433 drosophila
15	3849.5	32.1	1837	2 Q967R4	Q967R4 caenorhabdi
16	3849	32.0	1852	2 Q7Z002	Q7Z002 caenorhabdi
17	3830	31.8	1844	2 Q7Y2R6	Q7Y2R6 caenorhabdi
18	3824.5	31.8	1885	2 Q7Z003	Q7Z003 caenorhabdi
19	3665	30.5	1460	2 Q80TJ2	Q80TJ2 mus musculu
20	2941.5	24.5	1418	2 Q7JPB4	Q7JPB4 caenorhabdi
21	2813.5	23.4	1942	2 Q869H0	Q869H0 lymnaea sta
22	2098.5	17.4	1211	2 Q8MQ95	Q8MQ95 caenorhabdi
23	1727	14.4	541	2 Q6PE92	Q6PE92 mus musculu
24	1720.5	14.3	1810	2 Q44930	Q44930 alptasia pa
25	1678	14.0	2327	1 CCAH_MOUSE	O55017 mus musculu
26	1674	13.9	2339	1 CCAH_HUMAN	Q00975 homo sapien
27	1673	13.9	2331	2 Q9TTA4	Q9TTA4 bos taurus
28	1665.5	13.9	1599	2 Q7PNK9	Q7PNK9 anopheles g
29	1665.5	13.8	2259	1 CCAH_RABIT	O02343 oryctolagus
30	1661	13.8	2333	2 Q890E9	Q890E9 rattus norv
31	1660	13.8	2295	2 Q9Z3K6	Q9Z3K6 rattus norv

32	1656	13.8	2304	2 Q9BMO4	Q9BMO4 blattella g
33	1653.5	13.7	2272	1 CCAE_MOUSE	Q61290 mus musculu
34	1652.5	13.7	1891	2 Q97017	Q97017 stylophora
35	1650	13.7	2312	1 CCAE_HUMAN	Q15878 homo sapien
36	1649.5	13.7	1984	2 Q28644	Q28644 oryctolagus
37	1646.5	13.7	1847	2 Q6RKB0	Q6RKB0 brachydanio
38	1642.5	13.7	2336	1 CCAH_RAT	Q02294 rattus norv
39	1642.5	13.7	2357	2 Q9PUM6	Q9PUM6 gallus gall
40	1642	13.7	1985	1 CCAE_MOUSE	Q9J187 mus musculu
41	1642	13.7	2223	1 CCAE_DISOM	P56699 discopyge o
42	1639.5	13.6	1984	2 Q7TNI3	Q7TNI3 mus musculu
43	1636	13.6	1993	2 P90670	P90670 aplysia cal
44	1634.5	13.6	1984	2 O08562	O08562 rattus norv
45	1632.5	13.6	2222	1 CCAE_RAT	Q07652 rattus norv

ALIGNMENTS

RESULT 1
CCAG RAT
ID CCAG RAT STANDARD; PRT; 2254 AA.
AC O54898;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Voltage-dependent T-type calcium channel alpha-1G subunit (Voltage-gated calcium channel alpha subunit Cav3.1).
DE gated calcium channel alpha subunit Cav3.1).
GN Name=Cacnalg;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Brain;
RX MEDLINE=98154730; PubMed=9495342; DOI=10.1038/36110;
RA Perez-Reyes E., Cribbs L.L., Daud A., Lacerda A.E., Barclay J., Williamson M.P., Fox M., Rees M., Lee J.-H.;
RT "Molecular characterization of a neuronal low-voltage-activated T-type calcium channel.";
RL Nature 391:896-900(1998).
CC -I- FUNCTION: Voltage-sensitive calcium channels (VSCC) mediate the entry of calcium ions into excitable cells and are also involved in a variety of calcium-dependent processes, including muscle contraction, hormone or neurotransmitter release, gene expression, cell motility, cell division and cell death. The isoform alpha-1G gives rise to T-type calcium currents. T-type calcium channels belong to the "low-voltage activated (LVA)" group and are strongly blocked by nickel and mibefradil. A particularity of this type of channels is an opening at quite negative potentials and a voltage-dependent inactivation. T-type channels serve pacemaking functions in both central neurons and cardiac nodal cells and support calcium signaling in secretory cells and vascular smooth muscle. They may also be involved in the modulation of firing patterns of neurons which is important for information processing as well as in cell growth processes.

-I- SUBCELLULAR LOCATION: Integral membrane protein.
-I- TISSUE SPECIFICITY: Highly expressed in brain. Moderate expression in heart; low expression in placenta, kidney and lung.
-I- DOMAIN: Each of the four internal repeats contains five hydrophobic transmembrane segments (S1, S2, S3, S5, S6) and one positively charged transmembrane segment (S4). S4 segments probably represent the voltage-sensor and are characterized by a series of positively charged amino acids at every third position.

-I- PTM: In response to raising of intracellular calcium, the T-type channels are activated by CaM-kinase II.
-I- SIMILARITY: Belongs to the calcium channel alpha-1 subunits family.

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EMBL: AF027984; AAC67372.1; --
DR PIR: T09053; T09053.
DR RGD: 68942; Cactnalg.
DR InterPro: IPR001682; Ca/Na pore.
DR InterPro: IPR002111; Cat channel_TrpL.
DR InterPro: IPR005821; Ion trans.
DR InterPro: IPR005820; M-channel nlg.
DR InterPro: IPR005445; TVDCCAlphal.
DR Pfam: PF00520; Ion trans; 4.
DR PRINTS: PR01629; TVDCCAlphal.
DR KEGG: K01629; TVDCCAlphal.
KW Calcium channel; Calcium-binding; Glycoprotein; Ion transport;
KW Ionic channel; Multigene family; Phosphorylation; Repeat;
KW Transmembrane; Voltage-gated channel.
FT REPEAT 68 398 I.
FT REPEAT 730 968 II.
FT REPEAT 1242 1519 III.
FT REPEAT 1564 1822 IV.
FT DOMAIN 1 80 Cytoplasmic (Potential).
FT TRANSMEM 81 101 S1 of repeat I.
FT DOMAIN 102 119 Extracellular (Potential).
FT TRANSMEM 120 141 S2 of repeat I (Potential).
FT DOMAIN 142 150 Cytoplasmic (Potential).
FT TRANSMEM 151 170 S3 of repeat I.
FT DOMAIN 171 175 Extracellular (Potential).
FT TRANSMEM 176 193 S4 of repeat I.
FT DOMAIN 194 213 Cytoplasmic (Potential).
FT TRANSMEM 214 234 S5 of repeat I (Potential).
FT DOMAIN 235 370 Extracellular (Potential).
FT TRANSMEM 371 395 S6 of repeat I.
FT DOMAIN 396 744 Cytoplasmic (Potential).
FT TRANSMEM 745 765 S1 of repeat II (Potential).
FT DOMAIN 766 778 Extracellular (Potential).
FT TRANSMEM 779 800 S2 of repeat II (Potential).
FT DOMAIN 801 806 Cytoplasmic (Potential).
FT TRANSMEM 807 825 S3 of repeat II (Potential).
FT DOMAIN 826 833 Extracellular (Potential).
FT TRANSMEM 834 857 S4 of repeat II (Potential).
FT DOMAIN 858 868 Cytoplasmic (Potential).
FT TRANSMEM 869 889 S5 of repeat II (Potential).
FT DOMAIN 890 940 Extracellular (Potential).
FT TRANSMEM 941 965 S6 of repeat II (Potential).
FT DOMAIN 966 1251 Cytoplasmic (Potential).
FT TRANSMEM 1252 1274 S1 of repeat III (Potential).
FT DOMAIN 1275 1292 Extracellular (Potential).
FT TRANSMEM 1293 1313 S2 of repeat III (Potential).
FT DOMAIN 1314 1323 Cytoplasmic (Potential).
FT TRANSMEM 1324 1343 S3 of repeat III (Potential).
FT DOMAIN 1344 1357 Extracellular (Potential).
FT TRANSMEM 1358 1379 S4 of repeat III (Potential).
FT DOMAIN 1380 1389 Cytoplasmic (Potential).
FT TRANSMEM 1390 1413 S5 of repeat III (Potential).
FT DOMAIN 1414 1490 Extracellular (Potential).
FT TRANSMEM 1491 1516 S6 of repeat III (Potential).
FT DOMAIN 1517 1578 Cytoplasmic (Potential).
FT TRANSMEM 1579 1599 S1 of repeat IV (Potential).
FT DOMAIN 1600 1613 Extracellular (Potential).
FT TRANSMEM 1614 1635 S2 of repeat IV (Potential).
FT DOMAIN 1636 1642 Cytoplasmic (Potential).
FT TRANSMEM 1643 1661 S3 of repeat IV (Potential).
FT DOMAIN 1662 1675 Extracellular (Potential).
FT TRANSMEM 1676 1699 S4 of repeat IV (Potential).
FT DOMAIN 1700 1713 Cytoplasmic (Potential).
FT TRANSMEM 1714 1734 S5 of repeat IV (Potential).
FT DOMAIN 1735 1794 Extracellular (Potential).
FT TRANSMEM 1795 1822 S6 of repeat IV (Potential).
FT DOMAIN 1823 2254 Cytoplasmic (Potential).
FT TRANSMEM 2255 290 Poly-Gly.
FT DOMAIN 291 496 Poly-His.

FT	DOMAIN	1527	1530	Poly-Glu.
FT	SITE	354	354	Calcium ion selectivity and permeability (By similarity).
FT	SITE	924	924	Calcium ion selectivity and permeability (By similarity).
FT	SITE	1465	1465	Calcium ion selectivity and permeability (By similarity).
FT	SITE	1770	1770	Calcium ion selectivity and permeability (By similarity).
FT	CARBOHYD	173	173	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	246	246	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	306	306	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	310	310	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	322	322	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	1427	1427	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	1430	1430	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	1666	1666	N-linked (GlcNAc. . .) (Potential).
SQ	SEQUENCE	2254 AA; 250405 MW; 697BBE06360CF0F6 CRC64;		
Query Match 96.9%; Score 11657; DB 1; Length 2254;				
Best Local Similarity 99.7%; Pred. No. 0;				
Matches 2219; Conservative 0; Mismatches 6; Indels 0; Gaps 0;				
QY	62	GAAGAGSTKDPGSAADSEAEGLPYALAPVWFYLSQDSRPESWCLRTVCNPFERVSML	121	
DB	30	GRQPGSTKDPGSAADSEAEGLPYALAPVWFYLSQDSRPESWCLRTVCNPFERVSML	89	
QY	122	VILLNCVTILGMFRPCEDIAQDSQRCILQAFDDFIFAFPAFVEMVVMVALGIFGKKCYLG	181	
DB	90	VILLNCVTILGMFRPCEDIAQDSQRCILQAFDDFIFAFPAFVEMVVMVALGIFGKKCYLG	149	
QY	182	DTWNRDLDFIVTAGMLEYSLDLQNVFSFSAVRTVRVLRPLRNRVPSMRILVTLTLDTP	241	
DB	150	DTWNRDLDFIVTAGMLEYSLDLQNVFSFSAVRTVRVLRPLRNRVPSMRILVTLTLDTP	209	
QY	242	MLGNVLLCFVFFIFIGIVGVQLWAGLLNRNCFLENFSLPLSVLDEPYQYQENEDSPF	301	
DB	210	MLGNVLLCFVFFIFIGIVGVQLWAGLLNRNCFLENFSLPLSVLDEPYQYQENEDSPF	269	
QY	302	ICSPRENGMRSRCSVPTLRGEGGGPPCSDLDTYETVNSSNTTCVNMNQYVNCAGEHN	361	
DB	270	ICSPRENGMRSRCSVPTLRGEGGGPPCSDLDTYETVNSSNTTCVNMNQYVNCAGEHN	329	
QY	362	PFKGAINFNDIGNYAWIAIQVITLEGWDMYFVMDAHSFYNYFIYFILLIIVGSFPMINL	421	
DB	330	PFKGAINFNDIGNYAWIAIQVITLEGWDMYFVMDAHSFYNYFIYFILLIIVGSFPMINL	389	
QY	422	CLVVIATQFSETKORESOLMRQVRFLSNASTLASFSGSCYBELLKYLVYLKKAAR	481	
DB	390	CLVVIATQFSETKORESOLMRQVRFLSNASTLASFSGSCYBELLKYLVYLKKAAR	449	
QY	482	RLAQVSRAGVRAGLLSSPVARSQBPQSGCSTRSHRLSVHLVHHHHHHHHVHLGN	541	
DB	450	RLAQVSRAGVRAGLLSSPVARSQBPQSGCSTRSHRLSVHLVHHHHHHHHVHLGN	509	
QY	542	GTLRVPASPEIQORDANGSRRLWLPPTPTSGGPPRGAEVSHSFYADCHLEPVRCQ	601	
DB	510	GTLRVPASPEIQORDANGSRRLWLPPTPTSGGPPRGAEVSHSFYADCHLEPVRCQ	569	
QY	602	APPRCPSEASGRVTGSGKYVPTVHTSPPEILKDKALVEVAPSPGPTLTSNIPDPGF	661	
DB	570	APPRCPSEASGRVTGSGKYVPTVHTSPPEILKDKALVEVAPSPGPTLTSNIPDPGF	629	
QY	662	SSMHKLLTOSTGACHSSCKISPCSKADSGACPDSCPYCARTGAGEPESADHVPDSD	721	
DB	630	SSMHKLLTOSTGACHSSCKISPCSKADSGACPDSCPYCARTGAGEPESADHVPDSD	689	
QY	722	SEAVYFTQDAQHSDLRDPHSRRRQSLGPDAPSSVLAFWRLICDTFRKIVDSKYFGRG	781	
DB	690	SEAVYFTQDAQHSDLRDPHSRRRQSLGPDAPSSVLAFWRLICDTFRKIVDSKYFGRG	749	
QY	782	IMIAILVNTLSMGIEYHEQPEELTNALEINIVTSLFALEMLLKLIYVGFYKIPYN	841	

750 IMIALVNTLSMGIEYHEQPEELTNALBISNIVFTSLFALEMLLKLIVYGPPIKPNYN 809
842 IPDGIVIVISWEIVGOQGGSLVLRTPRLMRVLKLVFLPALORQLVVLKMTMDNVATP 901
810 IPDGIVIVISWEIVGOQGGSLVLRTPRLMRVLKLVFLPALORQLVVLKMTMDNVATF 869
902 CMLLMFLFIFISILGMHLFGCKFASERDGTLPDRKNFDSLILWAIIVTVFQILTOEDWNKV 961
870 CMLLMFLFIFISILGMHLFGCKFASERDGTLPDRKNFDSLILWAIIVTVFQILTOEDWNKV 929
962 LYNMGMASTSSWAALYFIALMTFGNYVLFNLLVAILVEGFQAEADTKSESEPDFSPSVD 1021
930 LYNMGMASTSSWAALYFIALMTFGNYVLFNLLVAILVEGFQAEADTKSESEPDFSPSVD 989
1022 GDGRKRLALVALGEHALRKSLLPPLI IHTAATPMHSHPKSSSTGVGEALGSGSRRTSS 1081
990 GDGRKRLALVALGEHALRKSLLPPLI IHTAATPMHSHPKSSSTGVGEALGSGSRRTSS 1049
1082 SGSAEPGAHEMKCPPSARSPPHSPMSAASSTWSSRRNSLGRAPSLKRRSPSGERRS 1141
1050 SGSAEPGAHEMKCPPSARSPPHSPMSAASSTWSSRRNSLGRAPSLKRRSPSGERRS 1109
1142 LLSGEGQESQDEBESSEDRASPAGSDHRRHGRSLEREAKSFDLPDTLQVPLHRTASGR 1201
1110 LLSGEGQESQDEBESSEDRASPAGSDHRRHGRSLEREAKSFDLPDTLQVPLHRTASGR 1169
1202 SSASEHQDCNKSASGRILARTLRTDDPOLDDGDDNDDEGNLSKGERIQAWRSRLPACCRE 1261
1170 SSASEHQDCNKSASGRILARTLRTDDPOLDDGDDNDDEGNLSKGERIQAWRSRLPACCRE 1229
1262 RDSASVIFPPQSRFLLCRIITHKMFHVVLVIIFLNCITIAMERPKIDPHSAERIFL 1321
1230 RDSASVIFPPQSRFLLCRIITHKMFHVVLVIIFLNCITIAMERPKIDPHSAERIFL 1289
1322 TLSNYIFTAVFLAEMTKVVALGWCFCGQAYLRSSNNVLDGLLVILSVISVSDSG 1381
1290 TLSNYIFTAVFLAEMTKVVALGWCFCGQAYLRSSNNVLDGLLVILSVISVSDSG 1349
1382 TKILGMRLVRLRLTLRLPRVISAQGLKVETILMSSLKPIGNIIVVICCAFFIIFGILG 1441
1350 TKILGMRLVRLRLTLRLPRVISAQGLKVETILMSSLKPIGNIIVVICCAFFIIFGILG 1409
1442 VOLFKGFVFCQGEDTRNITNKSACAEASYWVRHKYFNDFNLGOALMSFLVLSKDGWVD 1501
1410 VOLFKGFVFCQGEDTRNITNKSACAEASYWVRHKYFNDFNLGOALMSFLVLSKDGWVD 1469
1502 IMYDGLDAVGVDQOPIIMHNPWMLLYFISFLIIVAFVFLNNFVGVVVENPHKCRHQHEE 1561
1470 IMYDGLDAVGVDQOPIIMHNPWMLLYFISFLIIVAFVFLNNFVGVVVENPHKCRHQHEE 1529
1562 EARRREKRLRLRLEKRRSKQMAEACQKPYSDYSRFRLLVHLCTSHYLDLFIITGVI 1621
1530 EARRREKRLRLRLEKRRSKQMAEACQKPYSDYSRFRLLVHLCTSHYLDLFIITGVI 1589
1622 GLNVVTWAMEHYQOQILDEALKICNYIFTVIFVESVFKLVAFAFRFPQDRNOLDLA 1681
1590 GLNVVTWAMEHYQOQILDEALKICNYIFTVIFVESVFKLVAFAFRFPQDRNOLDLA 1649
1682 IVLSISMITLEEVNLSLPINPTIIRIMRVLRIRVLRKLLKMAVGNRALLHTVMOALP 1741
1650 IVLSISMITLEEVNLSLPINPTIIRIMRVLRIRVLRKLLKMAVGNRALLHTVMOALP 1709
1742 QVGNLGLLFLMLFFIIFALGVLELFDLECDTHPECEGLGRHATFRNFGMAFLTIFRVSTG 1801
1710 QVGNLGLLFLMLFFIIFALGVLELFDLECDTHPECEGLGRHATFRNFGMAFLTIFRVSTG 1769
1802 DNWNGIMKDPDRDCQESTCNTVISPFIYFVSFVLTAQFVLNVNVIAMVLMKHLSEESKEA 1861
1770 DNWNGIMKDPDRDCQESTCNTVISPFIYFVSFVLTAQFVLNVNVIAMVLMKHLSEESKEA 1829
1862 KEAELEAELEEMKTLSPQHSPLGSPFLWPGVGVNSTDSPKPGAPHTTAAHGAASGF 1921
1830 KEAELEAELEEMKTLSPQHSPLGSPFLWPGVGVNSTDSPKPGAPHTTAAHGAASGF 1889

QY 1922 SLEHTPTWPHPEEVPVPLGPDLLITVRKSGVSRTHSLPNDSTWCRNGSTAERSLGHGWL 1981
Db 1990 SLEHTPTWPHPEEVPVPLGPDLLITVRKSGVSRTHSLPNDSTWCRNGSTAERSLGHGWL 1949
QY 1982 PKAOSGSLSVHSPADTSCILQPKDVHYLLQPHGAPTWGAIPKLPPLPPGRSPLAQRPLR 2041
Db 1950 PKAOSGSLSVHSPADTSCILQPKDVHYLLQPHGAPTWGAIPKLPPLPPGRSPLAQRPLR 2009
QY 2042 RQAAIRTDSDVQGLSGREDLLSEVSGPSCPLTRSSSFWGGSSIQVQQRSGIQSKVSKHI 2101
Db 2010 RQAAIRTDSDVQGLSGREDLLSEVSGPSCPLTRSSSFWGGSSIQVQQRSGIQSKVSKHI 2069
QY 2102 RLPAPCGLEPSWAKDPPETRSSLELDELTELWSIGDILLPSSQEBPLFRDLKCKYSVETQ 2161
Db 2070 RLPAPCGLEPSWAKDPPETRSSLELDELTELWSIGDILLPSSQEBPLFRDLKCKYSVETQ 2129
QY 2162 SCRRRPGFWLDEQRHRSIAVSCLDGSGOPRLCPSPSSLGQPLGQPGSRPKKLSPPGIS 2221
Db 2130 SCRRRPGFWLDEQRHRSIAVSCLDGSGOPRLCPSPSSLGQPLGQPGSRPKKLSPPGIS 2189
QY 2222 IDPPESQGSRRPPCGVCLRRRAPASDSDKPSVSPSLDSTAASPSPKDITLSLGLSDP 2281
Db 2190 IDPPESQGSRRPPCGVCLRRRAPASDSDKPSVSPSLDSTAASPSPKDITLSLGLSDP 2249
QY 2282 TDMDP 2286
Db 2250 TDMDP 2254
RESULT 2
Q9WUB8
ID Q9WUB8 PRELIMINARY; PRT; 2288 AA.
AC Q9WUB8;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE T-type calcium channel isoform.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
[1]
SEQUENCE FROM N.A.
RC TISSUE=Pancreas;
RX MEDLINE=20081696; PubMed=10615950;
RA Zhuang H., Bhattacharjee A., Hu F., Zhang M., Goswami T., Wang L.,
RA Wu S., Berggren P.O., Li M.;
RT "Cloning of a T-type Ca2+ channel isoform in insulin-secreting
RT cells.";
RL Diabetes 49:59-64(2000).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (by similarity).
CC -1- SIMILARITY: Belongs to the calcium channel alpha-1 subunits
family.
DR EMBL; AF125151; AA026858.1; -;
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0005891; C: voltage-gated calcium channel complex; IEA.
DR GO; GO:0005509; F: calcium ion binding; IEA.
DR GO; GO:0005245; F: voltage-gated calcium channel activity; IEA.
DR GO; GO:0006816; P: calcium ion transport; IEA.
DR GO; GO:0006812; P: cation transport; IEA.
DR InterPro; IPR001682; Ca/Na pore.
DR InterPro; IPR002111; Cat_channel_TripL.
DR InterPro; IPR002077; Ca_channel_alpha.
DR InterPro; IPR005821; Ion trans.
DR InterPro; IPR005820; M-channel_nlg.
DR InterPro; IPR005445; TVDCCAlphal.
DR Pfam; PF00520; Ion trans; 4.
DR PRINTS; PR00167; CACHANNEL.
DR PRINTS; PR01629; TVDCCALPHAL.
KW Calcium; Calcium channel; Calcium transport; Calcium-binding;
KW Ion transport; Ionic channel; Transmembrane; Transport;
KW Voltage-gated channel.

SQ	SEQUENCE	2288 AA; 253476 NW; B89DBB5A1D81757F CRC64;	
	Query Match	95.98; Score 11532; DB 2; Length 2288;	
	Best Local Similarity	97.78; Pred. No. 0;	
	Matches 2206; Conservative	1; Mismatches 18; Indels 34; Gaps 2;	
Qy	62	GAAGAGTEKDPGSADSEAGLPYPALAPVVFYLSQDSRPRSWCLRTVCNPNFVRVSM 121	
Db	30	GRQPGSTKDPGSADSEAGLPYPALAPVVFYLSQDSRPRSWCLRTVCNPNFVRVSM 89	
Qy	122	VILLNCVTLGMFRCEDIACDSQRCRILOAFDDFIFAFAFVAVMVKVALGIGKKCYLG 181	
Db	90	VILLNCVTLGMFRCEDIACDSQRCRILOAFDDFIFAFAFVAVMVKVALGIGKKCYLG 149	
Qy	182	DTNRLDFFIVIAAGLVEYSLDQNVFSAVRTVRVLRPLRAINRVPMSRMLVTLTLLDTP 241	
Db	150	DTNRLDFFIVIAAGLVEYSLDQNVFSAVRTVRVLRPLRAINRVPMSRMLVTLTLLDTP 209	
Qy	242	MLGNVLLLCPPVFFIGVIGVQLWAGLLRNCRFLPENFSIPLSVDLPEYQOTENEDSPF 301	
Db	210	MLGNVLLLCPPVFFIGVIGVQLWAGLLRNCRFLPENFSIPLSVDLPEYQOTENEDSPF 269	
Qy	302	ICSPRENGMSCRSVPTLRGEGGGPPCSLDYETYNSSNTTCVNNQYVYTNCAGEHN 361	
Db	270	ICSPRENGMSCRSVPTLRGEGGGPPCSLDYETYNSSNTTCVNNQYVYTNCAGEHN 329	
Qy	362	PFKGAINDNIGYAMIAIFQVITLEGWVDIMYFVMDAHSFNFYIFILLIIVGSFFMINL 421	
Db	330	PFKGAINDNIGYAMIAIFQVITLEGWVDIMYFVMDAHSFNFYIFILLIIVGSFFMINL 389	
Qy	422	CLVVIATQFSETKQRESQLMREORVRFILSNASTLASFSEPGSCYBEELLKYLVIYLRKAAR 481	
Db	390	CLVVIATQFSETKQRESQLMREORVRFILSNASTLASFSEPGSCYBEELLKYLVIYLRKAAR 449	
Qy	482	RLAQSRAIGVRAAGLLSPVARSQEPQPSGSTRSHRLSVHLLVHHHHHHHHYHLGN 541	
Db	450	RLAQSRAIGVRAAGLLSPVARSQEPQPSGSTRSHRLSVHLLVHHHHHHHHYHLGN 509	
Qy	542	GTLVRPRASPEIQDRDANGSRRLMLPPSTPTSPGPPRGAEVHSFVHADCHLEPVRCQ 601	
Db	510	GTLVRPRASPEIQDRDANGSRRLMLPPSTPTSPGPPRGAEVHSFVHADCHLEPVRCQ 569	
Qy	602	APPRCPSEASGRVSGSKVYTVHTSPPEILKDKALVEVAPSPGPTLTSFNIPGPF 661	
Db	570	APPRCPSEASGRVSGSKVYTVHTSPPEILKDKALVEVAPSPGPTLTSFNIPGPF 629	
Qy	662	SSMHKLETOSTQACHSSCKISSPCKADSGACGPDSCPCYCATGAGPESADHWMPDSD 721	
Db	630	SSMHKLETOSTQACHSSCKISSPCKADSGACGPDSCPCYCATGAGPESADHWMPDSD 689	
Qy	722	SEAVYFTQDAQSHSLDRDPSRRRQSLGPDAPSPSVLAFWRLICDTFRKIVDSKYFGRG 781	
Db	690	SEAVYFTQDAQSHSLDRDPSRRRQSLGPDAPSPSVLAFWRLICDTFRKIVDSKYFGRG 749	
Qy	782	IMTALVNTLSMGIYEHEQPEELTNALEISNIVFTSLFALEMLKLLVYGPFGYIKNPYN 841	
Db	750	IMTALVNTLSMGIYEHEQPEELTNALEISNIVFTSLFALEMLKLLVYGPFGYIKNPYN 809	
Qy	842	IFDGVIVIVISWEIVGQGGGLSVLRTFRLMRVLKLVRLPALQRLVLMKTMNDVATF 901	
Db	810	IFDGVIVIVISWEIVGQGGGLSVLRTFRLMRVLKLVRLPALQRLVLMKTMNDVATF 869	
Qy	902	CMLMLFIFIFISILGMLHFCCKFASERDGTLPDRKNFDSLWAIIVTVFQILTOEDWNKV 961	
Db	870	CMLMLFIFIFISILGMLHFCCKFASERDGTLPDRKNFDSLWAIIVTVFQILTOEDWNKV 929	
Qy	962	LYNGMASTSWAALFYFALMTFGNYVLNLLVAILVEGFOAE-----1003	
Db	930	LYNGMASTSWAALFYFALMTFGNYVLNLLVAILVEGFOAEIIGKREASQOLSCIQLP 989	
Qy	1004	-----GPATKSESPDFPSVDGDKRKLALVALGEHAEIRKSLPLPILTHAATPM 1058	
Db	990	VNSQGGDATKSESPDFPSVDGDKRKLALVALGEHAEIRKSLPLPILTHAATPM 1049	

Qy	1059	SHPKSSSTGVGEALGSGSRRTSSSGSAEPGAAAHHEMKCPPSARSSPHSPSAASSWTSRR 1118	
Db	1050	SLPKSSSTGVGEALGSGSRRTSSSGSAEPGAAAHHEMKCPPSARSSPHSPSAASSWTSRR 1109	
Qy	1119	SSRNSLGRAPSLKRRSPSGERRSLLSGEGQESQDEBESSEEDRASPGSDHRRHGSLERE 1178	
Db	1110	SSRNSLGRAPSLKRRSPSGERRSLLSGEGQESQDEBESSEEDRASPGSDHRRHGSLERE 1169	
Qy	1179	AKSSFDLPDTLOVPLGHRHTASGRSASGHQDCNCKSASGRLARLTRTDDPOLDDGDDONDE 1238	
Db	1170	AKSSFDLPDTLOVPLGHRHTASGRSASGHQDCNCKSASGRLARLTRTDDPOLDDGDDONDE 1229	
Qy	1239	GNLSKGERIQAWVRSLPACCRERDSWSAYIFPPQSRPRLCHRIITHKMFDPHVVLVIF 1298	
Db	1230	GNLSKGERIQAWVRSLPACCRERDSWSAYIFPPQSRPRLCHRIITHKMFDPHVVLVIF 1289	
Qy	1299	LNCITIAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTVKVALGWCFCGQAYLRSSWN 1358	
Db	1290	LNCITIAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTVKVALGWCFCGQAYLRSSWN 1349	
Qy	1359	VLDGLLVLSVIDILVMSVSDSGTKILGMLRVLRLLRTRLRPLRVISRAOGLKLVVETILMS 1418	
Db	1350	VLDGLLVLSVIDILVMSVSDSGTKILGMLRVLRLLRTRLRPLRVISRAOGLKLVVETILMS 1409	
Qy	1419	SLKPIGNIIVVICAPFIIFGILGVQLFKGKFPVCOGEDTRNITNKSDCAEASYSRVWRHKY 1478	
Db	1410	SLKPIGNIIVVICAPFIIFGILGVQLFKGKFPVCOGEDTRNITNKSDCAEASYSRVWRHKY 1469	
Qy	1479	NFDNLQOALMSLFLVASKDGWVDIMYDGLDAGVDQOQIMNHNPMWLLYFISFLLIIVAF 1538	
Db	1470	NFDNLQOALMSLFLVASKDGWVDIMYDGLDAGVDQOQIMNHNPMWLLYFISFLLIIVAF 1529	
Qy	1539	VLMNFVGVVVENPHKCRQHQEERREKRLREKQR-----SKKQWAE 1587	
Db	1530	VLMNFVGVVVENPHKCRQHQEERREKRLREKQR-----SKKQWAE 1589	
Qy	1588	AOCKPYSDYSRPRLLVHLLCTSHYLDLFTGVIQVVTVMAMEHVQOQIIDEALKICN 1647	
Db	1590	AOCKPYSDYSRPRLLVHLLCTSHYLDLFTGVIQVVTVMAMEHVQOQIIDEALKICN 1649	
Qy	1648	YIFTVLFEVSEVPKLVAFAPRFFQDRMNQDLAIIVLLSIMGITLIEEIVNLSLPINPTI 1707	
Db	1650	YIFTVLFEVSEVPKLVAFAPRFFQDRMNQDLAIIVLLSIMGITLIEEIVNLSLPINPTI 1709	
Qy	1708	IRIMRVLRIRARVLKLLKMAVGRALLHTVMQALPOVGNLGLLFMLLFFIIPALGVELFGD 1767	
Db	1710	IRIMRVLRIRARVLKLLKMAVGRALLHTVMQALPOVGNLGLLFMLLFFIIPALGVELFGD 1769	
Qy	1768	LECDETHPCSGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMKDPDRDCDOESTCYNTVIS 1827	
Db	1770	LECDETHPCSGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMKDPDRDCDOESTCYNTVIS 1829	
Qy	1828	PIYFVSFVLTAQFVLNVVIVIAVLMKHLSESNKAEAEAEAEAELEEMKTLSPQHPSLG 1887	
Db	1830	PIYFVSFVLTAQFVLNVVIVIAVLMKHLSESNKAEAEAEAELEEMKTLSPQHPSLG 1889	
Qy	1888	SPFLWPVGEGVNSTDSKPGAPHTTAHGAASGFSLEHPTWPHPEVPVPLGPDLLTVR 1947	
Db	1890	SPFLWPVGEGVNSTDSKPGAPHTTAHGAASGFSLEHPTWPHPEVPVPLGPDLLTVR 1949	
Qy	1948	KSGVSRTHSLPNDSYMCRNGSTAESRSLGHRGWGLPKAQSGSILSVHSQPADTSCILQLPK 2007	
Db	1950	KSGVSRTHSLPNDSYMCRNGSTAESRSLGHRGWGLPKAQSGSILSVHSQPADTSCILQLPK 2009	
Qy	2008	DVHYLLQPHGAPTGAIPKLPPLPGSRPLAQRPRLRQAARTDSLDVQGLGSRDILLSEVS 2067	
Db	2010	DVHYLLQPHGAPTGAIPKLPPLPGSRPLAQRPRLRQAARTDSLDVQGLGSRDILLSEVS 2069	
Qy	2068	GPSCLPTRSSSFWGSSSIQVQORSGIQSKVSKHRLPAPCFGLEPSPWAKOPPETRSSLEL 2127	
Db	2070	GPSCLPTRSSSFWGSSSIQVQORSGIQSKVSKHRLPAPCFGLEPSPWAKOPPETRSSLEL 2129	

QY 2128 DTELSWISGDLPSSEPELPRDLKKYSVETOSCRPPGFWLDEORRHSHIAVCLDSG 2187
DTELSWISGDLPSSEPELPRDLKKYSVETOSCRPPGFWLDEORRHSHIAVCLDSG 2189
DTELSWISGDLPSSEPELPRDLKKYSVETOSCRPPGFWLDEORRHSHIAVCLDSG 2191
QY 2188 SQRLCPSPSLGQPLGGPGSRPKKLSPPSISIDPPESQSRPPCPSPGVCLRRRAPAS 2247
SQRLCPSPSLGQPLGGPGSRPKKLSPPSISIDPPESQSRPPCPSPGVCLRRRAPAS 2249
QY 2248 DSKDPSVSSPLDSTAASPSPKKOTLSLSGLSSDPTDMDP 2286
DSKDPSVSSPLDSTAASPSPKKOTLSLSGLSSDPTDMDP 2288
Db 2250 DSKDPSVSSPLDSTAASPSPKKOTLSLSGLSSDPTDMDP 2288

RESULT 3
Q9WUT2 PRELIMINARY; PRT; 2295 AA.
AC Q9WUT2
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Voltage-gated calcium channel, alpha-1-G subunit.
GN Name=Cacnalg;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=99189326; PubMed=10087148;
RA Klugbauer N.; Marais E.; Lacinova L.; Hofmann F.;
RT "A T-type calcium channel from mouse brain."
RL Pfugers Arch. 437:710-715(1999).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -1- SIMILARITY: Belongs to the calcium channel alpha-1 subunits family.
DR EMBL; AJ012569; CAB40793.1; -;
DR MGD; MGI:1201678; Cacnalg.
DR GO; GO:0016021; C: integral to membrane; TAS.
DR GO; GO:0005886; C: plasma membrane; IDA.
DR GO; GO:0005245; F: voltage-gated calcium channel activity; IDA.
DR InterPro; IPR001682; Ca/Na_pore.
DR InterPro; IPR002111; Cat_channel_TrpL.
DR InterPro; IPR002077; Ca_channel_alpha.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR005820; M-channel_nlg.
DR Pfam; PF00520; Ion_trans_4.
DR PRINTS; PR00167; CACHANNEL.
DR PRINTS; PR01629; TVDCCALPHA1.
KW Calcium; Calcium channel; Calcium transport; Calcium-binding;
KW Ion transport; Ionic channel; Transmembrane; Transport;
KW Voltage-gated channel.
SQ SEQUENCE 2295 AA; 253957 MW; FE817D054ED26984 CRC64;

Query Match 94.6%; Score 11372.5; DB 2; Length 2295;
Best Local Similarity 96.1%; Pred. No. 0;
Matches 2178; Conservative 12; Mismatches 34; Indels 43; Gaps 4;

QY 62 GAAGAGSTKDPGSDSEAGLPYPALAPVVFYVLSQDSRPSRCLRTVCNPFERSM 121
DTELSWISGDLPSSEPELPRDLKKYSVETOSCRPPGFWLDEORRHSHIAVCLDSG 2187
DTELSWISGDLPSSEPELPRDLKKYSVETOSCRPPGFWLDEORRHSHIAVCLDSG 2189
DTELSWISGDLPSSEPELPRDLKKYSVETOSCRPPGFWLDEORRHSHIAVCLDSG 2191
QY 30 GRQPGSTKDPGSDSEAGLPYPALAPVVFYVLSQDSRPSRCLRTVCNPFERSM 89
DTELSWISGDLPSSEPELPRDLKKYSVETOSCRPPGFWLDEORRHSHIAVCLDSG 2187
DTELSWISGDLPSSEPELPRDLKKYSVETOSCRPPGFWLDEORRHSHIAVCLDSG 2189
DTELSWISGDLPSSEPELPRDLKKYSVETOSCRPPGFWLDEORRHSHIAVCLDSG 2191
QY 122 VILLNCVTLGNFRPCEDIACDSQRCLIQAFDDDFIAFFAVEMVVMVVALGIFGKKCYLG 181
VILLNCVTLGNFRPCEDIACDSQRCLIQAFDDDFIAFFAVEMVVMVVALGIFGKKCYLG 149
VILLNCVTLGNFRPCEDIACDSQRCLIQAFDDDFIAFFAVEMVVMVVALGIFGKKCYLG 149
QY 182 DTNRLDFFVIAGLMVSLDLQNVFSAVRTVRLPLRINRVPNRLVLTLLDTP 241
DTNRLDFFVIAGLMVSLDLQNVFSAVRTVRLPLRINRVPNRLVLTLLDTP 241
DTNRLDFFVIAGLMVSLDLQNVFSAVRTVRLPLRINRVPNRLVLTLLDTP 209
QY 242 MGNVLLICFPVFFIGVGVQWAGLLRNRCFLPENFSLPSVDLBPYYQTEDESP 301
MGNVLLICFPVFFIGVGVQWAGLLRNRCFLPENFSLPSVDLBPYYQTEDESP 301
MGNVLLICFPVFFIGVGVQWAGLLRNRCFLPENFSLPSVDLBPYYQTEDESP 301

Db 210 MGNVLLICFPVFFIGVGVQWAGLLRNRCFLPENFSLPSVDLBPYYQTEDESP 269
QY 302 ICSPRENGMRSCRSVPTLRGEGGGPPCSLDYTYNSSNTTCCVNNQYVYTNCSAGHN 361
ICSPRENGMRSCRSVPTLRGEGGGPPCSLDYTYNSSNTTCCVNNQYVYTNCSAGHN 361
ICSPRENGMRSCRSVPTLRGEGGGPPCSLDYTYNSSNTTCCVNNQYVYTNCSAGHN 329
QY 362 PFKGAINFNDIGYAWIAIFQVITLEGWVDIMYFMDAHSFYNFYFILLIIVGSFFMNL 421
PFKGAINFNDIGYAWIAIFQVITLEGWVDIMYFMDAHSFYNFYFILLIIVGSFFMNL 421
PFKGAINFNDIGYAWIAIFQVITLEGWVDIMYFMDAHSFYNFYFILLIIVGSFFMNL 389
QY 422 CLVVIATQFSETKQESQRLMREQVRFLSNASTILASFEPGSCYEELIKYLVIILRKAAR 481
CLVVIATQFSETKQESQRLMREQVRFLSNASTILASFEPGSCYEELIKYLVIILRKAAR 481
CLVVIATQFSETKQESQRLMREQVRFLSNASTILASFEPGSCYEELIKYLVIILRKAAR 449
QY 482 RLAQVSRAGVRAGLLSSPVARSQEPQPSGSCSTRSHRRLSVHLLVHHHHHHHHYHGN 541
RLAQVSRAGVRAGLLSSPVARSQEPQPSGSCSTRSHRRLSVHLLVHHHHHHHHYHGN 541
RLAQVSRAGVRAGLLSSPVARSQEPQPSGSCSTRSHRRLSVHLLVHHHHHHHHYHGN 509
QY 542 GTLRVPASPEIQDRDANGSRRLMLPPSTPTSGGPPRGAEVSHSVHADCHLEPVRQ 601
GTLRVPASPEIQDRDANGSRRLMLPPSTPTSGGPPRGAEVSHSVHADCHLEPVRQ 601
GTLRVPASPEIQDRDANGSRRLMLPPSTPTSGGPPRGAEVSHSVHADCHLEPVRQ 569
QY 602 APPRCPEASGRTVSGKVPYVHTSPPEILKDKALVEVAPSPGPTLTSTFNIPGPF 661
APPRCPEASGRTVSGKVPYVHTSPPEILKDKALVEVAPSPGPTLTSTFNIPGPF 661
APPRCPEASGRTVSGKVPYVHTSPPEILKDKALVEVAPSPGPTLTSTFNIPGPF 629
QY 662 SSMHKLLETOSTGACHSSCKISSPCSKADGACPDSCPCYARTGAGEPESADHMPDSD 721
SSMHKLLETOSTGACHSSCKISSPCSKADGACPDSCPCYARTGAGEPESADHMPDSD 721
SSMHKLLETOSTGACHSSCKISSPCSKADGACPDSCPCYARTGAGEPESADHMPDSD 689
QY 722 SEAVYETQAOHSDLRDPHRRRQRRSGDPAEPPSVLAFWRLICDTRFKIVDSKYCRG 781
SEAVYETQAOHSDLRDPHRRRQRRSGDPAEPPSVLAFWRLICDTRFKIVDSKYCRG 781
SEAVYETQAOHSDLRDPHRRRQRRSGDPAEPPSVLAFWRLICDTRFKIVDSKYCRG 748
QY 782 IMTAILVNTLSMGIEYHEQPEELTNALEISNIVFTSLFALEMLKLLVYGFYKPNYN 841
IMTAILVNTLSMGIEYHEQPEELTNALEISNIVFTSLFALEMLKLLVYGFYKPNYN 841
IMTAILVNTLSMGIEYHEQPEELTNALEISNIVFTSLFALEMLKLLVYGFYKPNYN 808
QY 842 IFDGVIVVSWETVGGGGLSVLRTFLMRVLKLVRFPLPALQRLVLMKTMNDVATP 901
IFDGVIVVSWETVGGGGLSVLRTFLMRVLKLVRFPLPALQRLVLMKTMNDVATP 901
IFDGVIVVSWETVGGGGLSVLRTFLMRVLKLVRFPLPALQRLVLMKTMNDVATP 868
QY 902 CMLLMLEFIFESILGMHLFCKFASERDGTLPDRKNFDSLWAIIVTFQILTQEDMNVK 961
CMLLMLEFIFESILGMHLFCKFASERDGTLPDRKNFDSLWAIIVTFQILTQEDMNVK 961
CMLLMLEFIFESILGMHLFCKFASERDGTLPDRKNFDSLWAIIVTFQILTQEDMNVK 928
QY 962 LYNGMASTSSWAALYFIALMTFGNYVLFNLLVALVEGFOAE----- 1003
LYNGMASTSSWAALYFIALMTFGNYVLFNLLVALVEGFOAE----- 1003
LYNGMASTSSWAALYFIALMTFGNYVLFNLLVALVEGFOAE----- 988
QY 1004 -----GDATKSESPDPFSPVGDGDRKKRLALVALGERHAELKSLPLPILHTAATPM 1058
-----GDATKSESPDPFSPVGDGDRKKRLALVALGERHAELKSLPLPILHTAATPM 1058
-----GDATKSESPDPFSPVGDGDRKKRLALVALGERHAELKSLPLPILHTAATPM 1048
QY 1059 SHPKSSSTGVGEALGSGSRRTSSGSAEPGNAHHEKCPSPARSPPSPWAAASWTSRR 1118
SHPKSSSTGVGEALGSGSRRTSSGSAEPGNAHHEKCPSPARSPPSPWAAASWTSRR 1118
SHPKSSSTGVGEALGSGSRRTSSGSAEPGNAHHEKCPSPARSPPSPWAAASWTSRR 1108
QY 1109 SRRNSLGRAPSLKRRSPSGERRSLLSGEGQESQDEESSEDRA SPAGSDHRRHGSLE 1178
SRRNSLGRAPSLKRRSPSGERRSLLSGEGQESQDEESSEDRA SPAGSDHRRHGSLE 1178
SRRNSLGRAPSLKRRSPSGERRSLLSGEGQESQDEESSEDRA SPAGSDHRRHGSLE 1168
QY 1179 AKSFDLPDQLVPLHRTASGRSSASEHQDCNCKSASGRILARTLRTDDPOLDGGDDNDE 1238
AKSFDLPDQLVPLHRTASGRSSASEHQDCNCKSASGRILARTLRTDDPOLDGGDDNDE 1238
AKSFDLPDQLVPLHRTASGRSSASEHQDCNCKSASGRILARTLRTDDPOLDGGDDNDE 1228
QY 1239 GNLSKGRERIQAWVSRPLPACCRERDSYAFIPQSRFRLCHRIITHKMDHVLVIIF 1298
GNLSKGRERIQAWVSRPLPACCRERDSYAFIPQSRFRLCHRIITHKMDHVLVIIF 1298
GNLSKGRERIQAWVSRPLPACCRERDSYAFIPQSRFRLCHRIITHKMDHVLVIIF 1288
QY 1299 LNCITIAWERPKIDPHSAERIFLTLVNIYFVAVLAETVAVKVGWCFGQAYLRSSWN 1358
LNCITIAWERPKIDPHSAERIFLTLVNIYFVAVLAETVAVKVGWCFGQAYLRSSWN 1358
LNCITIAWERPKIDPHSAERIFLTLVNIYFVAVLAETVAVKVGWCFGQAYLRSSWN 1348

QY 1359 VLDGLLVISVIDILVSMVSDSGTKILGMLRVLRLLRTLRPRVSRAGLKLWVETLMS 1418
DB 1349 VLDGLLVISVIDILVSMVSDSGTKILGMLRVLRLLRTLRPRVSRAGLKLWVETLMS 1408
QY 1419 SLKPIGNVVICAFFIIFGILGVOLFPGKFFVCOGEDTNNITNKSDCAEASVRWRHKY 1478
DB 1409 SLKPIGNVVICAFFIIFGILGVOLFPGKFFVCOGEDTNNITNKSDCAEASVRWRHKY 1468
QY 1479 NFDNLGALMSLFLVASKDGDWDIMYDGLDVGVDQOPIINHNPMWMLLYFISFLLVAPF 1538
DB 1469 NFDNLGALMSLFLVASKDGDWDIMYDGLDVGVDQOPIINHNPMWMLLYFISFLLVAPF 1528
QY 1539 VLNMFVGVVVFENFKRQHQBEEFARREKRRLRLEKGRSKEKQWA----- 1586
DB 1529 VLNMFVGVVVFENFKRQHQBEEFARREKRRLRLEKGRSKEKQWADMLDDVJASGS 1588
QY 1587 -----EAOCKPYSDYSRFFLVAHLLCTSHYLDLFTGVIGLVNVTMAMEHYQQOQILD 1640
DB 1589 SASAASEAQCKPYSDYSRFFLVAHLLCTSHYLDLFTGVIGLVNVTMAMEHYQQOQILD 1648
QY 1641 EALKICNYIFTVIFVLESFVKLAFARFRFQDRWNQDLAIVLLSIMGITLBEIEVNL 1700
DB 1649 EALKICNYIFTVIFVLESFVKLAFARFRFQDRWNQDLAIVLLSIMGITLBEIEVNAS 1708
QY 1701 LPINPTIIRIMRVRIARVLLKLVKQVGRALLHTVMQALPOVGNLGLFWMLFFIIPAL 1760
DB 1709 LPINPTIIRIMRVRIARVLLKLVKQVGRALLHTVMQALPOVGNLGLFWMLFFIIPAL 1768
QY 1761 GVELFGDLECDTHPCGELGRHATFRNFGMAFLTLFRVSTGDNWNGIMKOPSRDCQEST 1820
DB 1769 GVELFGDLECDTHPCGELGRHATFRNFGMAFLTLFRVSTGDNWNGIMKOTLRDCQEST 1828
QY 1821 CYNTWISPIYFVSFVLTQFVLVNVVIAVLMKHLEESNKEAKEAELELEMKTLSP 1880
DB 1829 CYNTWISPIYFVSFVLTQFVLVNVVIAVLMKHLEESNKEAKEAELELEMKTLSP 1888
QY 1881 QPHSPGSLPMPGVEGVNSTDSKPGAPHTTAHIGAA-SGFSLEHPTMVPHEVPVPL 1939
DB 1889 QPHSPGSLPMPGVEGVNSTDSKPGAPHTTAHIGAA-SGFSLEHPTMVPHEVPVPL 1948
QY 1940 GPDLLTVKRSVSRTHSLPNDSYMCRNGSTABRSIGHRGWGLPKAQSGSILSVHSQPADT 1999
DB 1949 GPDLLTVKRSVSRTHSLPNDSYMCRNGSTABRSIGHRGWGLPKAQSGSILSVHSQPADT 2008
QY 2000 SCILQPKDVHLLQPHGAPTWGATPKLPGRSPLAQRPLRQAAIRTDSDLDVQGLGR 2059
DB 2009 SCILQPKDVHLLQPHGAPTWGATPKLPGRSPLAQRPLRQAAIRTDSDLDVQGLGR 2068
QY 2060 EDLLSEVSGPSCPLTRSSFWGSSIQVOQRSGISQKSVKHIRLPAPCPGLEPSPWAKDPP 2119
DB 2069 EDLLSEVSGPSCPLTRSSFWGSSIQVOQRSGISQKSVKHIRLPAPCPGLEPSPWAKDPP 2128
QY 2120 ETRSSLELDTLSWISGDLPLPSQOEPLPRDLKKCYSVETOSCRRRPGFWLDEORRHSI 2179
DB 2129 ETRSSLELDTLSWISGDLPLPSQOEPLPRDLKKCYSVETOSCRRRPGFWLDEORRHSI 2188
QY 2180 AVSCLDGSGOPRLCPSPSSILGGOPLGPGSRPKKLSPPSISIDPPESQGRPPCPSPGVC 2239
DB 2189 AVSCLDGSGOPRLCPSPSSILGGOPLGPGSRPKKLSPPSISIDPPESQGRPPCPSPGVC 2248
QY 2240 LRRRAPASDSDKPSVSSPLDSTAASPPKXDTLSLGLSDSDPTMDP 2286
DB 2249 LRRRAPASDSDKPSVSSPLDSTAASPPKXDTLSLGLSDSDPTMDP 2295

RESULT 4
Q6PFV8 PRELIMINARY; PRT: 2248 AA.
AC Q6PFV8
DT 05-JUL-2004 (Tremblrel. 27, Created)
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)

DE Cacna1g protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.2426038999;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalón D.K., Muzny K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Touchman J.W., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RX Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
RL EMBL: BC057399; AAH57399.1; -.
DR GO: 0016021; C: integral to membrane; TAS.
DR GO: 0005886; C: plasma membrane; IDA.
DR GO: 0005245; F: voltage-gated calcium channel activity; IDA.
DR InterPro: IPR001682; Ca/Na_pore.
DR InterPro: IPR002111; Ion channel.
DR InterPro: IPR005821; Cat_channel_TrpL.
DR InterPro: IPR005820; M-channel_nlg.
DR InterPro: IPR005445; TVDCCalpal.
DR Pfam: PF00520; Ion_trans_4.
DR PRINTS: PR01629; TVDCCALPAL.
DR Ion transport; Ionic channel; Transmembrane; Transport.
KW Ion transport; Ionic channel; Transmembrane; Transport.
SQ SEQUENCE 2248 AA; 248888 MW; 332CSA8D9115A64F CRC64;

Query Match 93.6%; Score 11263; DB 2; Length 2248;
Best Local Similarity 96.3%; Pred. No. 0;
Matches 2155; Conservative 12; Mismatches 40; Indels 30; Gaps 4;
QY 62 GAAGAGTEKDPGADSEAEGLYPALAPVVFVLSQDSRPSRWCRLTVCNPFVRSML 121
DB 30 GRCQPGSTKDPGADSEAEGLYPALAPVVFVLSQDSRPSRWCRLTVCNPFVRSML 89
QY 122 VILNCVTLGMFRCEDIACDSQRCRILQAFDFPIFAFFAVEMVVKVVALGIFGKCYLG 181
DB 90 VILNCVTLGMFRCEDIACDSQRCRILQAFDFPIFAFFAVEMVVKVVALGIFGKCYLG 149
QY 182 DTWNRLOFFVIAGWLEYSLDLQNVSPSAVTRVRLPLRAINRVPMSRLIVTLIDTLP 241
DB 150 DTWNRLOFFVIAGWLEYSLDLQNVSPSAVTRVRLPLRAINRVPMSRLIVTLIDTLP 209
QY 242 MGNVLLICFFVFFIFGIVGVQLWAGLLRNCFLPENFSLPLSVLDLEPYOTENEDSPF 301
DB 210 MGNVLLICFFVFFIFGIVGVQLWAGLLRNCFLPENFSLPLSVLDLEPYOTENEDSPF 269
QY 302 ICSPRENGMRSRCSVPTLRGEGGGPPCSLDYTYNSSNTTCVNNQYVTCNCSAGEHN 361
DB 270 ICSPRENGMRSRCSVPTLRGEGGGPPCGLDYAYNSSNTTCVNNQYVTCNCSAGEHN 329
QY 362 PFKGAINFDNIGYAWIAIFQVITLEGWVDIMVFMVDAHSFYNFYFVILLIIVGSFFMINL 421

||||| 330 PFKGAINEDNIGAWIAIFQVITLEGWVDIMYFMDAHSFYNFYIFILLII----- 380
QY 422 CLVVIATQFSETKQRESQLMREORVRFLSNASTLASPSEPGSCYEELLYVILRKAAR 481
Db 381 -----FSETKQRESQLMREORVRFLSNASTLASPSEPGSCYEELLYVILRKAAR 432
QY 482 RLAQVSRAGVYRAGLSSPVARSQOEPOPSGCTSRSHRRLSVHHLVHHHHHHHHYHLGN 541
Db 433 RLAQVSRAGVYRAGLSSPVVVGQEPQPSGCSHRRLSVHHLVHHHHHHHHYHLGN 492
QY 542 GTLRVPASPEIQDRDANGSRRLMPPSTPTPSGPPRGAESVHSFYHADCHLEPVRCQ 601
Db 493 GTLRVPASPEIQDRDANGSRWMLPPSTPTPSGPPRGAESVHSFYHADCHLEPVRCQ 552
QY 602 APPRCPSAAGRTVSGSKVPTVHTSPPPPEILKDKALVEVAPSGPPTLTSFNIPGPF 661
Db 553 APPRCPSAAGRTVSGSKVPTVHTSPPPPEMLKDKALVEVAPSGPPTLTSFNIPGPF 612
QY 662 SSMHKLLETQSTGACHSSCKISSPCSKADSGACGPDSCPYCARTCAGEPESADHVPDSD 721
Db 613 SSMHKLLETQSTGACHSSCKISSPCSKADSGACGPDSCPYCARTCAGEPESADHVPDSD 672
QY 722 SEAVYFTQDAQHSDLRDPHRRRRLSGPDAEPSSVLAFWRLICDTFRKIYVDSKYFGRG 781
Db 673 SEAVYFTQDAQHSDLRDPH-RRRPSLGPDAEPSSVLAFWRLICDTFRKIYVDSKYFGRG 731
QY 782 IMIAILVNTLSMGIEYHQBPELTNALEISINIVFTSLFALEMLKLLVYGFYIKPNYN 841
Db 732 IMIAILVNTLSMGIEYHQBPELTNALEISINIVFTSLFALEMLKLLVYGFYIKPNYN 791
QY 842 IFDGVIVVISWEIVGQGGGLSVLRTFRLMRVLKLVFLPALOROLVLMKTDWNVATF 901
Db 792 IFDGVIVVISWEIVGQGGGLSVLRTFRLMRVLKLVFLPALOROLVLMKTDWNVATF 851
QY 902 CMLLMFIFIFISILGMHLFGCKFASERDGDTLPRKNFDSLILWALTIVFQILITQEDWNVK 961
Db 852 CMLLMFIFIFISILGMHLFGCKFASERDGDTLPRKNFDSLILWALTIVFQILITQEDWNVK 911
QY 962 LYNGMASTSSWAALYFIALMTFGNYLVNLLVAILVEGFAEGDATKSESEBDFPSPSVD 1021
Db 912 LYNGMASTSSWAALYFIALMTFGNYLVNLLVAILVEGFAEGDATKSESEBDFPSPSVD 971
QY 1022 GDGRKRLALVALGEHAELRKSLLPPLIIHTAATPMASHKSSSTGVCEALGSSRRSTSS 1081
Db 972 GDGRKRLALVALGEHSELRKSLLPPLIIHTAATPMSLPKSSSTGVCEALGSSRRSTSS 1031
QY 1082 SGSAEPGAAHHEMKCPPGARSPPHSPWASAASWTSSRSLGRAPSLKRSPSGERRS 1141
Db 1032 SGSAEPGTAHHEMKSPGARSPPHSPWASAASWTSSRSLGRAPSLKRSPSGERRS 1091
QY 1142 LLSGEGQESQDEEESSEEDRASPAGSDHRRGSLEREAKSSFDLPDITLQVPLHRTASGR 1201
Db 1092 LLSGEGQESQDEEESSEEDRASPAGSDHRRGSLEREAKSSFDLPDITLQVPLHRTASGR 1151
QY 1202 SSASEHQDCNKSASGRILARTLTDPPOLDGDDNDDEGNLSKGERIQAWVRSRLPACCRE 1261
Db 1152 SSASEHQDCNKSASGRILARTLRADDPDLPDGDGDDDEGNLSKGERLARAWRARLPACCRE 1211
QY 1262 RDSMSAYIFPQSPFRLLCHRIITHKMDHVVVLIIIFLNCITIAMERKIDPHSAERIFL 1321
Db 1212 RDSMSAYIFPQSPFRLLCHRIITHKMDHVVVLIIIFLNCITIAMERKIDPHSAERIFL 1271
QY 1322 TLSNYIFTAVFLAEMTVKVALGWCFCGQAYLRSSNNVLDGLLVLISVIDILVSNVSDSG 1381
Db 1272 TLSNYIFTAVFLAEMTVKVALGWCFCGQAYLRSSNNVLDGLLVLISVIDILVSNVSDSG 1331
QY 1382 TKILGMLRVLLRLTLRLPLRVISRAQGLKVETILMSSLKPIGNIWIVICCAFFIIFGLG 1441
Db 1332 TKILGMLRVLLRLTLRLPLRVISRAQGLKVETILMSSLKPIGNIWIVICCAFFIIFGLG 1391
QY 1442 VOLFKGKFFVCOGEDTRNITNKSDCAEASYRWVRHKYNFDNLGOALMSLFLVLSKDGWVD 1501
|||||

Db 1392 VOLFKGKFFVCOGEDTRNITNKSDCAEASYRWVRHKYNFDNLGOALMSLFLVLSKDGWVD 1451
QY 1502 IMYDGLDAVGVDQOPIMNHNPMMLLYFISFLLIIVAFVFLNMFVGVVVFENFHKROHQBEE 1561
Db 1452 IMYDGLDAVGVDQOPIMNHNPMMLLYFISFLLIIVAFVFLNMFVGVVVFENFHKROHQBEE 1511
QY 1562 BARREERKRLRLRLEKRR-----SKEQMAEAOCKPYYSYDSRFRLLVHHLCTS 1610
Db 1512 BARREERKRLRLRLEKRRNLMDDVIAAGSSASASEAOCKPYYSYDSRFRLLVHHLCTS 1571
QY 1611 HYDLFLITGVIGLVNVTMAMEHYQQOILDEALKICNYIFTVI FVFESVFLKLVAFARFR 1670
Db 1572 HYDLFLITGVIGLVNVTMAMEHYQQOILDEALKICNYIFTVI FVLESVFLKLVAFGRFR 1631
QY 1671 FQDRWNOLDLAILVLLSIMGITLLEIEVNLSPINPTIIRIMRVLIARIVLKLKMAVGR 1730
Db 1632 FQDRWNOLDLAILVLLSIMGITLLEIEVNLSPINPTIIRIMRVLIARIVLKLKMAVGR 1691
QY 1731 ALLHTVMOALPOVGNLGLLFLMFFIPAALGVELFGDLECDETHPCBGLGRHATFRNFGM 1790
Db 1692 ALLHTVMOALPOVGNLGLLFLMFFIPAALGVELFGDLECDETHPCBGLGRHATFRNFGM 1751
QY 1791 AFLTLFRVSTGDNWNGIMKDPDRCDQESTCYNTVISPIYFVSFVLTAAQFVLNVNVI 1850
Db 1752 AFLTLFRVSTGDNWNGIMKDLRCDQESTCYNTVISPIYFVSFVLTAAQFVLNVNVI 1811
QY 1851 MKHLEENKEAKEBAELAELEEMKTLSPQPHSPLSGPFLWPGVEGVNSTDSPKPGAPH 1910
Db 1812 MKHLEENKEAKEBAELAELEEMKTLSPQPHSPLSGPFLWPGVEGVNSTDSPKPGAPH 1871
QY 1911 TTAHIGAA-SGFSLEHPTMVPHEVPVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGST 1969
Db 1872 TTAHIGAA-SGFSLEHPTMVPHEVPVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGST 1931
QY 1970 AERSLGHGWLKPAQSGSILSVHSQPADTSCILQPKDVHLLYLPQHGAPTGAIPKLPP 2029
Db 1932 AERSLGHGWLKPAQSGSILSVHSQPADTSCILQPKDVHLLYLPQHGAPTGAIPKLPP 1991
QY 2030 PGRSFLAQRPLRQAAIARTDSDLVQGLGSRDDLSEVSGPCLTRSSFWGGSSIQVQQ 2089
Db 1992 PGRSFLAQRPLRQAAIARTDSDLVQGLGSRDDLSEVSGPCLTRSSFWGGSSIQVQQ 2051
QY 2090 RSGIQSKVSHIRLPAPCPGLEPSWAKDPPETRSLSLEDTLSLWISGDLPLSSQBEPLP 2149
Db 2052 RSGIQSKVSHIRLPAPCPGLEPSWAKDPPETRSLSLEDTLSLWISGDLPLSSQBEPLP 2111
QY 2150 RDLKKCYSVETQSCRRRPFGLWDEQRHRSIAVSCLDGSGQRLCPSPSLGGQPLGGPGS 2209
Db 2112 RDLKKCYSVETQSCRRRPFGLWDEQRHRSIAVSCLDGSGQRLCPSPSLGGQPLGGPGS 2171
QY 2210 RPKKKLSPPSISIDPPSQSRPPCSPGVCLRRRAPASDSDKDVSSPLDSTAASPSPK 2269
Db 2172 RPKKKLSPPSISIDPPSQSRPPCSPGVCLRRRAPASDSDKDVSSPLDSTAASPSPK 2231
QY 2270 DTLSLSGLSSDPTDMDP 2286
Db 2232 DALSLGLSSDPTDMDP 2248

RESULT 5

CCAG HUMAN

ID CCAG HUMAN STANDARD; PRT: 2377 AA.

AC 043497; 043498; 094770; Q9NYU4; Q9NYU5; Q9NYU6; Q9NYU7; Q9NYU8;

AC Q9NYU9; Q9NYV0; Q9NYV1; Q9UHN9; Q9UHP0; Q9ULU6; Q9UNG7; Q9YST2;

AC Q9YST3;

DT 15-JUL-1999 (Rel. 38, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE voltage-dependent r-type calcium channel alpha-1G subunit (Voltage-

DE gated calcium channel alpha subunit Cav3.1) (Cav3.1c) (NBR13).

GN Name=CACNA1G; Synonyms=KIAA1123;

OS Homo sapiens (Human);

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CC NCBI_TaxID=9606;
CC (1)
CC SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING (ISOFORMS 4 AND 5).
CC TISSUE=Brain;
CC MEDLINE=20014446; PubMed=10548410; DOI=10.1016/S0304-3940(99)00716-8;
CC RA Mittman S., Guo J., Agnew W.S.;
CC "Structure and alternative splicing of the gene encoding alphaIG, a
CC human brain T calcium channel alpha subunit.";
CC Neurosci. Lett. 274:143-146(1999).
CC (2)
CC SEQUENCE FROM N.A. (ISOFORM 1).
CC TISSUE=Brain;
CC MEDLINE=20115462; PubMed=10648811; DOI=10.1016/S0014-5793(99)01756-1;
CC RA Cribbs L.L., Gomora J.C., Daud A.N., Lee J.-H., Perez-Reyes E.,
CC "Molecular cloning and functional expression of ca(v)3.1c, a T-type
CC calcium channel from human brain.";
CC FEBS Lett. 466:54-58(2000).
CC (3)
CC SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING (ISOFORMS 1-2 AND 6-13).
CC TISSUE=Brain;
CC MEDLINE=20158909; PubMed=10692398; DOI=10.1074/jbc.275.9.6090;
CC RA Montell A., Chemin J., Bourinet E., Mennessier G., Lory P.,
CC Nargeot J.;
CC "Molecular and functional properties of the human alphaIG subunit that
CC forms T-type calcium channels.";
CC J. Biol. Chem. 275:6090-6100(2000).
CC (4)
CC SEQUENCE FROM N.A. (ISOFORM 14).
CC RA Kishi F.;
CC Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
CC (5)
CC SEQUENCE OF 550-2377 FROM N.A. (ISOFORM 13).
CC TISSUE=Brain;
CC MEDLINE=22158633; PubMed=12168954;
CC RA Nakajima D., Okazaki N., Yamakawa H., Kikuno R., Ohara O., Nagase T.;
CC "Construction of expression-ready cDNA clones for KIAA genes: manual
CC curation of 330 KIAA cDNA clones.";
CC DNA Res. 9:99-106(2002).
CC (6)
CC SEQUENCE OF 750-2377 FROM N.A. (ISOFORM 13).
CC TISSUE=Brain;
CC MEDLINE=20039618; PubMed=10574461;
CC RA Hirosewa M., Nagase T., Ishikawa K.-I., Kikuno R., Nomura N.,
CC Ohara O.;
CC "Characterization of cDNA clones selected by the GeneMark analysis
CC from size-fractionated cDNA libraries from human brain.";
CC DNA Res. 6:329-336(1999).
CC (7)
CC SEQUENCE FROM N.A. (ISOFORM 3), AND GENE STRUCTURE.
CC TISSUE=Prostatic carcinoma;
CC MEDLINE=99421245; PubMed=10493502;
CC RA Toyota M., Ho C., Ohe-Toyota M., Baylin S.B., Issa J.-P.J.;
CC "Inactivation of CACNA1G, a T-type calcium channel gene, by aberrant
CC methylation of its 5' CpG island in human tumors.";
CC Cancer Res. 59:4535-4541(1999).
CC (8)
CC SEQUENCE OF 1126-1444; 1778-1927 AND 2021-2312 FROM N.A.
CC TISSUE=Brain;
CC MEDLINE=98154730; PubMed=9495342; DOI=10.1038/36110;
CC RA Perez-Reyes E., Cribbs L.L., Daud A., Lacerda A.E., Barclay J.,
CC Williamson M.P., Fox M., Rees M., Lee J.-H.;
CC "Molecular characterization of a neuronal low-voltage-activated T-type
CC calcium channel.";
CC Nature 391:896-900(1998).
CC (1)- FUNCTION: Voltage-sensitive calcium channels (VSCC) mediate the
CC entry of calcium ions into excitable cells and are also involved
CC in a variety of calcium-dependent processes, including muscle
CC contraction, hormone or neurotransmitter release, gene expression,
CC cell motility, cell division and cell death. The isoform alpha-IG
CC gives rise to T-type calcium currents. T-type calcium channels
CC belong to the "low-voltage activated (LVA)" group and are strongly
CC blocked by mibefradil. A particularity of this type of channels is

an opening at quite negative potentials and a voltage-dependent
inactivation. T-type channels serve pacemaking functions in both
central neurons and cardiac nodal cells and support calcium
signaling in secretory cells and vascular smooth muscle. They may
also be involved in the modulation of firing patterns of neurons
which is important for information processing as well as in cell
growth processes.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=14;
Comment=Additional isoforms seem to exist;
Name=5;
IsoId=O43497-1; Sequence=Displayed;
Name=1;
IsoId=O43497-2; Sequence=VSP_000940, VSP_000943, VSP_000946;
Name=2;
IsoId=O43497-3; Sequence=VSP_000940, VSP_000944, VSP_000946;
Name=3;
IsoId=O43497-4; Sequence=VSP_000940;
Name=4;
IsoId=O43497-5; Sequence=VSP_000940, VSP_000943, VSP_000946,
VSP_000948;
Name=6;
IsoId=O43497-6; Sequence=VSP_000943, VSP_000946;
Name=7;
IsoId=O43497-7; Sequence=VSP_000943, VSP_000947;
Name=8;
IsoId=O43497-8; Sequence=VSP_000940, VSP_000943, VSP_000947;
Name=9;
IsoId=O43497-9; Sequence=VSP_000940, VSP_000946;
Name=10;
IsoId=O43497-10; Sequence=VSP_000940, VSP_000945;
Name=11;
IsoId=O43497-11; Sequence=VSP_000946;
Name=12;
IsoId=O43497-12; Sequence=VSP_000947;
Name=13;
IsoId=O43497-13; Sequence=VSP_000944, VSP_000946;
Name=14;
IsoId=O43497-14; Sequence=VSP_000941, VSP_000942;
-!- TISSUE SPECIFICITY: Highly expressed in brain, in particular in
the amygdala, subthalamic nuclei, cerebellum and thalamus.
Moderate expression in heart; low expression in placenta, kidney
and lung. Also expressed in colon and bone marrow and in tumoral
cells to a lesser extent. Highly expressed in fetal brain, but
also in peripheral fetal tissues as heart, kidney and lung,
suggesting a developmentally regulated expression.
-!- DOMAIN: Each of the four internal repeats contains five
hydrophobic transmembrane segments (S1, S2, S3, S5, S6) and one
positively charged transmembrane segment (S4). S4 segments
probably represent the voltage-sensor and are characterized by a
series of positively charged amino acids at every third position.
-!- DOMAIN: The linker region between repeat III and IV probably play
a role in the inactivation of the channel. The C-terminal part may
be implicated in the anchoring of the protein to the membrane,
this by interfering/restricting its lateral diffusion.
-!- PTM: In response to raising of intracellular calcium, the T-type
channels are activated by CaM-kinase II.
-!- SIMILARITY: Belongs to the calcium channel alpha-1 subunits
family.

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or send an email to license@sib-sib.ch).

EMBL; AF134986; AAF19347.1; -
EMBL; AF134985; AAF19346.1; -
EMBL; AF227744; AAF37689.1; -
EMBL; AF227745; AAF37690.1; -

DR EMBL; AF227746; AAF37691.1; --
 DR EMBL; AF227747; AAF37692.1; --
 DR EMBL; AF227748; AAF37693.1; --
 DR EMBL; AF227749; AAF37694.1; --
 DR EMBL; AF227750; AAF37695.1; --
 DR EMBL; AF227751; AAF37696.1; --
 DR EMBL; AF124351; AAD34352.1; --
 DR EMBL; AB032949; BAA86437.2; --
 DR EMBL; AB012043; BAA36409.1; --
 DR EMBL; AF126965; AAD29400.1; --
 DR EMBL; AF126966; AAD29401.1; --
 DR EMBL; AF190860; AAF35287.1; --
 DR EMBL; AF029228; AAD12731.1; --
 DR EMBL; AF029229; AAD12732.1; --
 DR Genew; HGNC:1394; CACNA1G.; --
 DR MIM; 604065; --
 DR GO; GO:0005891; C: voltage-gated calcium channel complex; TAS.
 DR GO; GO:0008332; P: low voltage-gated calcium channel activity; TAS.
 DR GO; GO:0006810; P: transport; TAS.
 DR InterPro; IPR001682; Ca_Na_Pore.
 DR InterPro; IPR002077; Ca_channel_alpha.
 DR InterPro; IPR002111; Cat_channel_TrpL.
 DR InterPro; IPR005821; Ion_trans.
 DR InterPro; IPR005820; M-channel_nlg.
 DR InterPro; IPR005445; TVDCCAlphal.
 DR Pfam; PF00520; Ion_trans; 4.
 DR PRINTS; PR00167; CACHANNEL.
 DR PRINTS; PR01629; TVDCCAlphal.
 KW Alternative splicing; Calcium channel; Calcium-binding; Glycoprotein;
 KW Ion transport; Ionic channel; Multigene family; Phosphorylation;
 KW Repeat; Transmembrane; Voltage-gated channel.
 FT REPEAT 68 398 I.
 FT REPEAT 729 967 II.
 FT REPEAT 1263 1540 III.
 FT REPEAT 1596 1854 IV.
 FT DOMAIN 1 80 Cytoplasmic (Potential).
 FT TRANSMEM 81 101 S1 of repeat I (Potential).
 FT DOMAIN 102 119 Extracellular (Potential).
 FT TRANSMEM 120 141 S2 of repeat I (Potential).
 FT DOMAIN 142 150 Cytoplasmic (Potential).
 FT TRANSMEM 151 170 S3 of repeat I (Potential).
 FT DOMAIN 171 175 Extracellular (Potential).

Query Match 89.2%; Score 10732.5; DB 1; Length 2377;
 Best Local Similarity 88.3%; Pred. No. 0;
 Matches 2078; Conservative 33; Mismatches 109; Indels 133; Gaps 7;
 62 GAAGAGTEKDPGSAEGLPYALAPVVFYLSQDSRPSRSLRTVCNPFERUSML 121
 30 GRPGSAEKDPGSAEGLPYALAPVVFYLSQDSRPSRSLRTVCNPFERISML 89
 122 VILLNCVTLGMRPCEDIACDSQRILQAPDDPIFAFFAVEMVVMVVALGIFGKKCYLG 181
 90 VILLNCVTLGMRPCEDIACDSQRILQAPDDPIFAFFAVEMVVMVVALGIFGKKCYLG 149
 182 DTNRLDFFIVIAGLMSYSLDLQNVFSAVRTVRLPLRAINRVPNRLVTLTLLDTP 241
 150 DTNRLDFFIVIAGLMSYSLDLQNVFSAVRTVRLPLRAINRVPNRLVTLTLLDTP 209
 242 MLGNVLLCFFVFIIGLVGVLWAGLIRNRCFLPENFSLSDVLEPYQTENEDSPF 301
 210 MLGNVLLCFFVFIIGLVGVLWAGLIRNRCFLPENFSLSDVLEPYQTENEDSPF 269
 302 ICSPRENGMRSRCSVPTLRGEGGGPPCSLDYETYNSSNTTCNNQYNTNCAGEHN 361
 270 ICSPRENGMRSRCSVPTLRGEGGGPPCGLDYEAYNSSNTTCNNQYNTNCAGEHN 329
 362 PFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFNFYIFILLIIVGFFMINL 421
 330 PFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFNFYIFILLIIVGFFMINL 389
 422 CLVVIATQFSETKORESQLMREQVRFLSNASTLASPFGSCYEELLKYLVIYILRKAAR 481

Db 390 CLVVIATQFSETKORESQLMREQVRFLSNASTLASPFGSCYEELLKYLVIYILRKAAR 449
 Qy 482 RLAQVSRAGVRAGLLSSPVARSQOEPPQSGSCSTRSHRRLSVHHLVHHHHHHHHYHLCN 541
 Db 450 RLAQVSRAGVRAGLLSSPVARSQOEPPQSGSCSTRSHRRLSVHHLVHHHHHHHHYHLCN 509
 Qy 542 GTLRVPASPEIQDRDANGSRRLMLPPSTPTPGSGPRGASVHSFVHADCHLEPVRCQ 601
 Db 510 GTLRVPASPEIQDRDANGSRRLMLPPSTPTPGSGPRGASVHSFVHADCHLEPVRCQ 569
 Qy 602 APPRCPSEASGRVTGSGKVYPTVHTSPPPPIKDKALVEVAPSGPPPTLTSFNIPGPGF 661
 Db 570 APPRCPSEASGRVTGSGKVYPTVHTSPPPPIKDKALVEVAPSGPPPTLTSFNIPGPGF 629
 Qy 662 SSMHKLLETOSTGACHSCSKISSPCSKADGACGPDSCPYCARTGAGEPEADHVMPDSD 721
 Db 630 SSMHKLLETOSTGACHSCSKISSPCSKADGACGPDSCPYCARTGAGEPEADHVMPDSD 689
 Qy 722 SEAVYEFTQAOHSDLRDPSRRORSIGDPAEPPSSVLAFWRLICDTPRKIVDSKYFGRG 781
 Db 690 SEAVYEFTQAOHSDLRDPSRRORSIGDPAEPPSSVLAFWRLICDTPRKIVDSKYFGRG 748
 Qy 782 IMTAILNVTLSMGIEYHEQPEELTNALEISNIVFTSLFALEMLKLLVYGGFYIKNPYN 841
 Db 749 IMTAILNVTLSMGIEYHEQPEELTNALEISNIVFTSLFALEMLKLLVYGGFYIKNPYN 808
 Qy 842 IFDGVIVIVSWEIVGQGGGLSVLRTFRLMRVLKVRFLPALQRLVLMKTMNDNVATP 901
 Db 809 IFDGVIVIVSWEIVGQGGGLSVLRTFRLMRVLKVRFLPALQRLVLMKTMNDNVATP 868
 Qy 902 CMLLMFLIFIFSLIGMHLFGCKFASERDGTLPKKNFDSLMAIVTVFQILTQEDMNKV 961
 Db 869 CMLLMFLIFIFSLIGMHLFGCKFASERDGTLPKKNFDSLMAIVTVFQILTQEDMNKV 928
 Qy 962 LYNGMASTSSWAALYFIATMTFGNYVLFNLLVALIVEGFOAE----- 1003
 Db 929 LYNGMASTSSWAALYFIATMTFGNYVLFNLLVALIVEGFOAEISKREDASGQSLCTQLP 988
 Qy 1004 -----GDATKSESEPPDFPSVDGDRKRLALVALGAEHLKSLPLLIHTAATPM 1058
 Db 989 VDSQGGDANKSESEPPDFPSVDGDRKRLALVALGAEHLKSLPLLIHTAATPM 1048
 Qy 1059 SHPKSSSTGVGEALGSGSRRTSSGSAEPGNAHMKPCPSARSPSPHSAASWTSRR 1118
 Db 1049 SLPKSTGTGELGALGPASRETSSGSAEPGAA--HEMKSPSPASRSPSPHSAASWTSRR 1107
 Qy 1119 SSRNLSGRAPSLKRRSPSGRRRLSLGEGOSDEESSBEDRASPAGSDHRRHGSLERE 1178
 Db 1108 SSRNLSGRAPSLKRRSPSGRRRLSLGEGOSDEESSBEDRASPAGSDHRRHGSLERE 1167
 Qy 1179 AKSSFDPDLTQVPLHRTASGRSSASEHQDCNGKSASGLARTLRTDDPQDGDNDDE 1238
 Db 1168 AKSSFDPDLTQVPLHRTASGRSSASEHQDCNGKSASGLARTLRTDDPQDGDNDDE 1227
 Qy 1239 GNLSKGRERIOAWRSRLPACCRERDSVAIFPPQSRFLCHRIITHKMFHDVVLVIF 1298
 Db 1228 GNLSKGRERVRAWIRARLPACCLERDSVAIFPPQSRFLCHRIITHKMFHDVVLVIF 1287
 Qy 1299 LNCITIAWERPKDPHSAERIIFLTLSNYIFTAVFLAEMTVKVAWGCFGQAYLRSSWN 1358
 Db 1288 LNCITIAWERPKDPHSAERIIFLTLSNYIFTAVFLAEMTVKVAWGCFGQAYLRSSWN 1347
 Qy 1359 VLDGLLVLIISVIDILVSMVSDSGTKILGMLRVLRLRLTLPLRVLISRAQGLKLVETLMS 1418
 Db 1348 VLDGLLVLIISVIDILVSMVSDSGTKILGMLRVLRLRLTLPLRVLISRAQGLKLVETLMS 1407
 Qy 1419 SLKPIGNIVVICCAFFIIFGLVQLFKGKFFVQCGEDTRNITNKSQCAEASVWRHKKY 1478
 Db 1408 SLKPIGNIVVICCAFFIIFGLVQLFKGKFFVQCGEDTRNITNKSQCAEASVWRHKKY 1467
 Qy 1479 NFONLGQALMSLFLVASKGWDIMYDGLDAVGVDQOPIMNHNPMMLLYFTSLIIVAF 1538
 Db 1468 NFONLGQALMSLFLVASKGWDIMYDGLDAVGVDQOPIMNHNPMMLLYFTSLIIVAF 1527

QY	1539	VLNMFVGVVNFHKKCHQHEEERREKRLRLEKKR-----SKEQMAE	1587
Db	1528	VLNMFVGVVNFHKKCHQHEEERREKRLRLEKKRLMLDVIASGSSAASE	1587
QY	1588	AQCKPYSDYSRPFLLVHLLCTSHYLDLFTIGVGLNVVWMAEHVQOQILDEALKICN	1647
Db	1588	AQCKPYSDYSRPFLLVHLLCTSHYLDLFTIGVGLNVVWMAEHVQOQILDEALKICN	1647
QY	1648	YIFTVIFVFSVFKLVAFRRFPQDRWQDLIAVLLSIMGITLIEIEVNLSPINPTI	1707
Db	1648	YIFTVIFVFSVFKLVAFRRFPQDRWQDLIAVLLSIMGITLIEIEVNLSPINPTI	1707
QY	1708	IRIMVRLIARVLIKIVKVMRALLHVMQALPOVGNLGLLFWLFFIIFAALGVLEFGD	1767
Db	1708	IRIMVRLIARVLIKIVKVMRALLHVMQALPOVGNLGLLFWLFFIIFAALGVLEFGD	1767
QY	1768	LECETHPCBGLGHATFRNFGMAFLTLFRVSTGDNWNGIMKPSRDCDQESTCYNTVIS	1827
Db	1768	LECETHPCBGLGHATFRNFGMAFLTLFRVSTGDNWNGIMKDLTRCDQESTCYNTVIS	1827
QY	1828	PIYFVSFVLTAQFVLNVVIAVLMKHLSEESKEAEAELEEMKTLSPQHSPLG	1887
Db	1828	PIYFVSFVLTAQFVLNVVIAVLMKHLSEESKEAEAELEEMKTLSPQHSPLG	1887
QY	1888	SPFLWPGVEGVNSTDSKPKGAPHTTAHIGASGFSLEHT-----	1927
Db	1888	SPFLWPGVEGVNSTDSKPKGALHPAAHARSASHFSLEHTDRQLFDITISLLIQSLEWEL	1947
QY	1928	-----	1927
Db	1948	KLMDELACGPGQSPAPFAPSILGSGDPQIPLAEMEALSLTSEIVSEFSPCSLALTDLSLPD	2007
QY	1928	-----MVPHPEVPVPLGPDLLTVRKSGVSRTHSLNDSYMCENGSTAESL	1974
Db	2008	DMHTLLLSALESNMQPHTELP---GPDLLTVRKSGVSRTHSLNDSYMCRHGSTAGPL	2064
QY	1975	GRHGGLPKAOGSGLSVHSOPADTSCILQPKDVHYLLOPHGAPTWGAIPKLPPGCRSP	2034
Db	2065	GRHGGLPKAOGSGLSVHSOPADTSYILOPKDAPHLQLPHSAFTWTGTPKLPPGCRSP	2124
QY	2035	LAQRLRQAAIRTDLDVQGLGSRDLSLSEVSGSPCLPTRSSFWGSSSTQVQORGIQ	2094
Db	2125	LAQRLRQAAIRTDLDVQGLGSRDLSLSEVSGSPCLPCLARAYFWGSSSTQVQORSH	2184
QY	2095	SKVSGHILPAPCPGLEPSWAKDPETRSSLELDTLSWISGDL--PSSQEPLFPRLDK	2153
Db	2185	SKISKHMTTPAPCPGPEPNWKGPPETRSSLELDTLSWISGDLPLPGGQEEPPSRDLK	2244
QY	2154	KCYSVETOSCRRRPGFMDQORRHIAVSCLDGSGQPRLCPSGLGQPLGGPSRPPK	2213
Db	2245	KCYSVETOSCRRRPFTSWLDEQRHIAVSCLDGSGQPHGLTDPNLSGQPLGGPSRPPK	2304
QY	2214	KLSPFSISIDPPESQGRPPSPGVCLRRRAPASDKPSVSSPLDSTAAPSPPKOTLS	2273
Db	2305	KLSPFSITIDPPESQGRTPSPGICLRRRAPSDSKDPLASGPPDSMAAPSPPKOVLS	2364
QY	2274	LSGLSSDPTMDP	2286
Db	2365	LSGLSSDPAIDLDP	2377
RESULT 6			
Q62PX4	Q62PX4	PRELIMINARY;	PRT; 1389 AA.
AC	Q62PX4;		
DT	05-JUL-2004	(TrEMBLrel. 27, Created)	
DT	05-JUL-2004	(TrEMBLrel. 27, Last sequence update)	
DT	05-JUL-2004	(TrEMBLrel. 27, Last annotation update)	
DE	MKIAA1123	protein (Fragment).	
CN	Name=MKIAA1123;		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		

OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Brain;		
RX	PubMed=14621295;		
RA	Okazaki N., Kikuno R., Ohara R., Inamoto S., Koseki H., Hiraoka S.,		
RA	Saga Y., Nagase T., Ohara O., Koga H.;		
RT	"Prediction of the coding sequences of mouse homologues of KIAA gene:		
RT	III. the complete nucleotide sequences of 500 mouse KIAA-homologous		
RT	cDNAs identified by screening of terminal sequences of cDNA clones		
RT	randomly sampled from size-fractionated libraries.";		
RL	DNA Res. 10:167-180(2003).		
CC	-!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).		
CC	-!- SIMILARITY: Belongs to the calcium channel alpha-1 subunits		
CC	family.		
DR	EMBL; AK129294; BAC98104.1; -.		
DR	GO; GO:0016021; C:integral to membrane; TAS.		
DR	GO; GO:0005886; C:plasma membrane; IDA.		
DR	GO; GO:0005245; F:voltage-gated calcium channel activity; IDA.		
DR	InterPro; IPR001682; Ca/Na_pore.		
DR	InterPro; IPR002111; Cat_channel_TpL.		
DR	InterPro; IPR002077; Ca_channel_alpha.		
DR	InterPro; IPR005821; Ion_trans.		
DR	InterPro; IPR005820; M+channel_nlg.		
DR	Pfam; PF00520; Ion_trans; 3.		
DR	PRINTS; PR00167; CACHANNEL.		
KW	Calcium; Calcium channel; Calcium transport; Calcium-binding;		
KW	Ion transport; Ionic channel; Transmembrane; Transport;		
KW	Voltage-gated channel.		
FT	NON_TER 1		
SQ	SEQUENCE 1389 AA; 153067 MW; DA31535CA3C03B10 CRC64;		
Query Match 56.6%; Score 6809.5; DB 2; Length 1389;			
Best Local Similarity 94.8%; Pred. No. 0;			
Matches 1317; Conservative 8; Mismatches 29; Indels 35; Gaps 3;			
QY	933	LPDRKNFDSLLWAIVTVFOILTOEDWNKVLNGMASTSSWAALYFIALMTFGNYVFNLL	992
Db	1	LPDRKNFDSLLWAIVTVFOILTOEDWNKVLNGMASTSSWAALYFIALMTFGNYVFNLL	60
QY	993	VAILVEGFOAE-----GDATKSESPDFPSVDGDGDRKKR	1029
Db	61	VAILVEGFOAEIGTKREDTSGQLSCQLPVNSQGGDATKSESPDFPSVDGDGDRKKR	120
QY	1030	LALVALGEHAELRKSLLPPLIHTAATPMGHPKSSSTGVCEALGSGSRRTSSGSAEPGA	1089
Db	121	LALVALGEHSELRLKSLLPPLIHTAATPMGLPKSSSTGVGEALGSGSRRTSSGSAEPGT	180
QY	1090	AHEMKCPPSARSPSPSFWSAASWTSRRSRNSLGRAPSLKRRSPGERRSLLSGEGOE	1149
Db	181	AHEMKGPPSARSPSPSFWSAASWTSRRSRNSLGRAPSLKRRSPGERRSLLSGEGOE	240
QY	1150	SQDEEESSEDRASPAGSDHRRHGSLEAREAKSSFDLPTTLQVPLHRTASGRSSASHOD	1209
Db	241	SQDEEESSEDRASPAGSDHRRHGSLEAREAKSSFDLPTTLQVPLHRTASGRSSASHOD	300
QY	1210	CNGKSASGRLARTLRDTPQLDGDNDNDEGNLSKGERIQAWRSRLPACCRERDSWAYI	1269
Db	301	CNGKSASGRLARTLRADDPPLDGDGDDEGNLSKGERLRAWVRARLPACCRERDSWAYI	360
QY	1270	FPQSRFLLCHRIITHKMFHDVVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFT	1329
Db	361	FPQSRFLLCHRIITHKMFHDVVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFT	420
QY	1330	AVFLAEMTVKVALGCMFCGQAYLRSRNSVNLGDLVLSVIDILVMSVSGTKILGMLR	1389
Db	421	AVFLAEMTVKVALGCMFCGQAYLRSRNSVNLGDLVLSVIDILVMSVSGTKILGMLR	480
QY	1390	VLRLRLRLPLRVISRAQGLKLVETLMSLSKPIGNIWTICCAFFIIFGLGVLPKGF	1449
Db	481	VLRLRLRLPLRVISRAQGLKLVETLMSLSKPIGNIWTICCAFFIIFGLGVLPKGF	540

QY 1450 FVCGEDTRNTKNSDCAEASRYRWYHXYKYNEDNIGALMSLFLVILASKDGDWIDIMYDGLDA 1509
Db 541 FVCGEDTRNTKNSDCAEASRYRWYHXYKYNEDNIGALMSLFLVILASKDGDWIDIMYDGLDA 600
QY 1510 VGVDQOIPMNPNWMLLYFISFLIATVAFVFLNMFGVVVENFHKCRQHQEHEEARRREK 1569
Db 601 VGVDQOIPMNPNWMLLYFISFLIATVAFVFLNMFGVVVENFHKCRQHQEHEEARRREK 660
QY 1570 RLRLKLEKRR-----SKQMAEACKPKYYSYSPRLLVHLCTSHYLDLPIT 1618
Db 661 RLRLKLEKRRNMLDDVITASGSSAASEAQCKPYYSYSPRLLVHLCTSHYLDLPIT 720
QY 1619 GVIGLVVTVMAHGVQOQIILDEALKICNYIIFTVIFVESVFKLVAFAPRFFQDRNQL 1678
Db 721 GVIGLVVTVMAHGVQOQIILDEALKICNYIIFTVIFVESVFKLVAFAPRFFQDRNQL 780
QY 1679 DLAVLLSIMGITLLEIEEIVNLSLPINPTIIRIMRVLRARVLRKLLKMAVGNRALLHTVMQ 1738
Db 781 DLAVLLSIMGITLLEIEEIVNLSLPINPTIIRIMRVLRARVLRKLLKMAVGNRALLHTVMQ 840
QY 1739 ALPOVGNLGLLFFMLFFIIPALGVVELFGDLBCDETHPCGEGIGRATFRNFGMAFLTFRV 1798
Db 841 ALPOVGNLGLLFFMLFFIIPALGVVELFGDLBCDETHPCGEGIGRATFRNFGMAFLTFRV 900
QY 1799 STGDNWNGIMKDPKSDCDQESTCYNVTLSPIYFVSFVLTAQFVLVNVVIAVLKMLHEEN 1858
Db 901 STGDNWNGIMKDPKSDCDQESTCYNVTLSPIYFVSFVLTAQFVLVNVVIAVLKMLHEEN 960
QY 1859 KEAKEEAELEAELEEMKTLSPQPHSPGLSGPFLPGVEGVNSTDPKPGAPHTTAHIGAA 1918
Db 961 KEAKEEAELEAELEEMKTLSPQPHSPGLSGPFLPGVEGVNSTDPKPGAPHTTAHIGAA 1020
QY 1919 -SGFSLEHTVWPHEEVVPLGPDLLTVRKSGVSRTHSLPNDSTYMCNMGSTABSLGHR 1977
Db 1021 SSGFSLEHTVWPHEEVVPLGPDLLTVRKSGVSRTHSLPNDSTYMCNMGSTABSLGHR 1080
QY 1978 GWGLPKAQSGILSVHSPADTSCITQIPKDVHVLLOPHGAPTWGATPKLPGRSPPLAQ 2037
Db 1081 GWGLPKAQSGILSVHSPADTSCITQIPKDVHVLLOPHGAPTWGATPKLPGRSPPLAQ 1140
QY 2038 RPLRQAARTDSDVQGLSGREDLLSVSGPSCPLTRSSFWGSSSIQVQORSGIOSKV 2097
Db 1141 RPLRQAARTDSDVQGLSGREDLLSVSGPSCPLTRSSFWGSSSIQVQORSGIOSKV 1200
QY 2098 SKHRLPAPCGLPSPWAKDPETRRSSLELDELTELISGDLPLSPQSEPLPRDLKKCY 2157
Db 1201 SKHRLPAPCGLPSPWAKDPETRRSSLELDELTELISGDLPLSPQSEPLPRDLKKCY 1260
QY 2158 VETOSCRPPGFMDQRRHSIAVCLDSGSPRLCPSPSLGGQPLGGGRSPKKLSP 2217
Db 1261 VEAQSCRRPPGSLDQRRHSIAVCLDSGSPRLCPSPSLGGQPLGGGRSPKKLSP 1320
QY 2218 PSISIDPPESOGSRPPCPGVLRRRASPDKPSVSSPLDSTAASPSPKKDLTSLSG 2277
Db 1321 PSISIDPPESOGSRPPCPGVLRRRASPDKPSVSSPLDSTAASPSPKKDLTSLSG 1380
QY 2278 SSDPTMDP 2286
Db 1381 SSDPTMDP 1389
RESULT 7
CCAH RAT
ID CCAH RAT STANDARD; PRT; 2359 AA.
AC Q9BQ60;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Voltage-dependent T-type calcium channel alpha-1H subunit (Voltage-gated calcium channel alpha subunit Cav3.2).
GN Name=Cacnalh;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
(1)
SEQUENCE FROM N.A.
RP TISSUE=Brain;
RX PubMed=11073957; DOI=10.1074/jbc.M008215200;
RA McRory J.E., Santi C.M., Hamming K.S.C., Mezeyova J., Sutton K.G., Baillie D.L., Stea A., Snutch T.P.;
RT "Molecular and functional characterization of a family of rat brain T-type calcium channels";
RL J. Biol. Chem. 276:3999-4011(2001).
CC -!- FUNCTION: Voltage-sensitive calcium channels (VSCC) mediate the entry of calcium ions into excitable cells and are also involved in a variety of calcium-dependent processes, including muscle contraction, hormone or neurotransmitter release, gene expression, cell motility, cell division and cell death. The isoform alpha-1H gives rise to T-type calcium currents. T-type calcium channels belong to the "low-voltage activated (LVA)" group and are strongly blocked by nickel and mibefradil. A particularity of this type of channels is an opening at quite negative potentials, and a voltage-dependent inactivation. T-type channels serve pacemaking functions in both central neurons and cardiac nodal cells and support calcium signaling in secretory cells and vascular smooth muscle. They may also be involved in the modulation of firing patterns of neurons which is important for information processing as well as in cell growth processes.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Expressed in brain.
CC -!- DOMAIN: Each of the four internal repeats contains five hydrophobic transmembrane segments (S1, S2, S3, S5, S6) and one positively charged transmembrane segment (S4). S4 segments probably represent the voltage-sensor and are characterized by a series of positively charged amino acids at every third position.
CC -!- PTM: In response to raising of intracellular calcium, the T-type channels are activated by CaM-kinase II.
CC -!- SIMILARITY: Belongs to the calcium channel alpha-1 subunits family.

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EMBL; AF290213; AACG35187.1; -;
RGD; 68943; Cacnalh.
DR InterPro; IPR001682; Ca/Na_pore.
DR InterPro; IPR002111; Cat_channel_TrpL.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR005820; M-channel_nlg.
DR Pfam; PF00520; Ion_trans_4.
DR PRINTS; PR01629; TVDCCALPHAL.
KW Calcium channel; Glycoprotein; Ion transport; Ionic channel;
KW Multigene family; Phosphorylation; Repeat; Transmembrane;
KW Voltage-gated channel.
FT REPEAT 87 422 I.
FT REPEAT 776 1015 II.
FT REPEAT 1292 1569 III.
FT REPEAT 1607 1868 IV.
FT DOMAIN 1 100 Cytoplasmic (Potential).
FT DOMAIN 101 119 S1 of repeat I (Potential).
FT DOMAIN 120 139 Extracellular (Potential).
FT DOMAIN 140 160 S2 of repeat I (Potential).
FT DOMAIN 161 169 Cytoplasmic (Potential).
FT TRANSMEM 170 184 S3 of repeat I (Potential).
FT TRANSMEM 185 193 Extracellular (Potential).
FT TRANSMEM 194 212 S4 of repeat I (Potential).
FT TRANSMEM 213 232 Cytoplasmic (Potential).
FT TRANSMEM 233 253 S5 of repeat I (Potential).
FT TRANSMEM 254 394 Extracellular (Potential).

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FT	TRANSMEM	395	419	S6 of repeat I (Potential).
FT	DOMAIN	420	790	Cytoplasmic (Potential).
FT	TRANSMEM	791	811	S1 of repeat II (Potential).
FT	DOMAIN	812	824	Extracellular (Potential).
FT	TRANSMEM	825	846	S2 of repeat II (Potential).
FT	DOMAIN	847	852	Cytoplasmic (Potential).
FT	TRANSMEM	853	871	S3 of repeat II (Potential).
FT	DOMAIN	872	879	Extracellular (Potential).
FT	TRANSMEM	880	903	S4 of repeat II (Potential).
FT	DOMAIN	904	914	Cytoplasmic (Potential).
FT	TRANSMEM	915	935	S5 of repeat II (Potential).
FT	DOMAIN	936	987	Extracellular (Potential).
FT	TRANSMEM	988	1012	S6 of repeat II (Potential).
FT	DOMAIN	1013	1301	Cytoplasmic (Potential).
FT	TRANSMEM	1302	1324	S1 of repeat III (Potential).
FT	DOMAIN	1325	1342	Extracellular (Potential).
FT	TRANSMEM	1343	1363	S2 of repeat III (Potential).
FT	DOMAIN	1364	1373	Cytoplasmic (Potential).
FT	TRANSMEM	1374	1393	S3 of repeat III (Potential).
FT	DOMAIN	1394	1407	Extracellular (Potential).
FT	TRANSMEM	1408	1429	S4 of repeat III (Potential).
FT	DOMAIN	1430	1439	Cytoplasmic (Potential).
FT	TRANSMEM	1440	1463	S5 of repeat III (Potential).
FT	DOMAIN	1464	1540	Extracellular (Potential).
FT	TRANSMEM	1541	1566	S6 of repeat III (Potential).
FT	DOMAIN	1567	1621	Cytoplasmic (Potential).
FT	TRANSMEM	1622	1642	S1 of repeat IV (Potential).
FT	DOMAIN	1643	1656	Extracellular (Potential).
FT	TRANSMEM	1657	1678	S2 of repeat IV (Potential).
FT	DOMAIN	1679	1685	Cytoplasmic (Potential).
FT	TRANSMEM	1686	1704	S3 of repeat IV (Potential).
FT	DOMAIN	1705	1718	Extracellular (Potential).
FT	TRANSMEM	1719	1742	S4 of repeat IV (Potential).
FT	DOMAIN	1743	1756	Cytoplasmic (Potential).
FT	TRANSMEM	1757	1777	S5 of repeat IV (Potential).
FT	DOMAIN	1778	1840	Extracellular (Potential).
FT	TRANSMEM	1841	1868	S6 of repeat IV (Potential).
FT	DOMAIN	1869	2359	Cytoplasmic (Potential).
FT	DOMAIN	521	531	Poly-His.
FT	DOMAIN	1594	1597	Calcium ion selectivity and permeability
FT	SITE	378	378	(By similarity).
FT	SITE	971	971	Calcium ion selectivity and permeability
FT	SITE	1515	1515	(By similarity).
FT	SITE	1813	1813	Calcium ion selectivity and permeability
FT	SITE	192	192	(By similarity).
FT	CARBOHYD	192	192	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	271	271	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	1477	1477	N-linked (GlcNAc. . .) (Potential).
FT	SEQUENCE	2359	2359	AA; 261138 MW; F738083E94180081 CRC64;
Qy	Query Match	51.8%;	Score 6226; DB 1; Length 2359;	
Qy	Best Local Similarity	56.3%;	Pred. No. 3.5e-296;	
Qy	Matches 1356;	Conservative 248;	Mismatches 518; Indels 286; Gaps 58;	
Db	30	LARGWTRRRMERAPRGRDSPV-ASRSSTTCGP-PCGAAGAG-STEKDPGS---AD---S	78	
Db	6	LAADVVPVPGASPPAPAAVPRASPGAPGREGGSGSVLAPESPTECGADLGAD	65	
Qy	79	EAEGLPYPALAPVFFVYLSQDSRPNCLRTVCNPFVRSVMLVILNCVTLGMFRPCED	138	
Db	66	EEQVPVPPALAAVFFCLGQTRPRSWCLRLVCNPFVRSVMLVILNCVTLGMFRPCED	125	
Qy	139	IACDSQRCILQAFDDPIFAFAVEMVVKVALGIFGKCYLGDWNRLLDFFVIVAGMLE	198	
Db	126	VECRSERCSTLEAFDDPIFAFAVEMVVKVALGIFGKCYLGDWNRLLDFFVIVAGMME	185	
Qy	199	YSLDLQNVFSAVTRVRLRPLRAINRVPSMRILVTLTLLDTPMLGNVLLLCFFVFFIFG	258	
Db	186	YSLDGHVSLSAITRVRLRPLRAINRVPSMRILVTLTLLDTPMLGNVLLLCFFVFFIFG	245	

Qy	259	IVGVQLWAGLLRNRCFLPENFSLPSVD--LEPYVQTEENEDSPFCQPRENGMRSCSV 317	
Db	246	IVGVQLWAGLLRNRCFLDSAFVRNNLTFLRPYQTEEGEENPFICSRDRNGKQKSHI 305	
Qy	318	PT---LRGEGGGPPCSLDIETY-----NSSNTTCVNWNOYVYTCNAGEHNPFGKAI 367	
Db	306	PSRRELRVQ-----CTLGWEAYGQOABDGGAGRNACINWQYVYVCRSGEFNPHNGAI 359	
Qy	368	NFDNIGYAWIALFOVITLLEGWVDIMYFVMDAHSFYNYFIYFILLIIVGSPFMINICLVVIA 427	
Db	360	NFDNIGYAWIALFOVITLLEGWVDIMYFVMDAHSFYNYFIYFILLIIVGSPFMINICLVVIA 419	
Qy	428	TOFSETKQRESQMLRQEVRFSLNASLTASFSEFGSCYEELLYLVILRKAAERLAQVS 487	
Db	420	TOFSETKQRENQMLRQEVRFSLNASLTASFSEFGSCYEELLYLVILRKAAERLAQVS 479	
Qy	488	RAIGVRAGLLSPVAR-----SGQEPQSGSCSTRSHRLSVHILV-HHHHHHHHHYHLGN 541	
Db	480	ARWQSRWRKVDPSSTVHGQGGPRPRAG-----RTASVHILVYHHHHHHHHYHFSH 534	
Qy	542	GTLRVPRASPEIQDRDANGSRRLM--LPPPTPTSPGPPRGASVHSFYHADCHLEPVR 599	
Db	535	GGPR--RSPE-----PGAGDNLRVACAPPSPSPGHGPP-DSESVHSIYHADCHVEGPQ 587	
Qy	600	COAPPPRCPEASGRTVSGS---KYPTV-----HTSPPEILKDKALVEVAVSP 646	
Db	588	ERARVAHSIATAASLKLASGLTGMNYTILPSGTVNSKGTSSRPKGLRG-----AGAP 641	
Qy	647	GPPTLTSTFNI--PPGPFSSMHKLLETQSTGACHSSCK-ISSPC-----SKADSGACPDSCP 700	
Db	642	GAHVHSLSLGSPRYEKIQDVVGQGLGRASSHLSGLSVPCPLSPQAGTLTCLKSCP 701	
Qy	701	YCATGAGGP--ESADHVMPPDSSEAVYFTQDAQHSDLRDP-----HRRRRR 747	
Db	702	YCA-SALEPPEFEFGSGESGSDAHGVYFTQDVHRGDCRDPQVQHPHVGTECHNERR 760	
Qy	748	S-LGPDAAESSVLAFWRLICDTFRKIVDSKYFGRGIMAILVNTLSMGIEVHEQPEELTN 806	
Db	761	TPLRKASQGGGIGHLWASFSGKLRIVDKYFNRMGIMAILVNTLSMGIEVHEQPEELTN 820	
Qy	807	ALBISNIVTSLFALMLKLIVYGFYIKNPYINFDGIVIVISVWEIVGQGGGLSVL 866	
Db	821	ALBISNIVTSMFALMLKLACGLGYIRNPYINFDGIVIVISVWEIVGQGGGLSVL 880	
Qy	867	RTFLMRVLKIVFLPALORQLVLMKTDNVATFCMLLMFLFIFISILGMLFGCKFAS 926	
Db	881	RTFLRLVRLKIVFLPALRRQLVLMRTDNVATFCMLLMFLFIFISILGMLFGCKFSL 940	
Qy	927	ERD-GDTLPDRKNFDSLLMAIVTVFQILTQEDWNKVLVYNGMASTSSWAALFYFALMTFGN 985	
Db	941	KTDSGDTVDRKNFDSLLMAIVTVFQILTQEDWNKVLVYNGMASTSSWAALFYFALMTFGN 1000	
Qy	986	YVLNLLVAILVGFQAGDATKSESEPDFFSPVDGDKRKL-----ALVALG 1036	
Db	1001	YVLNLLVAILVGFQAGDATKSDTDEDTKSTQLEGDFDKLRDLRATENKMYSLAVTPN 1060	
Qy	1037	EHAELRSLPLLIHTAATPMSPKSS-STGVGEALGSGSRRTSSGSAEPGAAHEMK 1095	
Db	1061	GHLEGRSLPLLIHTAATPMTPKSSPNLDVAHAL-LDSRR-SSSGSDVPQLG--DQK 1116	
Qy	1096	CPPSARSPPHPSAAASWTSSRNSLGRAPSLKRSFSGRRSLTSGEGESQDEE- 1154	
Db	1117	SLASLRSPCTPMGPNAGSSRRSNLSGRAPSLKRNOCGERESLUSGEGKSTDEA 1176	
Qy	1155	ESSREDRASPGSDHRRHRSLEAKSFDLPDTLVQVGLHRTASGRSSA---SEHQDCN 1211	
Db	1177	EDSRPTGTHPGASGPPRATFLRRAB-SLDRSTLDL-----CPPRPAALLPTKPHDCN 1229	
Qy	1212	GKASGRILARTLRTDDPQLDGGDDNDENGLSKGBRIQAWVRSLPACCRDSDSAIETP 1271	
Db	1230	GMVALPSEFFLRIIDSHKEDAAEFDDIEDSCCFRLHKVLEPYAPQWCRSRESWALYFP 1289	
Qy	1272	QOSRRLCHRIITHKMFHDVVLVIFLNCITIAERPKIDPHSAERIFLITLSNYIFTAV 1331	

gives rise to T-type calcium currents. T-type calcium channels belong to the "low-voltage activated (LVA)" group and are strongly blocked by nickel and mibefradil. A particularity of this type of channels is an opening at quite negative potentials, and a voltage-dependent inactivation. T-type channels serve pacemaking functions in both central neurons and cardiac nodal cells and support calcium signaling in secretory cells and vascular smooth muscle. They may also be involved in the modulation of firing patterns of neurons which is important for information processing as well as in cell growth processes.

!- SUBCELLULAR LOCATION: Integral membrane protein.

!- ALTERNATIVE PRODUCTS:

Event=Alternative splicing; Named isoforms=2;

Isoid=095180-1; Sequence=Displayed;

Name=2; Synonyms=ALH-b;

Isoid=095180-2; Sequence=VSP 000949;

TISSUE SPECIFICITY: Expressed in kidney, liver, heart, brain.

Isoform 2 seems to be testis-specific.

!- DOMAIN: Each of the four internal repeats contains five positively charged transmembrane segments (S1, S2, S3, S5, S6) and one hydrophobic transmembrane segment (S4). S4 segments possibly represent the voltage-sensor and are characterized by a series of positively charged amino acids at every third position.

!- PTM: In response to raising of intracellular calcium, the T-type channels are activated by CaM-kinase II.

!- SIMILARITY: Belongs to the calcium channel alpha-1 subunits family.

!- CAUTION: AT-AC pre mRNA splicing gives rise to the isoform 1 shown in this entry. The additional 20 amino acids found in the Ref.4 and Ref.6 sequences are due to a misunderstanding of the real type of splicing mechanism involved.

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EMBL; AF051946; AAC67239.3; -

EMBL; AF073931; AAD17668.1; -

EMBL; AE006466; AAK61268.1; ALT_SEQ.

EMBL; AF420779; CAD12646.1; -

EMBL; AF031703; CAC42094.1; ALT_SEQ.

EMBL; AF223562; AAF60162.1; -

EMBL; AF223563; AAF60163.1; -

Genew; HGNC:1395; CACNA1H.

MIM; 607904; -

GO; GO:0005891; C: voltage-gated calcium channel complex; TAS.

GO; GO:0008332; F: low voltage-gated calcium channel activity; TAS.

GO; GO:0006936; P: muscle contraction; TAS.

GO; GO:0007520; P: myoblast fusion; TAS.

GO; GO:0008016; P: regulation of heart rate; TAS.

GO; GO:0006810; P: transport; TAS.

InterPro; IPR001682; Ca/Na pore.

InterPro; IPR002111; Cat channel_TrpL.

InterPro; IPR005821; Ion_trans_nlg.

InterPro; IPR005820; Mr-channel_nlg.

InterPro; IPR005445; TVDCCALPHal.

Pfam; PF00520; Ion_trans; 4.

PRINTS; PR01629; TVDCCALPHal.

Alternative splicing; Calcium channel; Calcium-binding; Glycoprotein; Ion transport; Tonic channel; Multigene family; Phosphorylation; Repeat; Transmembrane; Voltage-gated channel.

REPEAT 87 422

REPEAT 79 1018

REPEAT 1281 1558

REPEAT 1602 1863

DOMAIN 1 100

DOMAIN 101 119

DOMAIN 120 139

Extracellular (Potential).

Cytoplasmic (Potential).

S1 of repeat I (Potential).

S2 of repeat I (Potential).

S3 of repeat I (Potential).

S4 of repeat I (Potential).

S5 of repeat I (Potential).

S6 of repeat I (Potential).

S1 of repeat II (Potential).

S2 of repeat II (Potential).

S3 of repeat II (Potential).

S4 of repeat II (Potential).

S5 of repeat II (Potential).

S6 of repeat II (Potential).

S1 of repeat III (Potential).

S2 of repeat III (Potential).

S3 of repeat III (Potential).

S4 of repeat III (Potential).

S5 of repeat III (Potential).

S6 of repeat III (Potential).

S1 of repeat IV (Potential).

S2 of repeat IV (Potential).

S3 of repeat IV (Potential).

S4 of repeat IV (Potential).

S5 of repeat IV (Potential).

S6 of repeat IV (Potential).

Cytoplasmic (Potential).

Poly-His.

Poly-Ser.

Poly-Arg.

Calcium ion selectivity and permeability (By similarity).

Calcium ion selectivity and permeability (By similarity).

Calcium ion selectivity and permeability (By similarity).

Calcium ion selectivity and permeability (By similarity).

Calcium ion selectivity and permeability (By similarity).

N-linked (GlcNAc...) (Potential).

N-linked (GlcNAc...) (Potential).

Score 6222; DB 1; Length 2353;

Best Local Similarity 56.7%; Pred. No. 5.5e-236;

Mismatches 208; Conservative 208; Gaps 62;

Matches 1370;

FT	TRANSMEM	140	160	S2 of repeat I (Potential).
FT	DOMAIN	161	169	Cytoplasmic (Potential).
FT	TRANSMEM	170	184	S3 of repeat I (Potential).
FT	DOMAIN	185	193	Extracellular (Potential).
FT	TRANSMEM	194	212	S4 of repeat I (Potential).
FT	DOMAIN	213	232	Cytoplasmic (Potential).
FT	TRANSMEM	233	254	S5 of repeat I (Potential).
FT	DOMAIN	254	294	Extracellular (Potential).
FT	TRANSMEM	295	419	S6 of repeat I (Potential).
FT	DOMAIN	420	793	Cytoplasmic (Potential).
FT	TRANSMEM	794	814	S1 of repeat II (Potential).
FT	DOMAIN	815	827	Extracellular (Potential).
FT	TRANSMEM	828	849	S2 of repeat II (Potential).
FT	DOMAIN	850	855	Cytoplasmic (Potential).
FT	TRANSMEM	856	874	S3 of repeat II (Potential).
FT	DOMAIN	875	882	Extracellular (Potential).
FT	TRANSMEM	883	906	S4 of repeat II (Potential).
FT	DOMAIN	907	917	Cytoplasmic (Potential).
FT	TRANSMEM	918	938	S5 of repeat II (Potential).
FT	DOMAIN	939	990	Extracellular (Potential).
FT	TRANSMEM	991	1015	S6 of repeat II (Potential).
FT	DOMAIN	1016	1290	Cytoplasmic (Potential).
FT	TRANSMEM	1291	1313	S1 of repeat III (Potential).
FT	DOMAIN	1314	1331	Extracellular (Potential).
FT	TRANSMEM	1332	1352	S2 of repeat III (Potential).
FT	DOMAIN	1353	1362	Cytoplasmic (Potential).
FT	TRANSMEM	1363	1382	S3 of repeat III (Potential).
FT	DOMAIN	1383	1396	Extracellular (Potential).
FT	TRANSMEM	1397	1418	S4 of repeat III (Potential).
FT	DOMAIN	1419	1428	Cytoplasmic (Potential).
FT	TRANSMEM	1429	1452	S5 of repeat III (Potential).
FT	DOMAIN	1453	1529	Extracellular (Potential).
FT	TRANSMEM	1530	1555	S6 of repeat III (Potential).
FT	DOMAIN	1556	1616	Cytoplasmic (Potential).
FT	TRANSMEM	1617	1637	S1 of repeat IV (Potential).
FT	DOMAIN	1638	1651	Extracellular (Potential).
FT	TRANSMEM	1652	1673	S2 of repeat IV (Potential).
FT	DOMAIN	1674	1680	Cytoplasmic (Potential).
FT	TRANSMEM	1681	1699	S3 of repeat IV (Potential).
FT	DOMAIN	1700	1713	Extracellular (Potential).
FT	TRANSMEM	1714	1737	S4 of repeat IV (Potential).
FT	DOMAIN	1738	1751	Cytoplasmic (Potential).
FT	TRANSMEM	1752	1772	S5 of repeat IV (Potential).
FT	DOMAIN	1773	1835	Extracellular (Potential).
FT	TRANSMEM	1836	1863	S6 of repeat IV (Potential).
FT	DOMAIN	1864	2353	Cytoplasmic (Potential).
FT	TRANSMEM	520	530	Poly-His.
FT	DOMAIN	1107	1110	Poly-Ser.
FT	TRANSMEM	1583	1586	Poly-Arg.
FT	DOMAIN	378	378	Calcium ion selectivity and permeability (By similarity).
FT	SITE	974	974	Calcium ion selectivity and permeability (By similarity).
FT	SITE	1504	1504	Calcium ion selectivity and permeability (By similarity).
FT	SITE	1808	1808	Calcium ion selectivity and permeability (By similarity).
FT	CARBOHYD	192	192	N-linked (GlcNAc...) (Potential).
FT	CARBOHYD	271	271	N-linked (GlcNAc...) (Potential).

Query Match 51.7%; Score 6222; DB 1; Length 2353;

Best Local Similarity 56.7%; Pred. No. 5.5e-236;

Mismatches 208; Conservative 208; Gaps 62;

Matches 1370;

QY 25 PPGRLAGWTTRRRERAPSRDSP--VASRSSTTCFPGGAAGSTGKDFPGGADSAEG 82

DB 19 PPGPALVG-----ASPSPGAPGREAERGSSELGVSPSPSPAAERGAELGA--DEQR 69

QY 83 LPYPALAPVFFYLSQDSRPRSWCLRTVCNPFWRVSMVLINCVTLGMFRPCEDACD 142

DB 70 VDPALAAATVFFCLGQTTTRPSWCLRLVCNPFWRVSMVLINCVTLGMFRPCEDVECG 129

QY 143 SQRCILQAFDDFIAPFAFVAVMVKMVALGIFGKKCYLGDITWNLDFPFIIVAGMLEYSLD 202

Db 130 SERCNLEAFDAFAFAFAVEMVKNVAGLFGQKCYLGDTWNRLDFFIVVAGMEYSLD 189
Qy 203 LONVSFAVTRVRLRPLRAINRVPMSRMLVTLTLLDTPMLGNVLLLCFFVFFIFGIVG 262
Db 190 GHNSLSAIRVTRVRLRPLRAINRVPMSRMLVTLTLLDTPMLGNVLLLCFFVFFIFGIVG 249
Qy 263 QLMAGLNRNCFLENFSLPLSDV-LEPYOTENEDESPPICSOPIRENGMRSRCSVPLR 321
Db 250 QLMAGLNRNCFLOSFAFVRNNLTLRPRYYOTEEGENPFCSSRRDGMQKCSHP- 306
Qy 322 GEGGGPPCSDLDYTN-----SSNTTCVNNQYITNCSAGBNPFKGAINFDNIGY 374
Db 307 GRRELBMCTLGWEAYTOQAEVGAARNAACINNNQYINVCSDGSPHNGAINFNDIGY 366
Qy 375 AWIAIFQVITLEGWVDIMFYMDAHSFYNYFILLIIVGFFMINCLVVIATQFSSTK 434
Db 367 AWIAIFQVITLEGWVDIMFYMDAHSFYNYFILLIIVGFFMINCLVVIATQFSSTK 426
Qy 435 QRESQMBEORVFLSNASTLASSEPGSCYEELIKYLVYLKRAARELAQVRAIGVRA 494
Db 427 QRESQMBEORVFLSNASTLASSEPGSCYEELIKYVGHIFRKYKRSLRYARWQSRW 486
Qy 495 GLLSPVARSGOEPOPSGCTSRHR-----LSVHLV-HHHHHHHVHLGNTLRV 546
Db 487 RKKVDPSAVOQGP-----GHRORAGHTASVHLVTHHHHHHHVHFGSGSPR 538
Qy 547 PRASPEIQDRDANGSRRLML-PPPTPTPGGPPRGAESVHSFYHADCHLE--PVRCQA 602
Db 539 PGPEPGACD-----TRLVRAGAPSPSPGPGPP-DAESVHSIYHADCHIEGQERARV 591
Qy 603 PPPPCSEASGR-TVGSKV-YPTV-----HTSPPEILKDKALVEVASP-----646
Db 592 AHAAATAAASURLATGLTMYNPTILPSGVSGSGSTSPGPK-----GKWAQGPOTG 644
Qy 647 --GPPTLTSFNIPOPPSSMHKLETOSTGAC--HSS-----CKISSPCSKADGACGPD 697
Db 645 GHGFLSLS-----PDYEKI PHVGEHGLQAPCHLSGLSVPCPLPSP--PAGTLTCLK 698
Qy 698 SCPCYART-GAGEPESADHVPDSDSEAVYFTQDAQHSIDLDP-----740
Db 699 SCPCYTRALEDPEGELSGESGSDSGRGVYFTQDVRGDRWDPRPPRATDTPGPGGS 758
Qy 741 HSRRRORSLGDPASPSSVLAFWRLLICDTRKIVDSKYFGRGIMAILVNTLSMGIEVHEQ 800
Db 759 PORAQORAAP-GEFGMGRMLWVTFSGKRLRIVDSKYFSRGIMAILVNTLSMGIEVHEQ 817
Qy 801 PEELTNALEISNIIVFTSLFALEMLLKLVYGPFGYKPNYNI FQGVIVISVWEIVGQG 860
Db 818 PEELTNALEISNIIVFTSNFALEMLLKLVACGLGYIRPNYNI FQGVIVISVWEIVGQAD 877
Qy 861 GGLSVLRTFLRMVRLKLVRLPALQRLVRLMKTMDNVATFCMLLMFLFIFISILGMHLF 920
Db 878 GGLSVLRTFLRLVRLKLVRLPALRRLQVLVKTMDNVATFCTLLMLFIFISILGMHLF 937
Qy 921 GCKFASERD-CDTLPDRKNFSLWAIVTVQILTQEDWNVKLVNGMASTSSWAALYFIA 979
Db 938 GCKFSLKTDGTPDRKNFSLWAIIVTVQILTQEDWNVKLVNGMASTSSWAALYFVA 997
Qy 980 LMTFGNYVFLNVAIVLVEGFOAGSDATKSESEDPFSPSVVDGDRKRLALVAL-----1035
Db 998 LMTFGNYVFLNVAIVLVEGFOAGSDANRSDTDKTSVHFEEDFHKLURELQTTLEKWS 1057
Qy 1036 -----GEHAELRKSLLPLLIHTAATPMHSPKSSS-TGVGALGSGSRRTSSSGSABPGA 1089
Db 1058 LAVTPNGHLEGRGSLSPPLINCTAATPMTPKSPFLDAAFLPSDRSGSSSGDPPLG- 1116
Qy 1090 AHHEKCPSPARSPPHSPWASASWTSRRSRNSLGRAPSLKRRSPGERSILSGEGQE 1149
Db 1117 ---DQKPASLRSSPCAPWPGSGWSSRRSSWSLGRAPSLKRRSQCCERESLLSGEGK 1173
Qy 1150 SODEEESSEEDRASPA--GSDHRHRSILEREAKSSFDLPDTL-----QVPLH-----R 1196

Db 1174 STDDE--AEDGRAAPGPRAFLPRAESLDPRPLPAALPPTKCRDRDQOVVALPSDPFLR 1231
Qy 1197 TASGRSSASEHODCNGKASGASGLARTLTDDPDQDDDDNDEGNLSKGERIOAWYRSRLP 1256
Db 1232 IDSHREDAAELEDDSDSCCLRLHKVLEPYKPO-----W-----1265
Qy 1257 ACCEROSWASAYIPPOSRELLCHRIITHQMFQHVVLVVIIFLNCITTIAMERPDKIDPHSA 1316
Db 1266 --CSREAWALYLFSPQNRFRVSCQKVIITHQMFQHVVLVVIIFLNCVTIATLSRDPIDPOST 1323
Qy 1317 ERIEFLTSNYIFTAVFLAEMTVKVALGWCFCGEQAYLRSSWNVDGLGLVLVLSVIDILVSM 1376
Db 1324 ERFVLSVSNYIFTALFVAEMVAVGALLSGEHAYLOSSNNLDGLLVVSLVDIVAM 1383
Qy 1377 VSDSGTILGMLRVLRLTLRLPLRVISRAOGLKLVVETLMSKPKIGNIVVICAPFII 1436
Db 1384 ASAGGAKILGVLRLTLRLPLRVISRAOGLKLVVETLMSKPKIGNIVVICAPFII 1443
Qy 1437 FGIILGVOLFQKFPVCOGEDTRNITNKSDCAEASVVRVHRKYNFNDNLGOALMSLFLVASK 1496
Db 1444 FGIILGVOLFQKFPVCOGEDTRNITNKSDCAEASVVRVHRKYNFNDNLGOALMSLFLVASK 1503
Qy 1497 DGWVDIMYDGLDVGVDQOQIMNHNPNWMLLYFISFLIIVAFVFLNMFGVVVFNPHKCRQ 1556
Db 1504 DGWVDIMYDGLDVGVDQOQVONHNPNWMLLYFISFLIIVAFVFLNMFGVVVFNPHKCRQ 1563
Qy 1557 HQEERARRREKRLRLKRRSKEKOMABAQCKPYYSYDYSRFLRVHHLCTSHYDLF 1616
Db 1564 HQEERARRREKRLRLRRRRSTFPS-PEAQRPPYADYSPTRRSISLCTSHYDLF 1622
Qy 1617 ITGVIGLVNVTMAHEHYOQOIIDEALKICNYIETVIVFESVFKLVAPAFRRFODRW 1676
Db 1623 ITFICVNVITMSMEHYNPKSLDEALKYCNVFTIVFVEAALKLVAFGRFRFPKORW 1682
Qy 1677 QLDLAILLSIMGITLSEIEVNLSPINPTIIRMRVLRIARVLKLVKQAVGMALLHTV 1736
Db 1683 QLDLAILLSIMGITLSEIEVNSAALPINPTIIRMRVLRIARVLKLVKQAVGMALLHTV 1742
Qy 1737 MQALPQVGNLGLLPMFLFFIPAAAGVELFGDLECDETHPCBGLGRHATFRNFGMAFLTF 1796
Db 1743 VQALPQVGNLGLLPMFLFFIYALGVELFGLECEDNCPCEGLSRHATFSNFGMAFLTF 1802
Qy 1797 RVSTGDNWNGIMKDPDRDC---DOESTCYNTVISPIFYSVFLTAQFVLVNVVAVLMMKH 1853
Db 1803 RVSTGDNWNGIMKDTLRECSREDKCHLSYLPALSPVYFVTFVLVAQFVLVNVVAVLMMKH 1862
Qy 1854 LEENKEAKEAEALAEALAELEMTKLSPOHSPGLSGFLWPGVEGVNSDTSKPGAPHTTA 1913
Db 1863 LEENKEAREDAELDAIELEMA-----QPGSARRVDADRP-----1899
Qy 1914 HIGASGFSLEHPTMVPHPPEVPVPLGPDLLTVKSGVSRTHSLPNDSYMCRNGSTA---1970
Db 1900 -----PLQOESPGARDAPNLVARKVSVSRMLSLPNDSYMFRPVVPASAP 1943
Qy 1971 -----ERSLGRGWGLPKAQSGSILSVHSOPADTSCILQIPKDVH-----YLLQP 2015
Db 1944 HRPLOQVEMETYGAGTF---LGSVASVHSPPAESCASLQIPLAVSPPARSSEGEPLHALSP 2000
Qy 2016 HGAPTWCAIPKLPPPGRSPLAQRPLRROAAIRTDSDVOGLGSRREDLLSEV---SGPSC 2071
Db 2001 RGT-----AKSPSLRLLCQEAHVTDLSLEGK-IDSPRDTLDPAEPGEKTPVR 2047
Qy 2072 PLTRSSFWGSSSIQVOQRSGIOQSV--SKH-----IRLPAPCGLEPSWAKDPPETRS 2123
Db 2048 PVTQ-----GGSLOSPRPRPASVTRKHTFGQCVSSRPAAPGGEAEASDP-----2096
Qy 2124 SLELDTLSWISGDLPL-SSQEEPLFP-----RDLKKCYSVETQSCRRRFGFWLDE 2173
Db 2097 ---ADEEVSHITSSACPMQPTAEPHGPESVAGGERDLRLYSDAQQGLDKFCG-RADE 2152
Qy 2174 QRRHSIAVSLDSSGQRLCPSPSSLGQPLGGP--GSRPKKLSPPSISIDPP-ESQGS 2230
Db 2153 QWRPSAE---LGSGE-----PGEAKANG-PBAEPALGARKKKWSPPCISVEPBADEGS 2203

2231 -RPPCSFG-VCLRRAPA-----SDSKDPVSPLDSTAAS-----PSPKDTLSL 2274
 2204 ARPSAAGGGTTLRRPTSCSEATPHRDSLEPTBGSAGGDPAAKGRWGQASRAEHLTV 2263
 2275 SGLSSDPTDM-----DP 2286
 2264 PSFAFELDLGVPSGDP 2280

RESULT 9
 CCAH_MOUSE STANDARD; PRT: 2365 AA.
 AC 088427; 09JKUS;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Voltage-dependent T-type calcium channel alpha-1H subunit (Voltage-gated calcium channel alpha subunit Cav3.2).
 GN Name=Cacnalh;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALE/c;
 RA Mittman S.;
 RT "Exon organization of mouse Cacnalh.";
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 1923-1952 FROM N.A.
 RC STRAIN=CS7BL/6J;
 RA Cribbs L.L., Lee J.-H., Yang J., Daud A.N., Perez-Reyes E.;
 RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Voltage-sensitive calcium channels (VSCC) mediate the entry of calcium ions into excitable cells and are also involved in a variety of calcium-dependent processes, including muscle contraction, hormone or neurotransmitter release, gene expression, cell motility, cell division and cell death. The isoform alpha-1H gives rise to T-type calcium currents. T-type calcium channels belong to the "low-voltage activated (LVA)" group and are strongly blocked by nickel and mibefradil. A particularity of this type of channels is an opening at quite negative potentials, and a voltage-dependent inactivation. T-type channels serve pacemaking functions in both central neurons and cardiac nodal cells and support calcium signaling in secretory cells and vascular smooth muscle. They may also be involved in the modulation of firing patterns of neurons which is important for information processing as well as in cell growth processes.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- DOMAIN: Each of the four internal repeats contains five hydrophobic transmembrane segments (S1, S2, S3, S5, S6) and one positively charged transmembrane segment (S4). S4 segments probably represent the voltage-sensor and are characterized by a series of positively charged amino acids at every third position.
 CC -1- PTM: In response to raising of intracellular calcium, the T-type channels are activated by CaM-kinase II.
 CC -1- SIMILARITY: Belongs to the calcium channel alpha-1 subunits family.

DR InterPro; IPR001682; Ca/Na_pore.
 DR InterPro; IPR002111; Cat_channel_TripL.
 DR InterPro; IPR005821; Ion_trans.
 DR InterPro; IPR005820; Mech_channel_nlg.
 DR InterPro; IPR005445; TVDCCAlphal.
 DR Pfam; PF00520; Ion_trans; 4.
 DR PRINTS; PRO1629; TVDCCALPHA1.
 KW Calcium channel; Glycoprotein; Ion transport; Ionic channel;
 KW Multigene family; Phosphorylation; Repeat; Transmembrane;
 KW Voltage-gated channel.
 FT REPEAT 87 422 I.
 FT REPEAT 776 1015 II.
 FT REPEAT 1232 1569 III.
 FT REPEAT 1613 1874 IV.
 FT DOMAIN 1 100 Cytoplasmic (Potential).
 FT TRANSMEM 101 119 S1 of repeat I (Potential).
 FT DOMAIN 120 139 Extracellular (Potential).
 FT TRANSMEM 140 160 S2 of repeat I (Potential).
 FT DOMAIN 161 169 Cytoplasmic (Potential).
 FT TRANSMEM 170 184 S3 of repeat I (Potential).
 FT DOMAIN 185 193 Extracellular (Potential).
 FT TRANSMEM 194 212 S4 of repeat I (Potential).
 FT DOMAIN 213 232 S5 of repeat I (Potential).
 FT TRANSMEM 233 254 Extracellular (Potential).
 FT TRANSMEM 254 395 S6 of repeat I (Potential).
 FT DOMAIN 420 790 Cytoplasmic (Potential).
 FT TRANSMEM 791 811 S1 of repeat II (Potential).
 FT DOMAIN 812 824 Extracellular (Potential).
 FT TRANSMEM 825 846 S2 of repeat II (Potential).
 FT DOMAIN 847 852 Cytoplasmic (Potential).
 FT TRANSMEM 853 871 S3 of repeat II (Potential).
 FT DOMAIN 872 879 Extracellular (Potential).
 FT TRANSMEM 880 903 S4 of repeat II (Potential).
 FT DOMAIN 904 914 Cytoplasmic (Potential).
 FT TRANSMEM 915 935 S5 of repeat II (Potential).
 FT DOMAIN 936 987 Extracellular (Potential).
 FT TRANSMEM 988 1012 S6 of repeat II (Potential).
 FT DOMAIN 1013 1301 Cytoplasmic (Potential).
 FT TRANSMEM 1302 1324 S1 of repeat III (Potential).
 FT DOMAIN 1325 1342 Extracellular (Potential).
 FT TRANSMEM 1343 1363 S2 of repeat III (Potential).
 FT DOMAIN 1364 1373 Cytoplasmic (Potential).
 FT TRANSMEM 1374 1393 S3 of repeat III (Potential).
 FT DOMAIN 1394 1407 Extracellular (Potential).
 FT TRANSMEM 1408 1429 S4 of repeat III (Potential).
 FT DOMAIN 1430 1439 Cytoplasmic (Potential).
 FT TRANSMEM 1440 1463 S5 of repeat III (Potential).
 FT DOMAIN 1464 1540 Extracellular (Potential).
 FT TRANSMEM 1541 1566 S6 of repeat III (Potential).
 FT DOMAIN 1567 1627 Cytoplasmic (Potential).
 FT TRANSMEM 1628 1648 S1 of repeat IV (Potential).
 FT DOMAIN 1649 1662 Extracellular (Potential).
 FT TRANSMEM 1663 1684 S2 of repeat IV (Potential).
 FT DOMAIN 1685 1691 Cytoplasmic (Potential).
 FT TRANSMEM 1692 1710 S3 of repeat IV (Potential).
 FT DOMAIN 1711 1724 Extracellular (Potential).
 FT TRANSMEM 1725 1748 S4 of repeat IV (Potential).
 FT DOMAIN 1749 1762 Cytoplasmic (Potential).
 FT TRANSMEM 1763 1783 S5 of repeat IV (Potential).
 FT DOMAIN 1784 1846 Extracellular (Potential).
 FT TRANSMEM 1847 1874 S6 of repeat IV (Potential).
 FT DOMAIN 1875 2365 Poly-His.
 FT DOMAIN 2365 531 Poly-Arg.
 FT DOMAIN 531 1597 Calcium ion selectivity and permeability (By similarity).
 FT SITE 378 Calcium ion selectivity and permeability (By similarity).
 FT SITE 971 Calcium ion selectivity and permeability (By similarity).
 FT SITE 1515 Calcium ion selectivity and permeability (By similarity).
 FT SITE 1819 Calcium ion selectivity and permeability (By similarity).

Qy 1915 IGASGFSLEHPTWPHPEVPVPLGPDLLTVRKSGVSRTHSLPNDSYMCNCRNGSTAESRL 1974
Dy 1896 ---AQSSTAQPPSTAQSQGT-DPTENLLVVRKVSVMRLSLPNDSYMFPVAPAAAPH 1951
Qy 1975 CHRGWGLP-----KAQSGILSVHSQPADTSCILQP-----KDVHYLLQHPGAP 2019
Dy 1952 SH-----PLQVEMETVTPVTSAAHSPLEPRTSFQVPSAASSPARASDPLCALSPRDT 2006
Qy 2020 TWGAIPKLPPLPPRPLAQRPLRQAARTSLDVOGLGSRDILLSEVSGSCPLTRSSSF 2079
Dy 2007 -----RSLSLRILYRQENHAESLEQDIDGAGEDGIPDYTEPAENISMQAP 2054
Qy 2080 WG-----GSSIOVQSRSGIQSKVSHIRLPAPCPGLEPSWADPPETRSSLELDT 2129
Dy 2055 LGTURSPPCSPRPASVTRKTFQHCISR-----PTLGGDDAADAAP-----ADE 2102
Qy 2130 ELSWISGDLPLSPSOEELFP-----RDLKKYKSVETQSCRRRPPGFWLDE 2173
Dy 2103 EVSHITSSAHPWATEPHSPSPASPTAGPAKTVGSGRDPHRFCSVDQAQSFIDKFG-RPDA 2161
Qy 2174 QRRHSIAV-----SCLDSGS-----QPRLCPSFSSLGQPLGGPSRKKLSPPSIS 2221
Dy 2162 QRWSSVELNDGDHLESGVEPARASELEPAL-----GARRKKMSPPCIS 2206
Qy 2222 IDPP-ESOG-SRPPCSPG--VCLRRRAPSDS---KDPSSVSPDLSTAAAP-----2265
Dy 2207 IDPFTEDGSGRRPAPAEAGNTILRRTPSCAALHRDPCPESTEGTGTDGDPVAKGERWQ 2266
Qy 2266 -SPKXDTLSLGLSDSDPTM 2284
Dy 2267 ASCRAEHLTVNFAPEPLDM 2286

RESULT 10
CCAI HUMAN
ID CCAI HUMAN STANDARD; PRT; 2223 AA.
AC Q9P0X4; Q95504; Q7Z659; Q8NFX6; Q9NZC8; Q9UH15; Q9UH30; Q9ULU9;
AC Q9UNE6;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE 05-JUL-2004 (Rel. 44, Last annotation update)
DE Voltage-dependent T-type calcium channel alpha-1I subunit (Voltage-gated calcium channel alpha subunit Cav3.3) (Ca(v)3.3).
GN Name=CACNA1I; Synonyms=KIAA1120;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC TISSUE=Brain;
RX MEDLINE=99381950; PubMed=10454147; DOI=10.1016/S0304-3940(99)00319-5;
RA Mittman S., Guo J., Emerick M.C., Agnew W.S.;
RT "Structure and alternative splicing of the gene encoding alpha1I, a human brain T calcium channel alpha subunit."
RL Neurosci. Lett. 269:121-124(1999).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 3).
RC TISSUE=Brain;
RX MEDLINE=20287513; PubMed=10749850; DOI=10.1074/jbc.C000090200;
RA Monteil A., Chemin J., Leuranguer V., Altier C., Mennessier G., Bourinet E., Lory P., Nargeot J.;
RT "Specific properties of T-type calcium channels generated by the human alpha1I subunit."
RL J. Biol. Chem. 275:16530-16535(2000).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 4), AND VARIANT VAL-1040.
RC TISSUE=Brain;
RX MEDLINE=22074770; PubMed=12080115;
RA Gomora J.C., Murbartian J., Arias J.M., Lee J.-H., Perez-Reyes E.;
RT "Cloning and expression of the human T-type channel Ca(v)3.3: insights into prepulse facilitation";
RL Biophys. J. 83:229-241(2002).

103 SEQUENCE FROM N.A.
104 MEDLINE=20057165; PubMed=10591208; DOI=10.1038/990031;
105 Dunham I., Hunt A.R., Collins J.E., Bruskewich R., Beare D.M.,
106 Clump M., Smink L.J., Ainscough R., Almeida J.P., Babbage A.K.,
107 Baggaley C., Bailey J., Barlow K.F., Bates K.N., Beasley O.P.,
108 Bird C.P., Blakey S.E., Bridgeman A.M., Buck D., Burgess J.,
109 Burdill W.D., Burton J., Carder C., Carter N.P., Chen Y., Clark G.,
110 Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R.,
111 Conroy D., Corby N.R., Coville G.J., Cox A.V., Davis J., Dawson E.,
112 Dhami P.D., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.G.,
113 Evans K.L., Fey J.M., Fleming K., French L., Garner A.A.,
114 Gilbert J.G.R., Goward M.E., Grafham D.V., Griffiths M.N.D., Hall C.,
115 Hall R.E., Hall-Tamlyn G., Heathcote R.W., Ho S., Holmes S.,
116 Hunt S.E., Jones M.C., Kershaw J., Kimberley A.M., King A.,
117 Laird G.K., Langford C.F., Leversha M.A., Lloyd C., Lloyd D.M.,
118 Martyn I.D., Mashreghi-Wohammadi M., Matthews L.H., McCann O.T.,
119 McElay J., McLaren R., Pearce A.V., Pearson D., Phillimore B.J.,
120 Odell C.N., Pavitt R., Pearce A.V., Ramsey H., Ramsey Y., Rogers L.,
121 Phillips S.H., Plumb R.W., Skuce C.D., Smalley S., Smith M.L.,
122 Scott C.E., Sehra H.K., Steward C.A., Sulston J.E., Swann R.M.,
123 Soderlund C., Spraggon L., Whiteley M.N., Willey D.L.,
124 Vaudin M., Wallis J.M., Williamson H., Wilmer T.E., Wilming L.,
125 Williams L., Williams S.A., Wilmshurst D.R., Beck S., Rogers J., Shimizu N.,
126 Wright C.L., Hubbard T., Bentley D., Asakawa S., Kudoh J.,
127 Minoshima S., Kawasaki K., Sasaki T., Aoki N., Mitsuoyama S.,
128 Shintani A., Shibuya K., Yoshizaki Y., Crabtree J., Deschamps S.,
129 Roe B.A., Chen F., Fu Y., Hu P., Hua A., Kenton S., Lai H., Lao H.I.,
130 Dorman A., Fang F., Lin S.-P., Loh P., Malaj E., Nguyen T., Pan H.,
131 Lewis J., Lewis S., Lin S.-P., Loh P., Malaj E., Nguyen T., Pan H.,
132 Phan S., Qi S., Qian Y., Ray L., Ren Q., Shaull S., Sloan D., Song L.,
133 Wang Q., Wang Y., Wang Z., White J., Murray J., Miller N., Minx P.,
134 Zhan M., Zhang G., Chisoe S., Graves D., Bradshaw H., Bourne S.,
135 Fulton R., Johnson D., Bemis G., Bentley D., Ozersky P., Rohlfing T.,
136 Hinds K., Kemp K., Latreille P., Layman D., Graves T., Hawkins J.,
137 Schreier P., Walker C., Wamsley A., Wohldmann P., Pepin K., Nelson J.,
138 Korfi I., Bedell J.A., Hillier L.W., Kurahashi H., Saitta S.,
139 Wilson R., Emanuel B.S., Shaikh T., Kurahashi H., Saitta S.,
140 Budarf M.L., McDermid H.E., Johnson A., Wong A.C.C., Morrow B.E.,
141 Edelmann L., Kim U.J., Shizuya H., Simon M.I., Dumanski J.P.,
142 Peyrard M., Kedra D., Seroussi E., Franssen I., Tapia I., Bruder C.E.,
143 O'Brien K.P., Wilkinson P., Bodenteich A., Hartman K., Hu X.,
144 Khan A.S., Lane L., Tikhunov Y., Wright H.,
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147 [5]
148 SEQUENCE OF 1200-2223 FROM N.A. (ISOFORM 1).
149 TISSUE=Brain;
150 MEDLINE=20039618; PubMed=10574461;
151 Hirosewa M., Nagase T., Ishikawa K.-I., Kikuno R., Nomura N.,
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153 "Characterization of cDNA clones selected by the GeneMark analysis from size-fractionated cDNA libraries from human brain."
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155 -!- FUNCTION: Voltage-sensitive calcium channels (VSCC) mediate the entry of calcium ions into excitable cells and are also involved in a variety of calcium-dependent processes, including muscle contraction, hormone or neurotransmitter release, gene expression, cell motility, cell division and cell death. Isoform alpha-1I gives rise to T-type calcium currents. T-type calcium channels belong to the "low-voltage activated (LVA)" group and are strongly blocked by nickel and mibefradil. A particularity of this type of channels is an opening at quite negative potentials, and a voltage-dependent inactivation. T-type channels serve pacemaking functions in both central neurons and cardiac nodal cells and support calcium signaling in secretory cells and vascular smooth muscle. They may also be involved in the modulation of firing patterns of neurons which is important for information processing as well as in cell growth processes. Gates in voltage ranges similar to, but higher than alpha 1G or alpha 1H (By similarity).
156 -!- SUBCELLULAR LOCATION: Integral membrane protein.
157 -!- ALTERNATIVE PRODUCTS:

Event=Alternative splicing; Named isoforms=4;
 Name=1; Synonyms=Delta36b;
 IsoId=Q9P0X4-1; Sequence=Displayed;
 Name=2;
 IsoId=Q9P0X4-2; Sequence=VSP_000951;
 Name=3; Synonyms=Alpha1-a;
 IsoId=Q9P0X4-3; Sequence=VSP_000950, VSP_000951;
 Name=4;
 IsoId=Q9P0X4-4; Sequence=VSP_000950;
 TISSUE SPECIFICITY: Brain specific.
 DOMAIN: Each of the four internal repeats contains five hydrophobic transmembrane segments (S1, S2, S3, S5, S6) and one positively charged transmembrane segment (S4). S4 segments probably represent the voltage-sensor and are characterized by a series of positively charged amino acids at every third position.
 !- PFM: In response to raising of intracellular calcium, the T-type channels are activated by CaM-kinase II (By similarity).
 !- SIMILARITY: Belongs to the calcium channel alpha-1 subunits family.
 !- CAUTION: Ref.4 (CAB62996) sequence differs from that shown due to erroneous gene model prediction.

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EMBL; AF129133; AAD45251.1; -
 EMBL; AF142567; AAF25722.1; -
 EMBL; AF211189; AAF44626.1; -
 EMBL; AF393329; AAM67414.1; -
 EMBL; AL008716; CAAL5494.1; -
 EMBL; AL022312; CAB62988.1; -
 EMBL; AL022319; CAB62996.1; ALT_SEQ.
 EMBL; AL022319; CAB52536.1; -
 EMBL; AB032946; BAA86434.1; -
 Genew; HGNC:1396; CACNA1I.
 MIM; 608230; -
 GO; GO:0005891; C:voltage-gated calcium channel complex; NAS.
 GO; GO:0008332; P:low voltage-gated calcium channel activity; NAS.
 GO; GO:0006816; P:calcium ion transport; NAS.
 InterPro; IPR001682; Ca/Na_pore.
 InterPro; IPR002111; Cat_channel_Trlp.
 InterPro; IPR002077; Ca_channel_alpha.
 InterPro; IPR005821; Ion_trans.
 InterPro; IPR005820; M_channel_nlg.
 InterPro; IPR005445; TVDCCAlphal.
 Pfam; PF00520; Ion_trans_4.
 PRINTS; PR00167; CACHANNEL.
 PRINTS; PR01629; TVDCCAlphal.
 Alternative splicing; Calcium channel; Calcium-binding; Glycoprotein;
 Ion transport; Ionic channel; Multigene family; Phosphorylation;
 Polymorphism; Repeat; transmembrane; Voltage-gated channel.
 REPEAT 66 401
 REPEAT 66 865
 REPEAT 1157 1434
 REPEAT 1472 1733
 REPEAT 1 78
 DOMAIN 79 99
 TRANSMEM 100 120
 DOMAIN 121 141
 TRANSMEM 142 148
 DOMAIN 149 168
 TRANSMEM 169 173
 DOMAIN 174 191
 TRANSMEM 192 211
 DOMAIN 212 232
 TRANSMEM 233 377
 DOMAIN 378 398
 TRANSMEM 399 640
 DOMAIN 640 640

FT	TRANSMEM	641	661	S1 of repeat II (Potential).
FT	DOMAIN	662	676	Extracellular (Potential).
FT	TRANSMEM	677	697	S2 of repeat II (Potential).
FT	DOMAIN	698	702	Cytoplasmic (Potential).
FT	TRANSMEM	703	721	S3 of repeat II (Potential).
FT	DOMAIN	722	729	Extracellular (Potential).
FT	TRANSMEM	730	753	S4 of repeat II (Potential).
FT	DOMAIN	754	764	Cytoplasmic (Potential).
FT	TRANSMEM	765	785	S5 of repeat II (Potential).
FT	DOMAIN	786	841	Extracellular (Potential).
FT	TRANSMEM	842	862	S6 of repeat II (Potential).
FT	DOMAIN	863	1166	Cytoplasmic (Potential).
FT	TRANSMEM	1167	1187	S1 of repeat III (Potential).
FT	DOMAIN	1188	1209	Extracellular (Potential).
FT	TRANSMEM	1210	1230	S2 of repeat III (Potential).
FT	DOMAIN	1231	1244	Cytoplasmic (Potential).

Query Match 45.0%; Score 5418; DB 1; Length 2223;
 Best Local Similarity 49.9%; Pred No. 1.2e-256; Gaps 68;
 Matches 1235; Conservative 243; Mismatches 533; Indels 462; Gaps 68;

Qy	12	TPPLRGSRPSSDP	-----	PGRLARGWTRRRMERAPRSRSDSPVASRSTTCFPGGAAG	65
Db <td>6 <td>SPSSSSAAAPAAEPGVITEQPGPR <th>-----</th> <td>SPSSPPGLEPLDGA</td> <td>45</td> </td></td>	6 <td>SPSSSSAAAPAAEPGVITEQPGPR <th>-----</th> <td>SPSSPPGLEPLDGA</td> <td>45</td> </td>	SPSSSSAAAPAAEPGVITEQPGPR <th>-----</th> <td>SPSSPPGLEPLDGA</td> <td>45</td>	-----	SPSSPPGLEPLDGA	45
Qy <td>66 <td>AGSTEKDPGSADSEAGLPPALAPVFPYLSQSRPRSWCLRTVCNPFVSRVSLVILL</td> <th>-----</th> <td>125</td> </td>	66 <td>AGSTEKDPGSADSEAGLPPALAPVFPYLSQSRPRSWCLRTVCNPFVSRVSLVILL</td> <th>-----</th> <td>125</td>	AGSTEKDPGSADSEAGLPPALAPVFPYLSQSRPRSWCLRTVCNPFVSRVSLVILL	-----	125	
Db <td>46 <td>-----DP</td> <th>-----</th> <td>HVPHPLDLAPIAFFCLRTQTTSPENWCIMVCPNPFVSRVSLVILL</td> <td>91</td> </td>	46 <td>-----DP</td> <th>-----</th> <td>HVPHPLDLAPIAFFCLRTQTTSPENWCIMVCPNPFVSRVSLVILL</td> <td>91</td>	-----DP	-----	HVPHPLDLAPIAFFCLRTQTTSPENWCIMVCPNPFVSRVSLVILL	91
Qy <td>126 <td>NCVTLGMPFCEDTACDSQRCRILOAFDDTFAFFAVEMVVMVALGFGKCYLGDTWN</td> <th>-----</th> <td>185</td> </td>	126 <td>NCVTLGMPFCEDTACDSQRCRILOAFDDTFAFFAVEMVVMVALGFGKCYLGDTWN</td> <th>-----</th> <td>185</td>	NCVTLGMPFCEDTACDSQRCRILOAFDDTFAFFAVEMVVMVALGFGKCYLGDTWN	-----	185	
Db <td>92 <td>NCVTLGMPFCDDMDCLSDRCKLQVDFDFFIFAMEMVLMKVALGFGKCYLGDTWN</td> <th>-----</th> <td>151</td> </td>	92 <td>NCVTLGMPFCDDMDCLSDRCKLQVDFDFFIFAMEMVLMKVALGFGKCYLGDTWN</td> <th>-----</th> <td>151</td>	NCVTLGMPFCDDMDCLSDRCKLQVDFDFFIFAMEMVLMKVALGFGKCYLGDTWN	-----	151	
Qy <td>186 <td>RLDFFIIVAGLMYSLDLQNVFSFSAVTRVRLRLRINRVPSRILVTLTLLDTPMLGN</td> <th>-----</th> <td>245</td> </td>	186 <td>RLDFFIIVAGLMYSLDLQNVFSFSAVTRVRLRLRINRVPSRILVTLTLLDTPMLGN</td> <th>-----</th> <td>245</td>	RLDFFIIVAGLMYSLDLQNVFSFSAVTRVRLRLRINRVPSRILVTLTLLDTPMLGN	-----	245	
Db <td>152 <td>RLDFFIIVAGMVEYSLDLQNLNLSAIRTVRLPLKAINRVPSRILVTLTLLDTPMLGN</td> <th>-----</th> <td>211</td> </td>	152 <td>RLDFFIIVAGMVEYSLDLQNLNLSAIRTVRLPLKAINRVPSRILVTLTLLDTPMLGN</td> <th>-----</th> <td>211</td>	RLDFFIIVAGMVEYSLDLQNLNLSAIRTVRLPLKAINRVPSRILVTLTLLDTPMLGN	-----	211	
Qy <td>246 <td>VLLCFFVFFIFGIVGVLWAGLNRCLFNPENSLPLSVLDLEPYQTEDESPFISQ</td> <th>-----</th> <td>305</td> </td>	246 <td>VLLCFFVFFIFGIVGVLWAGLNRCLFNPENSLPLSVLDLEPYQTEDESPFISQ</td> <th>-----</th> <td>305</td>	VLLCFFVFFIFGIVGVLWAGLNRCLFNPENSLPLSVLDLEPYQTEDESPFISQ	-----	305	
Db <td>212 <td>VLLCFFVFFIFGIVGVLWAGLNRCLFNPENFTIQGDVALPPYQPEDEMPFISL</td> <th>-----</th> <td>271</td> </td>	212 <td>VLLCFFVFFIFGIVGVLWAGLNRCLFNPENFTIQGDVALPPYQPEDEMPFISL</td> <th>-----</th> <td>271</td>	VLLCFFVFFIFGIVGVLWAGLNRCLFNPENFTIQGDVALPPYQPEDEMPFISL	-----	271	
Qy <td>306 <td>PRENGMSCRSVPTLRGEGGGPPCSL</td> <th>-----</th> <td>DYETVNSSNTT</td> <td>357</td> </td>	306 <td>PRENGMSCRSVPTLRGEGGGPPCSL</td> <th>-----</th> <td>DYETVNSSNTT</td> <td>357</td>	PRENGMSCRSVPTLRGEGGGPPCSL	-----	DYETVNSSNTT	357
Db <td>272 <td>SGDNGMGCHIEPPLKEQ</td> <th>-----</th> <td>GRECLSKDDVDFGAGQDLNAGLGVNNRYNVCT</td> <td>328</td> </td>	272 <td>SGDNGMGCHIEPPLKEQ</td> <th>-----</th> <td>GRECLSKDDVDFGAGQDLNAGLGVNNRYNVCT</td> <td>328</td>	SGDNGMGCHIEPPLKEQ	-----	GRECLSKDDVDFGAGQDLNAGLGVNNRYNVCT	328
Qy <td>358 <td>GEHPFKGAINFDNIGYAWIAIFQVITLEGVDMYFVMDAHSFYNYFYILLIIVGFF</td> <th>-----</th> <td>417</td> </td>	358 <td>GEHPFKGAINFDNIGYAWIAIFQVITLEGVDMYFVMDAHSFYNYFYILLIIVGFF</td> <th>-----</th> <td>417</td>	GEHPFKGAINFDNIGYAWIAIFQVITLEGVDMYFVMDAHSFYNYFYILLIIVGFF	-----	417	
Db <td>329 <td>GSANPHKGAINFDNIGYAWIIVFQVITLEGVDMYFVMDAHSFYNYFYILLIIVGFF</td> <th>-----</th> <td>388</td> </td>	329 <td>GSANPHKGAINFDNIGYAWIIVFQVITLEGVDMYFVMDAHSFYNYFYILLIIVGFF</td> <th>-----</th> <td>388</td>	GSANPHKGAINFDNIGYAWIIVFQVITLEGVDMYFVMDAHSFYNYFYILLIIVGFF	-----	388	
Qy <td>418 <td>MINCLVVIATQFSETQKRESQLMREORVRLPSNASTLASFSPGSCYEELLYLVYLR</td> <th>-----</th> <td>477</td> </td>	418 <td>MINCLVVIATQFSETQKRESQLMREORVRLPSNASTLASFSPGSCYEELLYLVYLR</td> <th>-----</th> <td>477</td>	MINCLVVIATQFSETQKRESQLMREORVRLPSNASTLASFSPGSCYEELLYLVYLR	-----	477	
Db <td>389 <td>MINCLVVIATQFSETQKREHRLMLEQRQYLS-SSTVASYAEPGDCYEELFYQYVCHLR</td> <th>-----</th> <td>447</td> </td>	389 <td>MINCLVVIATQFSETQKREHRLMLEQRQYLS-SSTVASYAEPGDCYEELFYQYVCHLR</td> <th>-----</th> <td>447</td>	MINCLVVIATQFSETQKREHRLMLEQRQYLS-SSTVASYAEPGDCYEELFYQYVCHLR	-----	447	
Qy <td>478 <td>KAARLAAQVSPAIGVRAGLLSSPVARSQEPQSGSCSTRSHRRLSVHLLVHHHHHHHH</td> <th>-----</th> <td>537</td> </td>	478 <td>KAARLAAQVSPAIGVRAGLLSSPVARSQEPQSGSCSTRSHRRLSVHLLVHHHHHHHH</td> <th>-----</th> <td>537</td>	KAARLAAQVSPAIGVRAGLLSSPVARSQEPQSGSCSTRSHRRLSVHLLVHHHHHHHH	-----	537	
Db <td>448 <td>KAKRALGLYQALQSRQAL-GPEAPAPAKPGP</td> <th>-----</th> <td>HAKEPRHY</td> <td>487</td> </td>	448 <td>KAKRALGLYQALQSRQAL-GPEAPAPAKPGP</td> <th>-----</th> <td>HAKEPRHY</td> <td>487</td>	KAKRALGLYQALQSRQAL-GPEAPAPAKPGP	-----	HAKEPRHY	487
Qy <td>538 <td>H- - - - - LGNGTLRVPRASPEIQDRDAN-GSRRLM-LPPPTPTSPGPPRGAESVHSFYHAD</td> <th>-----</th> <td>592</td> </td>	538 <td>H- - - - - LGNGTLRVPRASPEIQDRDAN-GSRRLM-LPPPTPTSPGPPRGAESVHSFYHAD</td> <th>-----</th> <td>592</td>	H- - - - - LGNGTLRVPRASPEIQDRDAN-GSRRLM-LPPPTPTSPGPPRGAESVHSFYHAD	-----	592	
Db <td>488 <td>HGKTGQG</td> <th>-----</th> <td>DEGRHLGSRHCQLHGPASP</td> <td>523</td> </td>	488 <td>HGKTGQG</td> <th>-----</th> <td>DEGRHLGSRHCQLHGPASP</td> <td>523</td>	HGKTGQG	-----	DEGRHLGSRHCQLHGPASP	523
Qy <td>593 <td>CHLEPVRCQAPPPPCPSAEGRTVSGKVPYTVHTSPPEILKDKALVEVAPSGPPLT</td> <th>-----</th> <td>652</td> </td>	593 <td>CHLEPVRCQAPPPPCPSAEGRTVSGKVPYTVHTSPPEILKDKALVEVAPSGPPLT</td> <th>-----</th> <td>652</td>	CHLEPVRCQAPPPPCPSAEGRTVSGKVPYTVHTSPPEILKDKALVEVAPSGPPLT	-----	652	
Db <td>524 <td>-----LC</td> <th>-----</th> <td>PQHSPLDA</td> <td>547</td> </td>	524 <td>-----LC</td> <th>-----</th> <td>PQHSPLDA</td> <td>547</td>	-----LC	-----	PQHSPLDA	547
Qy <td>653 <td>SFNIPPGFSSMHKLLETQSTGAC-HSSCKLSSPCSKADSGACGPDSCPYCARICAGRPE</td> <th>-----</th> <td>711</td> </td>	653 <td>SFNIPPGFSSMHKLLETQSTGAC-HSSCKLSSPCSKADSGACGPDSCPYCARICAGRPE</td> <th>-----</th> <td>711</td>	SFNIPPGFSSMHKLLETQSTGAC-HSSCKLSSPCSKADSGACGPDSCPYCARICAGRPE	-----	711	
Db <td>548 <td>S</td> <th>-----</th> <td>DPASCPCCOHEGDRRPSGLGSTDQSGSGS</td> <td>588</td> </td>	548 <td>S</td> <th>-----</th> <td>DPASCPCCOHEGDRRPSGLGSTDQSGSGS</td> <td>588</td>	S	-----	DPASCPCCOHEGDRRPSGLGSTDQSGSGS	588
Qy <td>712 <td>SADHVPDPSDEAVYETQDAQHSDLRDPHRRRQRSLGPDAPSPSSVLA--FWRLICDTF</td> <th>-----</th> <td>769</td> </td>	712 <td>SADHVPDPSDEAVYETQDAQHSDLRDPHRRRQRSLGPDAPSPSSVLA--FWRLICDTF</td> <th>-----</th> <td>769</td>	SADHVPDPSDEAVYETQDAQHSDLRDPHRRRQRSLGPDAPSPSSVLA--FWRLICDTF	-----	769	
Db <td>589 <td>A- - - - - DGDA</td> <th>-----</th> <td>RSEGDGASSELKEEBEQ</td> <td>633</td> </td>	589 <td>A- - - - - DGDA</td> <th>-----</th> <td>RSEGDGASSELKEEBEQ</td> <td>633</td>	A- - - - - DGDA	-----	RSEGDGASSELKEEBEQ	633

QY 770 RKIVDSYKFGRIAMIAIVNTLSMGIEYHEPOBELTNALIEISNIVFTSLFALEMLKLIV 829
DB 634 RGIIVDSYKFGRIAMIAIVNTLSMGIEYHEPOBELTNALIEISNIVFTSMFALEMLKLAA 693
QY 830 YGPEYIKNPNYIPDGVIIVISVMEIYQOQGGGLSVLRTFLRMVRLKLVFLPALORQV 899
DB 694 FGLFDYLRNPNYIPDFSIIIVISWEIYQADGGGLSVLRTFLLRLVLKLVFLPALORQV 753
QY 890 VLMKTMNVATFCMLLMFLFIFISILGMLHFGCKFASERD-GDTLPDRKNFDSLLWAIVT 948
DB 754 VLMKTMNVATFCMLLMFLFIFISILGMLHFGCKFASERD-GDTLPDRKNFDSLLWAIVT 813
QY 949 VFQILTEDNMVLYNGWASTSWAALYFIALMTFGNYVLFNLVAILVVEFGQAEADATK 1008
DB 814 VFQILTEDNMVLYNGWASTSWAALYFIALMTFGNYVLFNLVAILVVEFGQAEADANR 873
QY 1009 SESBPDPFSPSV-----DGDGRKRLALVALGEHAERKSLPLLIHT-----A 1054
DB 874 SYSDEQSSNIEBFDKLQEGLDSSGDPK--LCPIMPMPNGHLDPDL--PLGGHLGPAGA 929
QY 1055 ATPMSHPKSSSTGVEALGSGSRRTSSGSAEPAAGAAHEMKCPSPARSSPHSPWSAASSW 1114
DB 930 AGPA--PRLSQDPMLVALGSKSSVMSL---GRMSYDORSLSRSSSYTGPWGRSAW 984
QY 1115 TSRRSSNLGRAPSLKRRSPSGRRSILSGE-QGESQDEESSEE--DRASPAQSDH-- 1169
DB 985 ASRRSSWN-----SLKHKPSAEHESLISAERGGARVCEVAADGPPRAAPLTPHAH 1038
QY 1170 -----RHGSLEREAKSFDLPDLOVPGHLRTASGRSS--ASEHODCNCKS 1214
DB 1039 HIHGHPLAHRRHRRHRTLSLDRNDSVDLAEVPAVGAHPRAAWRAAGAPAGPHEDCNGRM 1098
QY 1215 ASGRLARLTLD-DPOLDDDDNDEGNLSKGERIQAWVRSRLPACCRERDSWASYIFPPQ 1273
DB 1099 PS--IAKDVFTKMGDRGRGDEEIDYTLCFVRKMDIVVKPDWCVEVDWVYLSPSE 1156
QY 1274 SRFLLCRIITHKMFDRHVLVIFPLNCITTIAMERPKIDPHSABRIFLTLSNYIFTAVFL 1333
DB 1157 NFRVLCQITIAHLKFDVVLAFIFLNCITTIALERPOIEAGSTERIFLTVSNNYIFTAIFV 1216
QY 1334 AMTVKVALGWCFOEQAYLRSSNVLGGLLVLSVIDILVSMVSDSTKILGMLVRL 1393
DB 1217 GEMTLKVVSLGLYFQEQAYLRSSNVLGGLLVLSVIDILVSMVSDSTKILGMLVRL 1276
QY 1394 LTLRLPLRVISRAQGLKLVWETLMSLPIGNIVVICCAFFIIFGILGVOLFKGFFVCQ 1453
DB 1277 LTLRLPLRVISRAQGLKLVWETLMSLPIGNIVVICCAFFIIFGILGVOLFKGFFVHCL 1336
QY 1454 GEDTRNITNKSACABASVYRWHRKYNFNLGOALMSLFLVASKOGWVDIMYDGLDAVGD 1513
DB 1337 GVDTRNITNRSDCMAANYRWVHHKYNFNLGOALMSLFLVASKOGWVIMYDGLDAVGD 1396
QY 1514 QOPIMNHPMLLYTIFSLIIVAFVILNMFVGVVNFHCKRQHOEEAREERREKRLRR 1573
DB 1397 QOPVTHNHPMLLYTIFSLIIVAFVILNMFVGVVNFHCKRQHOEEAREERREKRLRR 1456
QY 1574 LEKKERSKEQMAEQAQCPYGYDYSRFLVHHLCTSHYLDLFIITGVILGNVVTMAMEHY 1633
DB 1457 LEKKER-----KAQLPYATYCHTLLIISMCTSHYLDLFIITGVILGNVVTMAMEHY 1509
QY 1634 QOPQILDEALKTCNITFTVIFVESVFKLVAFAPRRFODRNQDLDAIVLLSINGITILE 1693
DB 1510 NQPTSLTALKYCNMTFTVFLVLEAVLKLAVFGLRRFFKDRWNQDLDAIVLLSINGITILE 1569
QY 1694 EIEVNLSTINTPIRIMEVRLARVLKLLKMAVGNRALLHTVMOALPOVGNLGLFLLML 1753
DB 1570 EIEINALPINPIRIMEVRLARVLKLLKMAVGNRALLHTVMOALPOVGNLGLFLLML 1629
QY 1754 FFIIFALGVELFGDLCEDETHPECEGLRHATFRNFGMAFLTILFRYSTGDNWNGIMKDPSSR 1813
DB 1630 FFIIFALGVELFGDLCEDETHPECEGLRHATFRNFGMAFLTILFRYSTGDNWNGIMKDTILR 1689
QY 1814 DC-QDESTCVNTV--ISPIYFVSFVLTAQFVLVNVVIAVMKHLSESNKEAELEAE 1870

DB 1690 DCTHDERSCLSLQFVSPFLYFVSFVLTAQFVLVNVVIAVMKHLDDSNKEAQEDAEMDAE 1749
QY 1871 LELEW-KTILSPOHSPGLGSP-----FLW----- 1892
DB 1750 LELEWANGLPGRPLTGPSPGAPGRPGAGGGGTEGGLCRRCYSPAQENLWLDVSULI 1809
QY 1893 --PGVEG-VNSTDSPKGPAPHTTAHGAASG----- 1920
DB 1810 IKDSLGEELTIIDNLSSGSIH--HYSPGACKKCHKDKQEVQLAETEAFSLNSDRSSSI 1866
QY 1921 -----FLEHPTWVP-----HREVPV-PLGPDLLTVRKSGVSRTHSLPN-DSY 1962
DB 1867 LLGDDLSLSDPTACPPGRKDSKGEIDPPPMRVGDLGECFFPLSTAVS-----PDPENF 1921
QY 1963 MCRNGSTAERSLGHRCWGLPKAQSGSILSVHSQPADTSCILQPKDVHY-----LLQPH 2016
DB 1922 LCEMEIIPNPV--RSW--LKHDSSQAPSPSPDASSPLLPMPAEFFPHPAVSASQKQPE 1977
QY 2017 GAPTWGAIPKLPPPG-----RSLAQRPRLRQAARTDSDVOGLGSRREDLLSEVSGPSC 2071
DB 1978 KGTGTGTLFKIALQGSWASLRSPRVNCTLLRQATGSDTSLDAS----- 2020
QY 2072 PLTRSSFWGSSIQVQORSGIQSKVSHIRLPAPCPGLEPSPWAKDPPETRSLELDTL 2131
DB 2021 -----PSSAGSLQTTLEDSLTLSDSPRALGPPAPAG----- 2054
QY 2132 SWITSGDLLSPSSOPELPPRLDKKCYSVETQSCRRRPGFWLDBORRHISIAVCLDSGQSR 2191
DB 2055 -----PRAGLSPAARRRL-----SLRGRLFLSLGLRAHQHSHS--SGGSTP 2095
QY 2192 LCPSPSL-----GGPLGPGSRPKKLSPPSIS---IDPPESQSRPPCSPGVCL 2240
DB 2096 GCTHDSMDPDSDEGRGGAGGGGSEHSETLSSLSLTLFCPPP-----PPAPGLTP 2149
QY 2241 RR-----RAP---ASDSKOPSVSPDLSTAAASPSPKDDTLS 2273
DB 2150 ARKFSSTSLAAPGRPHAAHLARSPSWADRSDKPPGRAPLPMGLGPLAPPQPL- 2208
QY 2274 LSGLSDDPTMDP 2286
DB 2209 -----PGELEP 2214
RESULT 11
CCAI RAT STANDARD; PET; 1835 AA.
ID_CCAI RAT
AC O920Y8; Q9E059;
DT 30-MAY-2000 (Rel. 39, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Voltage-dependent T-type calcium channel alpha-1I subunit (Voltage-gated calcium channel alpha subunit Cav3.3)- (CavT.3).
GN Name=Cacnali;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=101116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Brain;
RX MEDLINE=99165796; PubMed=10066244;
RA Lee J.-H., Daud A.N., Cribbs L.L., Lacerda A.E., Pereverzev A.,
RA Kloeckner U., Schneider T., Perez-Reyes E.,
RT "Cloning and expression of a novel member of the low voltage-activated
RT T-type calcium channel family.";
RL J. Neurosci. 19:1912-1921(1999).
RN [2]
RP REVISIONS TO 345; 1656 AND 1737.
RA Perez-Reyes E.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.

RC TISSUE=Brain;
RX PubMed-11073957; DOI=10.1074/jbc.M008215200;
RA McRory J.B., Santi C.M., Hamming K.S.C., Mezeyova J., Sutton K.G.,
RA Baillie D.B., Stea A., Snutch T.P.;
RT "Molecular and functional characterization of a family of rat brain T-
RT type calcium channels.";
RL J. Biol. Chem. 276:3999-4011(2001).
CC -!- FUNCTION: Voltage-sensitive calcium channels (VSCC) mediate the
CC entry of calcium ions into excitable cells and are also involved
CC in a variety of calcium-dependent processes, including muscle
CC contraction, hormone or neurotransmitter release, gene expression,
CC cell motility, cell division and cell death. Isoform alpha-1I
CC gives rise to T-type calcium currents. T-type calcium channels
CC belong to the "low-voltage activated (LVA)" group and are strongly
CC blocked by nickel and mibefradil. A particularity of this type of
CC channels is an opening at quite negative potentials, and a
CC voltage-dependent inactivation. T-type channels serve pacemaking
CC functions in both central neurons and cardiac nodal cells and
CC support calcium signaling in secretory cells and vascular smooth
CC muscle. They may also be involved in the modulation of firing
CC patterns of neurons which is important for information processing
CC as well as in cell growth processes. Gates in voltage ranges
CC similar to, but higher than alpha 1G or alpha 1H.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Brain.
CC -!- DOMAIN: Each of the four internal repeats contains five
CC hydrophobic transmembrane segments (S1, S2, S3, S5, S6) and one
CC positively charged transmembrane segment (S4). S4 segments
CC probably represent the voltage-sensor and are characterized by a
CC series of positively charged amino acids at every third position.
CC -!- PTM: In response to raising of intracellular calcium, the T-type
CC channels are activated by CaM-kinase II (By similarity).
CC -!- SIMILARITY: Belongs to the calcium channel alpha-1 subunits
CC family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF086827; AAD17796.2; -;
DR EMBL; AF290214; AAG35188.1; -;
DR InterPro; IPR001682; Ca/Na_pore.
DR InterPro; IPR002111; Cat channel TrpL.
DR InterPro; IPR002077; Ca channel_alpha.
DR InterPro; IPR005821; Ion trans_alpha.
DR InterPro; IPR005820; M+channel_nlg.
DR InterPro; IPR005445; TVDCCALPHAL.
DR Pfam; PF00520; Ion_trans; 4.
DR PRINTS; PR00167; CACHANNEL.
DR PRINTS; PR01629; TVDCCALPHAL.
KW Calcium channel; Calcium-binding; Glycoprotein; Ion transport;
KW Transmembrane; Multigene family; Phosphorylation; Repeat;
KW REPEAT 64 399 I.
FT REPEAT 584 823 II.
FT REPEAT 1116 1393 III.
FT REPEAT 1431 1692 IV.
FT DOMAIN 1 76
FT TRANSMEM 77 97
FT DOMAIN 98 115
FT TRANSMEM 116 137
FT DOMAIN 138 146
FT TRANSMEM 147 166
FT DOMAIN 167 171
FT TRANSMEM 172 189
FT DOMAIN 190 209
FT TRANSMEM 210 230
FT DOMAIN 231 371
FT TRANSMEM 372 396
FT TRANSMEM 396 400

FT DOMAIN 397 598
FT TRANSMEM 599 619
FT DOMAIN 620 632
FT TRANSMEM 633 654
FT DOMAIN 655 660
FT TRANSMEM 661 679
FT DOMAIN 680 687
FT TRANSMEM 688 711
FT DOMAIN 712 722
FT TRANSMEM 723 743
FT DOMAIN 744 795
FT TRANSMEM 796 820
FT DOMAIN 821 1125
FT TRANSMEM 1126 1148
FT DOMAIN 1149 1166
FT TRANSMEM 1167 1187
FT DOMAIN 1188 1197
FT TRANSMEM 1198 1217
FT DOMAIN 1218 1231
FT TRANSMEM 1232 1253
FT DOMAIN 1254 1263
FT TRANSMEM 1264 1287
FT DOMAIN 1288 1364
FT TRANSMEM 1365 1390
FT DOMAIN 1391 1445
FT TRANSMEM 1446 1466
FT DOMAIN 1467 1480
FT TRANSMEM 1481 1509
FT DOMAIN 1509 1528
FT TRANSMEM 1510 1542
FT DOMAIN 1529 1542
FT TRANSMEM 1543 1566
FT DOMAIN 1567 1580
FT TRANSMEM 1581 1601
FT DOMAIN 1602 1664
FT TRANSMEM 1665 1692
FT DOMAIN 1693 1835
FT SITE 355 355
FT SITE 779 779
FT SITE 1339 1339
FT SITE 1637 1637
FT CARBOHYD 171 171
FT CARBOHYD 242 242
FT CARBOHYD 309 309
FT CARBOHYD 1301 1301
FT CARBOHYD 1304 1304
FT CONFLICT 193 193
FT CONFLICT 291 291
FT CONFLICT 394 394
FT CONFLICT 406 406
FT CONFLICT 485 485
FT CONFLICT 512 512
FT CONFLICT 558 558
FT CONFLICT 683 683
FT CONFLICT 691 691
FT CONFLICT 739 740
FT CONFLICT 833 833
FT CONFLICT 846 846
FT CONFLICT 856 856
FT CONFLICT 905 905
FT CONFLICT 913 913
FT CONFLICT 936 936
FT CONFLICT 996 996
FT CONFLICT 1060 1060
FT CONFLICT 1094 1094
FT CONFLICT 1197 1198
FT CONFLICT 1229 1231
FT CONFLICT 1422 1422
FT CONFLICT 1623 1625

Cytoplasmic (Potential).
S1 of repeat II (Potential).
Extracellular (Potential).
S2 of repeat II (Potential).
Cytoplasmic (Potential).
S3 of repeat II (Potential).
Extracellular (Potential).
S4 of repeat II (Potential).
Cytoplasmic (Potential).
S5 of repeat II (Potential).
Extracellular (Potential).
S6 of repeat II (Potential).
Cytoplasmic (Potential).
S1 of repeat III (Potential).
Extracellular (Potential).
S2 of repeat III (Potential).
Cytoplasmic (Potential).
S3 of repeat III (Potential).
Extracellular (Potential).
S4 of repeat III (Potential).
Cytoplasmic (Potential).
S5 of repeat III (Potential).
Extracellular (Potential).
S6 of repeat III (Potential).
Cytoplasmic (Potential).
S1 of repeat IV (Potential).
Extracellular (Potential).
S2 of repeat IV (Potential).
Cytoplasmic (Potential).
S3 of repeat IV (Potential).
Extracellular (Potential).
S4 of repeat IV (Potential).
Cytoplasmic (Potential).
S5 of repeat IV (Potential).
Extracellular (Potential).
S6 of repeat IV (Potential).
Cytoplasmic (Potential).
Calcium ion selectivity and permeability
(BY similarity).
Calcium ion selectivity and permeability
(BY similarity).
Calcium ion selectivity and permeability
(BY similarity).
Calcium ion selectivity and permeability
(BY similarity).
N-linked (GlcNAc. . .) (Potential).
N-linked (GlcNAc. . .) (Potential).
N-linked (GlcNAc. . .) (Potential).
N-linked (GlcNAc. . .) (Potential).
M -> L (in Ref. 3).
V -> V (in Ref. 3).
V -> L (in Ref. 3).
E -> N (in Ref. 3).
C -> S (in Ref. 3).
D -> Y (in Ref. 3).
G -> S (in Ref. 3).
F -> S (in Ref. 3).
MH -> JD (in Ref. 3).
C -> Y (in Ref. 3).
F -> L (in Ref. 3).
S -> R (in Ref. 3).
L -> R (in Ref. 3).
M -> YW (in Ref. 3).
W -> G (in Ref. 3).
A -> R (in Ref. 3).
I -> M (in Ref. 3).
D -> CC (in Ref. 3).
SS -> TD (in Ref. 3).
Missing (in Ref. 3).
K -> Y (in Ref. 3).
FGM -> SAR (in Ref. 3).


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Db 1802 SGSVFHYASPDG 1814

RESULT 12
Q726S8
ID Q726S8 PRELIMINARY; PRT; 1994 AA.
AC Q726S8;
DT 01-OCT-2003 (Tremblrel. 25, Created)
DT 01-OCT-2003 (Tremblrel. 25, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE DJ172B20.1 (Calcium channel, voltage-dependent, alpha 1I subunit)
DE (Fragment).
GN Name=CACNA1I;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Phillips S.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL023219; CAD92537.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005261; F:cation channel activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR InterPro; IPR001682; Ca/Na_Pore.
DR InterPro; IPR002111; Cat_channel_TrpL.
DR InterPro; IPR00345; CytC_heme_BS.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR005820; M-channel_nlg.
DR Pfam; PF00520; Ion_trans_4.
DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
KW Ion transport; Ionic channel; Transmembrane; Transport.
FT NON TER 1
SQ SEQUENCE 1994 AA; 220004 MW; A5EPAE5FA32DCF76 CRC64;

Query Match 39.5%; Score 4750.5; DB 2; Length 1994;
Best Local Similarity 49.0%; Pred. No. 5-le-224;
Matches 1099; Conservative 214; Mismatches 485; Indels 447; Gaps 61;

Qy 229 MRILVTLDDTLPLMGNVLLLCFFVFFIFGIVGVQWAGLNRNCFPLPENSLPLSDVLE 288
Db 1 NRILVNLDDTLPLMGNVLLLCFFVFFIFGIVGVQWAGLNRNCFLEENTIQDVALP 60

Qy 289 PYYOTENEDESPFTCSQPRENGMRSRVSPTLRGEGGGPPCSL-----DYTYNGSSN 342
Db 61 PYYQPEDEDEMPFICSLSGDNGIMGCHIEIPLKEQ---GRECCLSKDDVDYDFGAGRODLN 117

Qy 343 TT--CVNWNQYTWCSAGEHNPFGAINFDNIGYAWIAIFQVITLEGWVDIMYVMDAHS 400
Db 118 ASGLCVNWNRYNVCRTGSANPHKGAINFDNIGYAWIVIFQVITLEGWVEIMYVMDAHS 177

Qy 401 FYNFIYFILLIIVGSFFMINCLVVIATQFSETKQRESOLMREORVRFSLNASTLASPSE 460
Db 178 FYNFIYFILLIIVGSFFMINCLVVIATQFSETKQREHRLMLEQRVLS--SSIVASYAE 236

Qy 461 PGSCYBEELLKYLIVLRKAARLARLAQVRAIGVRAGLSSPVARSQEPQSPGSCSTRSHRR 520
Db 237 PGDCVEEIEFQVVCILRKAKR-----RALGLYQALQS-----RR 270

Qy 521 LSVHHLVHHHHHHHHHHLNGTLRVPRASPEIQDRDANGSRRLMLPPPTPTPSGGPPR 580
Db 271 QAL-----GPE-----APAPAKPGP-----285

Qy 581 GAESVHSFYHADCHLEPVRCAPPRCPSSEASGRVTGSGKVYTVHTSPPEILKDKALV 640
Db 286 -----HAK---EPRHYQLCQHSPLDA-----TPHT-----LV 310

Qy 641 EVAPSPGPTTTSFNIPPGPFSSMKHLETOSTGAC--HSSCKISPCSKADSGACGPDSC 699
Db 311 Q-----PIPATLAS-----DPASCPCQCHEDGRPPSGLGSTDGQGGSGS- 350

Qy 700 PYCARTGAGEPESADHVMPSDSSEAVYEFTQDAQHSDLRDPHSRRRQRSLGDAEPSVL 759
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Db 351 ---GSSAGGEDEA-----DGDGA---RSSDGSASSELGKBEEBEQ-----ADGAVWL 392
Qy 760 A--FWRLICDTFRKIVDSKYFCRGIMIAILVNTLSMGIEYHEQPEELTNALEISNIVFTS 817
Db 393 CGDVWRETRAKLRGIVDSKYFNRGIMAILVNTVSMGIERHEQPEELTNALEICNVVFTS 452
Qy 818 LFALEMLLKLIVYCPFGYIKNPYNIPOGVIVVVISWEIVGQGGGLSVLRFRLMRVLKL 877
Db 453 MFALEMLLKLAAAGFLDYLRNPYNIPOGVIVVVISWEIVGQGGGLSVLRFRLMRVLKL 512
Qy 878 VRFLPALQROLVLMKTMNDVATFCMLLMLEFIFISILGMHLFGCKPFASERD-GDTLPDR 936
Db 513 VRFPALRRQLVLMKTMNDVATFCMLLMLEFIFISILGMHLFGCKFSRLTDTGDTVPDR 572
Qy 937 KNFDSLMLAIIVTVFQILTQEDMNKVLNGMASTSSWAALYFIALMTFGNYVLNLLVAIL 996
Db 573 KNFDSLMLAIIVTVFQILTQEDMNKVLNGMASTSSWAALYFIALMTFGNYVLNLLVAIL 632
Qy 997 VEGFOAEGDATKSESEPDFFSPSV-----DGDGDKRLALVALGHAELKRSLL 1046
Db 633 VEGFOAEGDANRSYSDQSSNIEEFDKLOEGDSSGDPK--LCPIPTMTPNGHLDPSL- 689
Qy 1047 PPLIIHT-----AATPMSHPKSSSTGVCEALGSGSRRTSSSGSABPAAHMKCPSPARS 1102
Db 690 -PLGHLGPAAGA--PRLSLQDPMLVALGSRKSSVMSL-----GRMSYQORSUSSRS 743
Qy 1103 SPHSPWASAASWTSSRSRSLRAPSLKRSRSPGERRSLLSGE--GQSDQDEESSES-- 1159
Db 744 SYYGWGRSAAWASRRSSWN-----SLKHKPPSAEHSLSAERGGGARVCEVAADSGP 797
Qy 1160 DRASPAGSDH-----RHGSLERAKSFDLPDLTQVGLHRTASGRSS- 1203
Db 798 PRAAPLHTPHAHTHHGFHLAHRHRRHRTLSLNRSDVLAELVPAVGAHPRAAWRAAG 857
Qy 1204 -ASHQDCNGKSGASRLARTLD-DPOLQDGDNDNDEGNLKGRIQAWRSRLPACCRE 1261
Db 858 PAPGHECNGRMP--TAKOVFTKMGDRGDEBEEDYTLCTFRVRQMDVYKEDWCEV 915
Qy 1262 RDSMSAYIFPPQSRFLLCRRITTHKMPDHVVLVIIFLNCITIAMERPKIDPHSAERIFL 1321
Db 916 REDMSVYLFSPENRFLVCTIIAHLFDVYVLAFLNCITIALERQIEAGSTERIFL 975
Qy 1322 TLSNYITAVFLAMTVKVALGWCFCGEQAYLRSSNVNLDGLLVLSVIDILVSMVDSG 1381
Db 976 TVSNYIFTAIPVGEMTLKWSLGLYFGEQAYLRSSNVNLDGLVFSVIDIWSLASAGG 1035
Qy 1382 TKILGMLRVLRLTLRLPLRVISRAQGLKLVETLMSSLKPIGNTVIWCAPFIIFGLG 1441
Db 1036 AKILGVLRVLRLTLRLPLRVISRAQGLKLVETLISLKPIGNTVIWCAPFIIFGLG 1095
Qy 1442 VQLFKGKFFVQCQGEDTRNTNKSDCAEASVRWRHKNFNDLQALMSLFLVASKDGWD 1501
Db 1096 VQLFKGKFFVCLGVDTNTRNSDCMAANYRWVHHKYNFNDLQALMSLFLVASKDGWN 1155
Qy 1502 IMYDGLDAVGVDQOPINWHPMMLLYFISFLIIIVAFVFLVNMVGVVVFENFKCRHQBE 1561
Db 1156 IMYNGLDVAVDQOPVTNHPMMLLYFISFLIIIVSFFVLMNVGVVVFENFKCRHQBE 1215
Qy 1562 EARRERKRLRLLEKRSKEKQMAEAOCKPYSDYSRFRLLVHLCTSHVLDLPTGVI 1621
Db 1216 EARRERKRLRLLEKRR-----KAQRLPYATYCHTRLIIHSMCTSHYLDLPTITFI 1269
Qy 1622 GLNVVTWAMEHYQOQILDEALKICNYITFTVIFVESVFLVAFARFRFFQDRWNQDLA 1681
Db 1269 CLNVVTWLSLEHYNQPTSLTALKYCNMYFTTVFVLEAVLKLVAFLGRFFKDRWNQDLA 1328
Qy 1682 IVLLSINGITLLEIEVNLSPINPTIIRIMVRLIARVLRKLLKLVAVGNRALLHTVMQALP 1741
Db 1329 IVLLSVMGITLLEIEINAALPINPTIIRIMVRLIARVLRKLLKLVAVGNRALLHTVMQALP 1389
Qy 1742 QVGNLGLLFWLFFIFALGVLELGDCEDETHCEGIGHATFRNCGMAFLTFPRVSTG 1801
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Db 1389 QVGNLGLL FMLLPIFYAALGVLEFGKLVNCDENPCGMSRHATFNFQMAFLTLFQVSTG 1448
Qy 1802 DNWNGIMKDPDRDC-DOESTCYNTV--ISPIYFVSFVLTAQFVLVNVVIAVLMKHLEEN 1858
Db 1449 DNWNGIMKDLTRDCTHDSRCLSLQVSPFLYFVSFVLTAQFVLVNVVIAVLMKHLDSDN 1508
Qy 1859 KEAKEBAELAELELEM-KTSLQPHSPGLSP----- 1889
Db 1509 KEAQEDAEMAELELEMAHGLGPGFRLPTSGPAGPGPGGAGGGGTGGLCRRCYCSPA 1568
Qy 1890 --FLW-----PGVEG-VNSTDSPKPGAPHTTAHGAASG----- 1920
Db 1569 QENLWDSVLI I KDSLEGLTIDNLGSGIFH---HYSSPAGCKKHDKQEVQLAETE 1625
Qy 1921 -----FSLHPTMP-----HPEEVPV-PLGPDILTVRKSGV 1951
Db 1626 AFSLNSDRSSILLGDDLSLEDTACPPGRKDSKGELDPPEPMRVGLDGCFFPLSGTAV 1685
Qy 1952 SRTHSLPN-DSYCMRNGSTAERSI-GHRGWGLPKAQSGLSVHSQPADTSCILQLPKDVH 2010
Db 1686 S-----PDENFLCEMEIIPNPV--RSW--LKHDSSQAPSPSPDASSPLLPMPAEFF 1736
Qy 2011 Y-----LLQPHGAPTWGAIPKLPPPG-----RSLAQRPLRQAAIRTSLDVQGLGR 2059
Db 1737 HPAVASAKQPEKGTGTGTLPKIALQGSWASLRSPVNCITLLRQATGSDTSLDAS----- 1791
Qy 2060 EDLLSEVSGPCPLTRSSFWGSGSIQVQORSIGQSKVSHIRLPAPCGLEPSWAXDPP 2119
Db 1792 -----PSSAGSLQTTLEDLSLSDSPRRAIGPPAPAG----- 1825
Qy 2120 ETRSSLELDTLSWISGDLPSQEEPLFPRLDLKKCYSVETQSCRRRPFGLWLDQRHSI 2179
Db 1826 -----PRAGLSPAARRL-----SLRGRGLSLRGLRAHOR 1856
Qy 2180 AVSCLDSSGQRLCSPSSL-----GQPLGPGSGRPKKLSPPSIS---IDPPESQ 2228
Db 1857 SHS---SGGSTPGCTHDSMDPDSDEGRGGAGGAGSEHSETLSLSLTLFCPPP--- 1911
Qy 2229 GSRPCSGVCLRR-----RAP-----ASDSKDSVSPSLDST 2261
Db 1912 ---PPAPGLTPTARKFSSTSLAAGRPHAALAHGLARSWAADRSKDPGRAPLPMG 1968
Qy 2262 AASPSPKDTLSLSGLSDPTMDP 2286
Db 1969 LGPLAPPQPL-----PGELEP 1985

RESULT 13
Q7POV4 PRELIMINARY; PRT; 1762 AA.
AC Q7POV4;
DT 01-MAR-2004 (TReMBLrel. 26, Created)
DT 01-MAR-2004 (TReMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE ENSANGP0000003024 (Fragment).
GN Name=ENSANG00000002480;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
ON NCBI_TaxID=180454;
RX [1]
RN SEQUENCE FROM N.A.
RP STRAIN=PEST;
RC Anopheles Genome Sequencing Consortium;
RA Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
RL -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC EMBL; AAA01008859; EAA08229.2; -
DR GO:0016021; C:integral to membrane; IEA.
DR GO:0005261; F:cation channel activity; IEA.
DR GO:0005245; F:voltage-gated calcium channel activity; IEA.
DR GO:0006816; P:calcium ion transport; IEA.

DR GO:0006812; P:cation transport; IEA.
DR InterPro; IPR001682; Ca/Na_pore.
DR InterPro; IPR002111; Cat channel_TrpL.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR005820; M+channel_nlg.
DR InterPro; IPR005445; TVDCCALPHAL.
DR Pfam; PF00520; Ion_trans; 4.
DR PRINTS; PR01629; TVDCCALPHAL.
KW Ion transport; Ionic channel; Transmembrane; Transport.
FT NON_TER 1762 1762
SQ SEQUENCE 1762 AA; 199928 MW; AF70F5349068EDE2 CRC64;

Query Match 34.8%; Score 4188.5; DB 2; Length 1762;
Best Local Similarity 48.9%; Pred. No. 1.4e-196;
Matches 918; Conservative 270; Mismatches 457; Indels 231; Gaps 49;

Qy 114 WFERVSMVLILNCVTGLMFRCEDIACDSQRCILQAFDDFIFFAFAVEMVVKVALGI 173
Db 2 WFERISMLVILLNCVTGLMYPQVDDACVTRCKLIQIFDDIIFAFSLEMTIKIVAMGA 61

Qy 174 FGKCKYLGDTNRLDFFIVIAQMLBYSLDLQNVFSASVTRVLRPLRAINRVPMSRLIV 233
Db 62 WKGCTVLADSWRLDFFIVLAGALEVCLQVENLNTAIRTIVLRPLRAINRIPMSRLIV 121

Qy 234 TLLDLPMLGNVLLCFVFFIFGIVGVQLWAGLLNRCF--LPENFSLPLSVDLPEYV 291
Db 122 MLLDLPMLGNVLLCFVFFIFGIVGVQLWAGLLNRQRCVKLPDNVS--PPSYLVSFY 180

Qy 292 QTENEDESFIQSCPENGMRSRSPVTLRGEGGGP---PCSLDYETYNSSNTTCVN 347
Db 181 EFSKEQD--YICSPEDSGHMLCONLPYR---IGPLCNDLSALPY--SENEPTATACVN 233

Qy 348 WNOYTYNCAGEINPFKGAINFEDNIGYAMIAIQVITLEGWVDIMYFVMDAISFYNIIF 407
Db 234 WNOYTYNCIQGNPFGTISFDNIGLAWVAIFLVISLEGWTDIMYVQDAHSFMDWYIF 293

Qy 408 ILIIVGSPFMNCLVVIATQPSYKQESQLMREQVRFLSNASTLASF---SPGSC 464
Db 294 VLLIVIGSPFMNCLVVIATQPSYKQESQLMREQVRFLSNASTLASF---SPGSC 352

Qy 465 YEELLKYLVLKAAARLAQVSRAGLSSPVARSGQPPQSPGSGSTRSHRLSVH 524
Db 353 YAEIVKYIGHLYRRFKRLIK-----KLRLYKYHMQKKEGLIPTPETITLSPNKAH 407

Qy 525 H-----LVHHH-----HHHHYHLNGTLVRPASPEIQDRDANGSRRLMLPPPS 570
Db 408 HPKCPRMGALLQOQHASITNLQOQKXKHDILQSSLSINRTGVTLNH-----PEPG 456

Qy 571 TPTPSG---GPPRGESV-----HSFYHADCHLEPVRCOAPPPPCPSE--ASGRTVG 617
Db 457 TIVPSADNVQSPSEVSEIVSLENIKNALNNSTYLNEDRKVLLKINNEDQSNQVVG 516

Qy 618 SGKYVPTV-----HTSP-----PPEILKOKALV---EVAPSPGPPT 650
Db 517 MGWLGNWVEGRSTFEQSSSLAPQDHCMPSLLSPSAGRRSSWMFVYVVLHTPT 576

Qy 651 LTSFNIIPGFPSSMHKLELTQSTGACHSSCKISPCSKADSGAGGDCPCYCARTGAGEP 710
Db 577 ITE---PFQDKNVY--CLEKMTQAAANPATSRRAPAST---RCRPASTTSTWRS----- 622

Qy 711 ESADHVMPSDSEAVYEFTQDAQHSDLRDPHSRRRQRSLGPDAPSPSVLAFWRLICDTFR 770
Db 623 -----LP-----AATSTTKTRAWRRSDRSAPSARGSRWCFRRTCHLTR 663

Qy 771 ----KIVDSKYFGRGIMAILVNTLSMGIEYHEQPELTNALEISNIVFTSLFALEMLK 826
Db 664 VLVKLVVDHKYFQOQILLAILINTLSMGIEYHDQPAELTAIVETSNTVFSIFAFAVEMILK 723

Qy 827 LLVVGPGCYIKNPYNIQDGVTVLVSWEI-----VQOQGGGLSVLRTFRLMRVLKVR 880
Db 724 VIABGPFYVANGFNVDGVIVILSVVELGQSYLGEQSGSLSVLRTFRLLRILKLVRF 783

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 13, 2005, 16:00:31 ; Search time 243 Seconds
(without alignments)
3606.580 Million cell updates/sec

Title: US-09-611-257A-37
Perfect score: 11904
Sequence: 1 MDEEDGAGAEESQPRSF.....PKDVLISLGLSDPADLDP 2266

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04.*
1: Geneseq1980s.*
2: Geneseq1990s.*
3: Geneseq2000s.*
4: Geneseq2001s.*
5: Geneseq2002s.*
6: Geneseq2003as.*
7: Geneseq2003bs.*
8: Geneseq2004as.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	11862.5	99.7	2273	AAE01019	Aae01019 Human T-t
2	11815.5	99.3	2377	ADQ89064	Adq89064 Human uro
3	11758.5	98.8	2243	AAy14589	Aay14589 Human T-t
4	11758.5	98.8	2243	ADJ68819	Adj68819 Human hea
5	11741	98.6	2250	AAy14586	Aay14586 Human T-t
6	11735.5	98.6	2261	AAy14587	Aay14587 Human T-t
7	11727	98.5	2268	AAy14588	Aay14588 Human T-t
8	11653	97.9	2266	AAAB66481	Aab66481 Human alp
9	11111	93.3	2428	AAy70720	Aay70720 Rat pancr
10	10962.5	92.1	2247	AAy14593	Aay14593 Rat T-typ
11	10945	91.9	2254	AAy14590	Aay14590 Rat T-typ
12	10939.5	91.9	2265	AAy14591	Aay14591 Rat T-typ
13	10925	91.8	2272	AAy14592	Aay14592 Rat T-typ
14	10774	90.5	2287	AAAB66475	Aab66475 Rat alpha
15	6315.5	53.1	1207	AAU00474	Aau00474 Human T-t
16	6218	52.2	2359	AAAB66476	Aab66476 Rat alpha
17	6212	52.2	2353	AAy06299	Aay06299 Human act
18	6212	52.2	2353	ABP72254	Abp72254 Human T-t
19	6212	52.2	2353	ADJ69322	Adj69322 Human hea
20	6211	52.2	2353	AAy06298	Aay06298 Human act
21	6178	51.9	2353	ABG30840	Abg30840 Human vol
22	5855.5	49.2	2038	AAy14595	Aay14595 Human T-t
23	5845.5	49.1	2044	AAy14594	Aay14594 Human T-t
24	5709.5	48.0	2034	AAy06300	Aay06300 Human act
25	5492.5	46.1	2175	AAU010535	Aau010535 Human T-t

26	5492.5	46.1	2175	6	ABU08511	Abu08511 Human T-t
27	5492.5	46.1	2175	8	ADH65265	Adh65265 Human TCC
28	5484	46.1	2188	5	AAU10536	Aau10536 Human T-t
29	5484	46.1	2188	6	ABU08512	Abu08512 Human T-t
30	5484	46.1	2188	8	ADH69267	Adh69267 Human TCC
31	5366	45.1	1835	2	AAy14597	Aay14597 Rat T-typ
32	5366	45.1	1835	8	ADH69268	Adh69268 Rat T-typ
33	5361.5	45.0	1823	2	AAy14596	Aay14596 Human T-t
34	5198.5	43.7	1792	4	AAAB66477	Aab66477 Rat brain
35	5043.5	42.4	982	4	AAAM23743	Aam23743 Human EST
36	3959.5	33.3	1854	2	AAW79161	Aaw79161 Human cal
37	3959.5	33.3	1854	4	AAAB66472	Aab66472 Protein e
38	3564.5	29.9	1657	8	ADN24183	Adn24183 Bacterial
39	3442	28.9	2435	4	ABBB60448	Abb60448 Drosophil
40	3427	28.8	644	4	AAAB66478	Aab66478 Human alp
41	3020.5	25.4	1859	4	ABGL10954	Abg10954 Novel hum
42	1960	16.5	853	4	AAAM93437	Aam93437 Human pol
43	1960	16.5	853	8	ADL31041	Adl31041 Human pro
44	1753	14.7	2264	8	ADM31026	Adm31026 Human cal
45	1752.5	14.7	2339	2	AAAR33549	Aar33549 Sequence

ALIGNMENTS

RESULT 1

AAE01019
ID AAE01019 standard; protein; 2273 AA.

AC AAE01019;

DT 17-JUL-2001 (first entry)

XX Human T-type low voltage activated calcium channel alpha1G-c protein.
XX Human T-type low voltage activated calcium channel alpha1G-c; stress; epilepsy; schizophrenia; depression; sleep disorder; Cushing's disease; endocrine disorder; respiratory disorder; peripheral muscle disorder; muscle excitability; fertilisation; contraception; hypertension; neuronal firing regulation; cardiovascular disorder; gene therapy; forensic analysis; epidemiological study; neuroleptic.
XX Homo sapiens.

XX Key Location/Qualifiers
FH Misc-difference 1138 /note= "Encoded by GAG"
FT Misc-difference 1142 /note= "Encoded by GAA"
FT Misc-difference 1680 /note= "Encoded by ACG"
FT Misc-difference 1683 /note= "Encoded by GAA"

PN WO200130844-A1.

XX 03-MAY-2001.

XX 06-OCT-2000; 2000WO-US027761.

XX 26-OCT-1999; 99US-00426998.

XX (ORTH) ORTHO-MCNEIL PHARM INC.

XX Dublin AE, Galindo JE, Pyati J, Zhu JY, Erlander MG;

XX WPI; 2001-300486/31.

XX N-ESDB; AAD04756.

XX New nucleic acid encoding human calcium channel protein, useful for identifying specific modulators and potential pharmaceuticals for treating e.g. epilepsy.

XX

QY 1794 LRDCDOESTCYNTWISPIYFVSFVLTAQVFLVNWVIAVMKHLBESNKEAELEAEL 1853
Db |||||||
QY 1801 LRDCDOESTCYNTWISPIYFVSFVLTAQVFLVNWVIAVMKHLBESNKEAELEAEL 1860
Db |||||||
QY 1854 ELEMKTLSPOHSPILGSPFLWPGVEGPDSPKPGALHPAAHARSASHFSLEHPTWOPH 1913
Db |||||||
QY 1861 ELEMKTLSPOHSPILGSPFLWPGVEGPDSPKPGALHPAAHARSASHFSLEHPTWOPH 1920
Db |||||||
QY 1914 PTELPGPDLLTVRKSGVSRTHSLPNDNSYMCRRHGSTAEGPLGHRGWGLPKAQSGLSVLSVHS 1973
Db |||||||
QY 1921 PTELPGPDLLTVRKSGVSRTHSLPNDNSYMCRRHGSTAEGPLGHRGWGLPKAQSGLSVLSVHS 1980
Db |||||||
QY 1974 QPADTSYLQPKAPHLLOHSAPTWCTIPIKLPGRSPLAORPLRQAAIRTDSDVQ 2033
Db |||||||
QY 1981 QPADTSYLQPKAPHLLOHSAPTWCTIPIKLPGRSPLAORPLRQAAIRTDSDVQ 2040
Db |||||||
QY 2034 GLGSRDILLAEVSGSPPLARAYFWGQSSSTQAQOHSRSHSKISKHMTTPAPCPGPEPNW 2093
Db |||||||
QY 2041 GLGSRDILLAEVSGSPPLARAYFWGQSSSTQAQOHSRSHSKISKHMTTPAPCPGPEPNW 2100
Db |||||||
QY 2094 KGKPPETRSSLELDTLSWISGDLPLPGQBEPPSPDLKKCYVSAQSCORRPTSMWDE 2153
Db |||||||
QY 2101 KGKPPETRSSLELDTLSWISGDLPLPGQBEPPSPDLKKCYVSAQSCORRPTSMWDE 2160
Db |||||||
QY 2154 QRRHSIAVCLDSGSOHLGTDPSNLGGQPLGGSPRKKLSPPSITIDPPESQGRTP 2213
Db |||||||
QY 2161 QRRHSIAVCLDSGSOHLGTDPSNLGGQPLGGSPRKKLSPPSITIDPPESQGRTP 2220
Db |||||||
QY 2214 PSPGICLRRRAPSDSKDPLASGPPDSMAASPSPKKDVLSLSGLSSDDPADLDP 2266
Db |||||||
QY 2221 PSPGICLRRRAPSDSKDPLASGPPDSMAASPSPKKDVLSLSGLSSDDPADLDP 2273
Db |||||||

RESULT 2

ADQ89064
ID ADQ89064 standard; protein; 2377 AA.
AC ADQ89064;
XX
XX
DT 21-OCT-2004 (first entry)
XX
XX
DE Human urological disorder related protein 4421 SEQ:16.
XX
XX
KW urological disorder; uropathic; cytostatic; urinary incontinence;
KW benign prostatic hyperplasia; human.
XX
XX
OS Homo sapiens.
XX
XX
PN WO2004065576-A2.
XX
XX
PD 05-AUG-2004.
XX
XX
PF 14-JAN-2004; 2004WO-US000750.
XX
XX
PR 15-JAN-2003; 2003US-0440318P.
PR 04-FEB-2003; 2003US-0444783P.
PR 27-MAR-2003; 2003US-0457901P.
PR 08-MAY-2003; 2003US-0468775P.
PR 19-MAY-2003; 2003US-0471614P.
PR 16-JUN-2003; 2003US-0478742P.
PR 18-JUL-2003; 2003US-0488529P.
PR 30-JUL-2003; 2003US-0491156P.
PR 02-SEP-2003; 2003US-0499594P.
PR 26-SEP-2003; 2003US-0506332P.
XX
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
XX
FI Karicheti V, Silos-Santiago I, Eliasof SD;
XX
XX
DR WPI; 2004-562167/54.
DR N-PSDB; ADQ89063.
XX
XX

PT Use of polypeptides related to urological disorders, e.g. 44390, 54181,
PT 211 or for identifying a compound capable of treating a urological
PT disorder or identifying and treating a subject having a urological
PT disorder.
XX
XX
PS Claim 1; SEQ ID NO 16; 542pp; English.
XX
CC The present invention describes the use of polypeptides related to
CC urological disorders for identifying a compound capable of treating a
CC urological disorder, identifying a subject having a urological disorder,
CC or treating a subject having a urological disorder. Also described: (1) a
CC method for identifying a compound capable of treating a urological
CC disorder; (2) a method for identifying a subject having a urological
CC disorder; and (3) a method for treating a subject having a urological
CC disorder. The compound has uropathic and cytostatic activities. The
CC polypeptides related to urological disorders are useful for identifying a
CC compound capable of treating a urological disorder, identifying a subject
CC having a urological disorder, or treating a subject having a urological
CC disorder. Disorders include urinary incontinence and benign prostatic
CC hyperplasia. The present sequence represents a human urological disorder
CC related protein, which is used in the exemplification of the present
CC invention.
XX
SQ Sequence 2377 AA;

Query Match 99.3%; Score 11815.5; DB 8; Length 2377;
Best Local Similarity 95.2%; Pred. No. 0;
Matches 2264; Conservative 1; Mismatches 1; Indels 111; Gaps 2;
QY 1 MDEEDGAGAEESGQPRSFMRNLDSGAGGPRGPGSAEKDPGSADSEAEGLYPALAPV 60
Db 1 MDEEDGAGAEESGQPRSFMRNLDSGAGGPRGPGSAEKDPGSADSEAEGLYPALAPV 60
QY 61 FFYLSQDSRPRSWCLRTVCNPFWRISMLVILLNCVTILGMFRPCEDIAQSQRILQAF 120
Db 61 FFYLSQDSRPRSWCLRTVCNPFWRISMLVILLNCVTILGMFRPCEDIAQSQRILQAF 120
QY 121 DDFIFAFVAVEMVVMVALGIFGKKCYLGDFTWNRDLFFIVIAAGMLEYSLDLQNVSFSAVR 180
Db 121 DDFIFAFVAVEMVVMVALGIFGKKCYLGDFTWNRDLFFIVIAAGMLEYSLDLQNVSFSAVR 180
QY 181 TVRVLRPLRAINRVPMSRILVLLDLTLPMLGNVLLCFFVFFIFGIVGVOLWAGLLNR 240
Db 181 TVRVLRPLRAINRVPMSRILVLLDLTLPMLGNVLLCFFVFFIFGIVGVOLWAGLLNR 240
QY 241 CFLPENFSLPLVDLERYQTENEDESPFICSPRENGMRSCRSVPTLRGDDGGPPCGL 300
Db 241 CFLPENFSLPLVDLERYQTENEDESPFICSPRENGMRSCRSVPTLRGDDGGPPCGL 300
QY 301 DYEAYNSSNTTCVNNQYVYTNCSAGEHNPFGAINFDNIGYAWIAIFQVITLEGWVDM 360
Db 301 DYEAYNSSNTTCVNNQYVYTNCSAGEHNPFGAINFDNIGYAWIAIFQVITLEGWVDM 360
QY 361 YFVMDAHSFYNIYFILLIIVGSFFMINLCLVATATOFSETKQRESQMRQRVFLSNA 420
Db 361 YFVMDAHSFYNIYFILLIIVGSFFMINLCLVATATOFSETKQRESQMRQRVFLSNA 420
QY 421 STLASFSEPGSCYBELLYLILRKAARRLAQVSRAGVRVGLSSPAPLGQETQPS 480
Db 421 STLASFSEPGSCYBELLYLILRKAARRLAQVSRAGVRVGLSSPAPLGQETQPS 480
QY 481 SCRSRRLSVHLLVHHHHHHHHYHLNGTILRAPRASPEIQDRDANGSRRLMLPPPSTP 540
Db 481 SCRSRRLSVHLLVHHHHHHHHYHLNGTILRAPRASPEIQDRDANGSRRLMLPPPSTP 540
QY 541 ALSCAPPGGAESVHSFYHADCHLEPVRCOAPPPPSSEASGRTVSGKVYPTVHTSPPE 600
Db 541 ALSCAPPGGAESVHSFYHADCHLEPVRCOAPPPPSSEASGRTVSGKVYPTVHTSPPE 600
QY 601 TLKEKALVEVAASSGPPTLTSLNIPPGPYSSMHKLLTQSTGACQSSCKISSPLKADSG 660
Db 601 TLKEKALVEVAASSGPPTLTSLNIPPGPYSSMHKLLTQSTGACQSSCKISSPLKADSG 660

QY	661	ACGPDSCPYCARAGAGVEVLADREMPDSDSEAYVEFTQDAQHSDDLDPHRRRQORSIGPDA	720	Db	1741	POVGNLGLLFWLLFFIFAALGVLEFGDLECDTHPCBCEGLGRHATFRNFGMAFLTLFRVST	1800
Db	661	ACGPDSCPYCARAGAGVEVLADREMPDSDSEAYVEFTQDAQHSDDLDPHRRRQORSIGPDA	720	QY	1783	GDNNWNGIMKOTLRCDQESCTCYNTVISPFIYFVSFLTAQFVNVVIAVLMKHLSEENKE	1842
QY	721	EPSSVLAFWRLICDTFRKIVDSKYFGRGIMAILVNTLSNGIYHPOBELTNALEISNI	780	Db	1801	GDNNWNGIMKOTLRCDQESCTCYNTVISPFIYFVSFLTAQFVNVVIAVLMKHLSEENKE	1860
Db	721	EPSSVLAFWRLICDTFRKIVDSKYFGRGIMAILVNTLSNGIYHPOBELTNALEISNI	780	QY	1843	AKERAELAELEEMKLTLSPOPHSPLGSPFLWPGVEGPDSPSPKPGALLHAAHARSASH	1902
QY	781	VFTSLFALEMLLKVLPVGPFGYIKNPYINFDGVIVVISWEIVGQGGGLSVLRTFRLMR	840	Db	1861	AKERAELAELEEMKLTLSPOPHSPLGSPFLWPGVEGPDSPSPKPGALLHAAHARSASH	1920
Db	781	VFTSLFALEMLLKVLPVGPFGYIKNPYINFDGVIVVISWEIVGQGGGLSVLRTFRLMR	840	QY	1903	FSLEHPT-----	1909
QY	841	VKLVRFLPALQRLVLMKTMNVATFCMLMLFIFIPISILGMHLPGCKFASERDGTIL	900	Db	1921	FSLEHPTDQLFDFTISLIIQGSLEWELKMDLDELAPGQSPAPSPSAPSLGSGDPOIPLAE	1980
Db	841	VKLVRFLPALQRLVLMKTMNVATFCMLMLFIFIPISILGMHLPGCKFASERDGTIL	900	QY	1910	-----MQPHPTLPGPDLLTVRKSG	1929
QY	901	PDRKNFDSLLWAIIVTVFQILTOEDWNKVLVNGMASTSSWAALVFIALMTGNTVLFNLV	960	Db	1981	MEALSITSEIIVSEPPSCSALATDSDSLPDDMTLILLSALESNNMQPHPTLPGPDLLTVRKSG	2040
Db	901	PDRKNFDSLLWAIIVTVFQILTOEDWNKVLVNGMASTSSWAALVFIALMTGNTVLFNLV	960	QY	1930	VSRTHSLPNDSTYMCRRHGTAEGLHGRWGGLPKAQSGLSVLSVHSGPADTSYILQPKDAP	1989
QY	961	AILVEGFOAEISKEEDASGOLSCIQLPVDQSOGGDANKSESEPFPSLDGDRKKCL	1020	Db	2041	VSRTHSLPNDSTYMCRRHGTAEGLHGRWGGLPKAQSGLSVLSVHSGPADTSYILQPKDAP	2100
Db	961	AILVEGFOAEISKEEDASGOLSCIQLPVDQSOGGDANKSESEPFPSLDGDRKKCL	1020	QY	1990	HLLQPHSAPTWTGIIPKLPPGCSPLAQRLRQAARTDSDVQGLSREDLLAEVSGPS	2049
QY	1021	ALVSLGEHPELRKSLPLPILITHAATPMSLPKSTSTGLGEALGPASRTSSSGSAEPGAA	1080	Db	2101	HLLQPHSAPTWTGIIPKLPPGCSPLAQRLRQAARTDSDVQGLSREDLLAEVSGPS	2160
Db	1021	ALVSLGEHPELRKSLPLPILITHAATPMSLPKSTSTGLGEALGPASRTSSSGSAEPGAA	1080	QY	2050	PPLARAYSWGQSSSTQAQOHSRSHSKISKHMTPPAPCPGPEPNWKGKPPETRSSLELDT	2109
QY	1081	HEMKSPPARSPHSPWGAASWTSRRSRNSLGRAPSLKRRSPSGERRSLLSGEGQESQ	1140	Db	2161	PPLARAYSWGQSSSTQAQOHSRSHSKISKHMTPPAPCPGPEPNWKGKPPETRSSLELDT	2220
Db	1081	HEMKSPPARSPHSPWGAASWTSRRSRNSLGRAPSLKRRSPSGERRSLLSGEGQESQ	1140	QY	2110	LSWISGDLPPGQOBEPPSPROLKKCYSEACORRPTSWLDEORRHISIAVSCLDGSGQ	2169
QY	1141	DEEESSEERASPDGHRHGRSLBREKASFPDLPTLOVGLHRTASGRGSAEHQDCN	1200	Db	2221	LSWISGDLPPGQOBEPPSPROLKKCYSEACORRPTSWLDEORRHISIAVSCLDGSGQ	2280
Db	1141	DEEESSEERASPDGHRHGRSLBREKASFPDLPTLOVGLHRTASGRGSAEHQDCN	1200	QY	2170	PHLGTDPNLGGQPLGCGSRPKKLSPPSITIDPPESQGPRTTSPGICLRRRAPSSDS	2229
QY	1201	GKSASGLARALRPDPPDLGGDDADDEGNLSKGERVRAWIRARLPACCLERDSWAVIFP	1260	Db	2281	PHLGTDPNLGGQPLGCGSRPKKLSPPSITIDPPESQGPRTTSPGICLRRRAPSSDS	2340
Db	1201	GKSASGLARALRPDPPDLGGDDADDEGNLSKGERVRAWIRARLPACCLERDSWAVIFP	1260	QY	2230	KDPLASGPPDSMAASPPKDVLSLGLSSDDPADLDP	2266
QY	1261	PQSRFLCHRIITHKMPDHVVLVIFLNCITIAMERPKIDPHSAERIFLTSNVIPTAV	1320	Db	2341	KDPLASGPPDSMAASPPKDVLSLGLSSDDPADLDP	2377
Db	1261	PQSRFLCHRIITHKMPDHVVLVIFLNCITIAMERPKIDPHSAERIFLTSNVIPTAV	1320	RESULT 3			
QY	1321	FLAEMTVKVALGWCFCGEQAYLRSSWNVDGLLVLSIDILVMSVDSGTKILGMLRVL	1380	AA14589			
Db	1321	FLAEMTVKVALGWCFCGEQAYLRSSWNVDGLLVLSIDILVMSVDSGTKILGMLRVL	1380	ID	AA14589	standard; protein; 2243 AA.	
QY	1381	RLRLTLRLRVLISRAQGLKLVVETLMSLKPIGNIVVICAPFIIFGILGVQLFKGKFFV	1440	XX	AA14589;		
Db	1381	RLRLTLRLRVLISRAQGLKLVVETLMSLKPIGNIVVICAPFIIFGILGVQLFKGKFFV	1440	AC			
QY	1441	COGEDTRNITKSDCAEASVWRVHKYFNFDNLGOALMSLFLVASKDGDWDIMYDGLDVG	1500	XX	07-DEC-1999	(first entry)	
Db	1441	COGEDTRNITKSDCAEASVWRVHKYFNFDNLGOALMSLFLVASKDGDWDIMYDGLDVG	1500	DT			
QY	1501	VDOQPINMHPMMLLFIISFLLVAFVFLNMVGVVVENFHKCRQHOEEEAARRREKRL	1560	XX		Human T-type voltage-gated Ca channel alpha-1-G (hCavTid).	
Db	1501	VDOQPINMHPMMLLFIISFLLVAFVFLNMVGVVVENFHKCRQHOEEEAARRREKRL	1560	DE		Human; T-type voltage-gated calcium channel; membrane; pore; ion;	
QY	1561	RRLEKKRR-----KAQCKPYYSRFRLLVHLCTSHYLDLPTITGV	1602	KW		activation; current; rat; screen; drug; cardiomyopathy; epileps.	
Db	1561	RRLEKKRR-----KAQCKPYYSRFRLLVHLCTSHYLDLPTITGV	1602	KW			
QY	1603	IGLNVVTWAMEHYOQPOLDEALKICNYIFTVIFVLESVEKLVAFGRFRFFQDRMNQDL	1662	OS		Homo sapiens.	
Db	1621	IGLNVVTWAMEHYOQPOLDEALKICNYIFTVIFVLESVEKLVAFGRFRFFQDRMNQDL	1680	XX	WO9929847-Al.		
QY	1663	AIVLISIMGITLEIEVNASLPINPTIIRIMRVLIARVLKLMVGMARLLDTWQAL	1722	PN			
Db	1681	AIVLISIMGITLEIEVNASLPINPTIIRIMRVLIARVLKLMVGMARLLDTWQAL	1740	PD	17-JUN-1999.		
QY	1723	POVGNLGLLFWLLFFIFAALGVLEFGDLECDTHPCBCEGLGRHATFRNFGMAFLTLFRVST	1782	PF	30-OCT-1998; 98WO-U023161.		
				PR	05-DEC-1997; 97US-00985809.		
				XX	(LOYO) UNIV LOYOLA CHICAGO.		
				PI	Perez-Reyes E, Cribbs LL;		
				XX	WPI; 1999-394972/33.		
				DR	N-PSDB; AAX83484.		

XX	PT	New T-type voltage-gated calcium channels.	Qy	661	ACGPDSCPCYCARAGAGEVELADREMPDSSEAVYEFTQDAQHSDLRDPHSRQRSILGPPA	720
XX	XX	Disclosure; Page 58-67; 138pp; English.	Db	661	ACGPDSCPCYCARAGAGEVELADREMPDSSEAVYEFTQDAQHSDLRDPHSRQRSILGPPA	720
XX	FS		Qy	721	EPSSVLAFWRLLICDTFRKI VDSKVFGRGIMTALVNTLSMGTYEHEQPEELTNALEISNI	780
XX	CC	This sequence represents a human T-type voltage-gated calcium (Ca)	Db	721	EPSSVLAFWRLLICDTFRKI VDSKVFGRGIMTALVNTLSMGTYEHEQPEELTNALEISNI	780
CC	CC	channel alpha-1-G designated hCav1d. Voltage gated channels are membrane	Qy	781	VFTSLFALEMLLKLLVYGPFGYIKNPYNI FGVIVIVISWEIVGQGGSLVLTFRMLR	840
CC	CC	bound glycosylated proteins formed of several subunits. The large alpha	Db	781	VFTSLFALEMLLKLLVYGPFGYIKNPYNI FGVIVIVISWEIVGQGGSLVLTFRMLR	840
CC	CC	subunits form a pore in the membrane that is selective for a given ionic	Qy	841	VLKLVRELPAQRQLVLMKTMNDVATFCMLLMLEFIFSTILGMHLFCCKFASERDGT	900
CC	CC	species. Each alpha subunit contains 4 domains (I, II, III and IV) and	Db	841	VLKLVRELPAQRQLVLMKTMNDVATFCMLLMLEFIFSTILGMHLFCCKFASERDGT	900
CC	CC	each domain contains 6 putative transmembrane helical segments (S1-S6). T	Qy	901	PDRKNFDSLLWAIIVTFQILTQEDWNKVLVNGMASTSSWAALYFIALMTFGNYVLFNLIV	960
CC	CC	-type Ca channels are activated at a lower voltage than L- or N-type	Db	901	PDRKNFDSLLWAIIVTFQILTQEDWNKVLVNGMASTSSWAALYFIALMTFGNYVLFNLIV	960
CC	CC	channels. Characteristics of T-type channels include short current time,	Qy	961	AILVEGFOAEISKREDASGQLSCIQLPVDVSGGDKANKSESEPDFFPSLSDGDRKKCL	1020
CC	CC	slow activation kinetics near threshold, fast inactivation kinetics and	Db	961	AILVEGFOAEISKREDASGQLSCIQLPVDVSGGDKANKSESEPDFFPSLSDGDRKKCL	1020
CC	CC	slow tail current. The sequences AAX83481-X83492 represent novel T-type	Qy	1021	ALVSLGEHPELRKSLPLPLIIHTAATPMSLPKSTSTGLGEALGPASRRTSSSGSAREPNA	1080
CC	CC	voltage-gated Ca channel genes from humans and rats. Each of the novel Ca	Db	998	ALVSLGEHPELRKSLPLPLIIHTAATPMSLPKSTSTGLGEALGPASRRTSSSGSAREPNA	1057
CC	CC	-channels contains a putative IVS4 region comprising the amino acid	Qy	1081	HEMKSPPSARSPSPHSAASWTSSRSRNSLGRAPSLKRRSPSGERRSLLSGGQSGSQ	1140
CC	CC	sequence AAY14598. Cells expressing the T-type voltage-gated calcium	Db	1058	HEMKSPPSARSPSPHSAASWTSSRSRNSLGRAPSLKRRSPSGERRSLLSGGQSGSQ	1117
CC	CC	channel proteins can be used to screen for drugs which affect calcium	Qy	1141	DEESSSEERASPAGSDHRRHRSGLEREAKSFDLPDTLQVPLGHRHTASGRGSAHQDCN	1200
CC	CC	channels. Methods are also disclosed for treating a disease or disorder	Db	1118	DEESSSEERASPAGSDHRRHRSGLEREAKSFDLPDTLQVPLGHRHTASGRGSAHQDCN	1177
CC	CC	associated with a deficiency in a native T-type calcium channel nucleic	Qy	1201	GKSASGLARALRDPDDPLDGDADDDEGNLSKGRVRAWIARLACVLERDSWYATFP	1260
CC	CC	acid, e.g. to treat cardiomyopathy, epilepsy, etc	Db	1178	GKSASGLARALRDPDDPLDGDADDDEGNLSKGRVRAWIARLACVLERDSWYATFP	1237
XX	SQ	Sequence 2243 AA;	Qy	1261	QPSFRLLCHRIITHKMPDHVVLVII FLNCITIAMERPKIDPHSAERIFLTLSNYIFAV	1320
		Query Match 98.8%; Score 11758.5; DB 2; Length 2243;	Db	1238	QPSFRLLCHRIITHKMPDHVVLVII FLNCITIAMERPKIDPHSAERIFLTLSNYIFAV	1297
		Best Local Similarity 98.9%; Pred. No. 0;	Qy	1321	FLAEMTVKVALGWCFCGEQAYLRSSWNVL DGLLVLSVIDILVMSVDSGTKILGMLRVL	1380
		Matches 2242; Conservative 0; Mismatches 1; Indels 23; Gaps 1;	Db	1298	FLAEMTVKVALGWCFCGEQAYLRSSWNVL DGLLVLSVIDILVMSVDSGTKILGMLRVL	1357
Qy	1	MDEEDGAGAESGQPRFMRNLDSGAGGRPGSGSAEKDPGSADSEAEGLPYPALAPVV	Qy	1381	RLLETLRPLRVI SRAOGLKLVETILMSLKIDIGNIVVICCAFFIIFGILGVQLFKGKFPV	1440
Db	1	MDEEDGAGAESGQPRFMRNLDSGAGGRPGSGSAEKDPGSADSEAEGLPYPALAPVV	Db	1358	RLLETLRPLRVI SRAOGLKLVETILMSLKIDIGNIVVICCAFFIIFGILGVQLFKGKFPV	1417
Qy	61	FFYLSQDSRPSWCLRTVCPNPFERISMLVILLNCVTLGMPRCPEDIAQSCRILQAF	Qy	1441	COGEDTRNITNKS DCAEAS YRWRHKYNFNDLGOALMSL FVLASKDGVWDIMYDGLDAVG	1500
Db	61	FFYLSQDSRPSWCLRTVCPNPFERISMLVILLNCVTLGMPRCPEDIAQSCRILQAF	Db	1418	COGEDTRNITNKS DCAEAS YRWRHKYNFNDLGOALMSL FVLASKDGVWDIMYDGLDAVG	1477
Qy	121	DDFIFAFVAVEMVKNVALGIFGKCYLGDWTNRDLDFIVAGMLEYSLDLQNVSFSAVR	Qy	1501	VDQOPIMNHNPMMLLYFTISFLLI VAFVFLNMFVGVVFNHFKCRHQHQBEEBARREERKL	1560
Db	121	DDFIFAFVAVEMVKNVALGIFGKCYLGDWTNRDLDFIVAGMLEYSLDLQNVSFSAVR	Db	1478	VDQOPIMNHNPMMLLYFTISFLLI VAFVFLNMFVGVVFNHFKCRHQHQBEEBARREERKL	1537
Qy	181	TVRVLRLPURLARNVPMSRILVTLTLLDLPMLGNVLLCFFVFFFIIGVGVQVMAGLLNR	Qy	1561	RLLEKRRKQACKPYSDYSRFRLLVHHLCTSHYLDLFTITGVIGLVNVTMAHEHYQQPOI	1620
Db	181	TVRVLRLPURLARNVPMSRILVTLTLLDLPMLGNVLLCFFVFFFIIGVGVQVMAGLLNR	Db	1538	RLLEKRRKQACKPYSDYSRFRLLVHHLCTSHYLDLFTITGVIGLVNVTMAHEHYQQPOI	1597
Qy	241	CFLPENFSLPLSVDLERYYTQENEDSPFICQPRENGMRSCRSVPTLRGDDGGGPPCGL	Qy	1621	LDEALKTCNYITFTVIFVLESVFKLVAFGFRFFQDRWNQDLDAIVLLSIMGITLSEIEVN	1680
Db	241	CFLPENFSLPLSVDLERYYTQENEDSPFICQPRENGMRSCRSVPTLRGDDGGGPPCGL	Db	1598	LDEALKTCNYITFTVIFVLESVFKLVAFGFRFFQDRWNQDLDAIVLLSIMGITLSEIEVN	1657
Qy	301	DYEAYNSSNTTCVNNQYTNCSAGEHNPFGKAINFONIGYAMTAPQVITLBSGVDIM	Qy	1681	ASLPINPTIIRIMRVLRARVLKLLKMAVGRALLDVTQMALPOVGNLGLLFFMLFFIFA	1740
Db	301	DYEAYNSSNTTCVNNQYTNCSAGEHNPFGKAINFONIGYAMTAPQVITLBSGVDIM	Db	1658	ASLPINPTIIRIMRVLRARVLKLLKMAVGRALLDVTQMALPOVGNLGLLFFMLFFIFA	1717
Qy	361	YFVMDAHSFYNIIFILLIIVGSFPMINCLVLTATQSETKQRESQLMRORVRFLSNA	Qy	1741	ALGVELFGDLECDETHPCGEGLRHATFRNFGMAFLTLFRVSTGDNWNGIMKDTLRDCQE	1800
Db	361	YFVMDAHSFYNIIFILLIIVGSFPMINCLVLTATQSETKQRESQLMRORVRFLSNA				
Qy	421	STLASFSFGPCGCBELLYVILIRKAAARRLAQVSRAGVRLGLSSPAPLGQGTQPS				
Db	421	STLASFSFGPCGCBELLYVILIRKAAARRLAQVSRAGVRLGLSSPAPLGQGTQPS				
Qy	481	SCSRSHRRLSVHLLVHHHHHHHHYHNGTILRAPRASPEI QDRDANGSRRLMLPPPTP				
Db	481	SCSRSHRRLSVHLLVHHHHHHHHYHNGTILRAPRASPEI QDRDANGSRRLMLPPPTP				
Qy	541	ALSGAPPGASVHSFYHADCHLBPVRCQAPPPSPSEASGRTVGSGKVYPTVHTSPPE				
Db	541	ALSGAPPGASVHSFYHADCHLBPVRCQAPPPSPSEASGRTVGSGKVYPTVHTSPPE				
Qy	601	TLKEKALVEVAASGPPTLTSLNTPPGPYSSMHKLLETQSTCACQSSCKISSPCLKADSG				
Db	601	TLKEKALVEVAASGPPTLTSLNTPPGPYSSMHKLLETQSTCACQSSCKISSPCLKADSG				

QY 661 ACPDSCPCYCARAGAGEVELADREMPDSDSEAVYEFTQDAQSDLRDPHSRRQSLGPD 720
DB 661 ACPDSCPCYCARAGAGEVELADREMPDSDSEAVYEFTQDAQSDLRDPHSRRQSLGPD 720
QY 721 EPSSVLAFWRLLCTDFRKLVDKSKYFGRGIMTALLVNTLSMGIEVHEQPEELTNALEISNI 780
DB 721 EPSSVLAFWRLLCTDFRKLVDKSKYFGRGIMTALLVNTLSMGIEVHEQPEELTNALEISNI 780
QY 781 VFTSLFALEMLLKLVLVYGPFGYIKNPYNI FGVIVIVISWEIVGQGGGLSVLFRFLMR 840
DB 781 VFTSLFALEMLLKLVLVYGPFGYIKNPYNI FGVIVIVISWEIVGQGGGLSVLFRFLMR 840
QY 841 VLKLVRFALQORQVLVLMKTMNDVATFCMLLMLEFIPTSLGWHLPCKKASERDGTLL 900
DB 841 VLKLVRFALQORQVLVLMKTMNDVATFCMLLMLEFIPTSLGWHLPCKKASERDGTLL 900
QY 901 PDRKNFDSLLWAI VTVFOILTQEDWNKVLVNGMASTSSWAALYFTALMTFGNYVLFNLLV 960
DB 901 PDRKNFDSLLWAI VTVFOILTQEDWNKVLVNGMASTSSWAALYFTALMTFGNYVLFNLLV 960
QY 961 AILVEGPOAEISKREDASGOLSCIQLPVDVSGGDANKSESEPFFPSLDGDRKKCL 1020
DB 961 AILVEGPOAE-----GDANKSESEPFFPSLDGDRKKCL 997
QY 1021 ALVSLGEHPELRKSLPPLIITHTAATPMSLPKSTSTGLGEALGPASRTSSGSAEPGAA 1080
DB 998 ALVSLGEHPELRKSLPPLIITHTAATPMSLPKSTSTGLGEALGPASRTSSGSAEPGAA 1057
QY 1081 HEMKSPPSARSPSPWASAASWTSRRSRNSLGRAPSLKRSPSGRRSLLSGEGQESQ 1140
DB 1058 HEMKSPPSARSPSPWASAASWTSRRSRNSLGRAPSLKRSPSGRRSLLSGEGQESQ 1117
QY 1141 DEESSEERASPAQSDHRRGSLEREAKSFDPDTLQVPLHRTASGRGSAHEQDCN 1200
DB 1118 DEESSEERASPAQSDHRRGSLEREAKSFDPDTLQVPLHRTASGRGSAHEQDCN 1177
QY 1201 GKSASGRALARALRPDDPLDGDADDDEGNLSKGERVRAIRARLPACVLERDSWSAYIFP 1260
DB 1178 GKSASGRALARALRPDDPLDGDADDDEGNLSKGERVRAIRARLPACVLERDSWSAYIFP 1237
QY 1261 POSRFLRLCHRIITHKMFHDVVLVIIPLNCITIAMERPKIDPHSAERIFLTLNVIYFVAV 1320
DB 1238 POSRFLRLCHRIITHKMFHDVVLVIIPLNCITIAMERPKIDPHSAERIFLTLNVIYFVAV 1297
QY 1321 FLAEMTVKVALGWCFCGQAYLRSSWNLVLDGLLVLSVIDILVMSVSDSGTKILGMLRVL 1380
DB 1298 FLAEMTVKVALGWCFCGQAYLRSSWNLVLDGLLVLSVIDILVMSVSDSGTKILGMLRVL 1357
QY 1381 RLRLTLRLRVLISRAQGLKLVVETLMSLSKIDIGNIIVWICCAFFIIFGILGVQLPKGKFFV 1440
DB 1358 RLRLTLRLRVLISRAQGLKLVVETLMSLSKIDIGNIIVWICCAFFIIFGILGVQLPKGKFFV 1417
QY 1441 COGEDTRNITNKSDCABASYRWRHKYNFNDNLGOALMSLFLVLSKDGWVDIMYDGLDAVG 1500
DB 1418 COGEDTRNITNKSDCABASYRWRHKYNFNDNLGOALMSLFLVLSKDGWVDIMYDGLDAVG 1477
QY 1501 VDOQPIMNHNPMWLLYFISFLLIIVAFVFNLFVGVVFNHFKRQHQEERARRRERKL 1560
DB 1478 VDOQPIMNHNPMWLLYFISFLLIIVAFVFNLFVGVVFNHFKRQHQEERARRRERKL 1537
QY 1561 RLLEKRRKACKQPKYISYDRFLVLVHLCTSHYLDLFIITGVIGLVNVTMAHEVYQQQOI 1620
DB 1538 RLLEKRRKACKQPKYISYDRFLVLVHLCTSHYLDLFIITGVIGLVNVTMAHEVYQQQOI 1597
QY 1621 LDEALKICNYITVTFVLESVFKLVAFGFRFFQDRWNQDLDAIVLLSIMGITLLEIEVNV 1680
DB 1598 LDEALKICNYITVTFVLESVFKLVAFGFRFFQDRWNQDLDAIVLLSIMGITLLEIEVNV 1657
QY 1681 ASLPINPTIIRIMRVLRILARVLKLLKMAVGMRALDVTWQALPQVGNLGLLFFMLFFIFA 1740
DB 1658 ASLPINPTIIRIMRVLRILARVLKLLKMAVGMRALDVTWQALPQVGNLGLLFFMLFFIFA 1717

QY 1741 ALGVELFGDLCEDETHPCCEGLGRHATFRNFGWAFILTLFRVSTGDNWNGIMKDTLDCDOE 1800
DB 1718 ALGVELFGDLCEDETHPCCEGLGRHATFRNFGWAFILTLFRVSTGDNWNGIMKDTLDCDOE 1777
QY 1801 STCYNTVISPITYFVSFVLTAQFVLVNVVIAVLMKHLEESNKEAEAELEAELEMKTL 1860
DB 1778 STCYNTVISPITYFVSFVLTAQFVLVNVVIAVLMKHLEESNKEAEAELEAELEMKTL 1837
QY 1861 SPQHPSLGSPFLPWPVEGPDSPSPKPGALHPAAHARSASHFSLEHPTMQHPTELPGP 1920
DB 1838 SPQHPSLGSPFLPWPVEGPDSPSPKPGALHPAAHARSASHFSLEHPTMQHPTELPGP 1897
QY 1921 DLLTVRSGVSRTHSLPNDSYMCVRHGSTAEGPLGHRGWLKPAQSGSVLSVHSQPADTYS 1980
DB 1998 DLLTVRSGVSRTHSLPNDSYMCVRHGSTAEGPLGHRGWLKPAQSGSVLSVHSQPADTYS 1957
QY 1981 ILQLPKDAPHLLQPHSAPTWTGTIPKLPPPGRSPLAQRPLRQAARTDLSLVQGLGSRD 2040
DB 1958 ILQLPKDAPHLLQPHSAPTWTGTIPKLPPPGRSPLAQRPLRQAARTDLSLVQGLGSRD 2017
QY 2041 LLAEVSGPSPPLARAYSFWGQSSSTQAOQHSHSKISKHMTTPAPCPGPEPNWGKGPPE 2100
DB 2018 LLAEVSGPSPPLARAYSFWGQSSSTQAOQHSHSKISKHMTTPAPCPGPEPNWGKGPPE 2077
QY 2101 RSSLELDTLSWISGDLPLPGQSEPPSPDLKKCYVSAQSCORRPTSWLDEQRRHSIA 2160
DB 2078 RSSLELDTLSWISGDLPLPGQSEPPSPDLKKCYVSAQSCORRPTSWLDEQRRHSIA 2137
QY 2161 VSCLDSSQPHLGTDPNLSGQPLGGSRPKKLSPPSITIDPPESQGRTPPSPGICL 2220
DB 2138 VSCLDSSQPHLGTDPNLSGQPLGGSRPKKLSPPSITIDPPESQGRTPPSPGICL 2197
QY 2221 RRRAPSSDSKDPPLASGPPDSMAASPPKOVLSLSGLSSDPADLDP 2266
DB 2198 RRRAPSSDSKDPPLASGPPDSMAASPPKOVLSLSGLSSDPADLDP 2243
RESULT 5
AAV14586
ID AAV14586 standard; protein; 2250 AA.
XX
AC AAV14586;
XX
DT 07-DEC-1999 (first entry)
XX
DE Human T-type voltage-gated Ca channel alpha-1-G (hCavT1a).
XX
KW Human; T-type voltage-gated calcium channel; membrane; pore; ion;
KW activation; current; rat; screen; drug; cardiomyopathy; epilepsy.
XX
OS Homo sapiens.
XX
PN WO9929847-A1.
XX
PD 17-JUN-1999.
XX
PF 30-OCT-1998; 98WO-US023161.
XX
PR 05-DEC-1997; 97US-00985809.
XX
PA (LOYO) UNIV LOYOLA CHICAGO.
XX
PI Perez-Reyes E, Cribbs LL;
XX
DR WPI; 1999-394972/33.
XX
DR N-PSDB; AAX83481.
XX
PT New T-type voltage-gated calcium channels.
XX
PS Disclosure; Page 31-40; 138pp; English.
XX
CC This sequence represents a human T-type voltage-gated calcium (Ca)
channel alpha-1-G designated hCavT1a. Voltage gated channels are membrane

CC bound glycosylated proteins formed of several subunits. The large alpha
 CC subunits form a pore in the membrane that is selective for a given ionic
 CC species. Each alpha subunit contains 4 domains (I, II, III and IV) and
 CC each domain contains 6 putative transmembrane helical segments (S1-S6). T
 CC -type Ca channels are activated at a lower voltage than L- or N-type
 CC channels. Characteristics of T-type channels include short current time,
 CC slow activation kinetics near threshold, fast inactivation kinetics and
 CC slow tail current. The sequences AAX83481-X83492 represent novel T-type
 CC voltage-gated Ca channel genes from humans and rats. Each of the novel Ca
 CC channels contains a putative IVS4 region comprising the amino acid
 CC sequence AAY14598. Cells expressing the T-type voltage-gated calcium
 CC channel proteins can be used to screen for drugs which affect calcium
 CC channels. Methods are also disclosed for treating a disease or disorder
 CC associated with a deficiency in a native T-type calcium channel nucleic
 CC acid, e.g. to treat cardiomyopathy, epilepsy, etc
 XX
 SQ Sequence 2250 AA;

Query Match	98.6%;	Score 11741;	DB 2;	Length 2250;
Best Local Similarity	98.6%;	Pred. No. 0;		
Matches 2241;	Conservative	1;	Mismatches	1;
			Indels	30;
			Gaps	2;
QY 1	MDEEDGAGAESGQPSR	FMLNDLSGAGRP	PGSAEKDPGSADSAEGLYPALAPVV	60
DB 1	MDEEDGAGAESGQPSR	FMLNDLSGAGRP	PGSAEKDPGSADSAEGLYPALAPVV	60
QY 61	FFYLSDSRPESWCLRTVCNPFERISMLVLLNCVTILGMP	RPCEDACDSORCRILQAF	120	
DB 61	FFYLSDSRPESWCLRTVCNPFERISMLVLLNCVTILGMP	RPCEDACDSORCRILQAF	120	
QY 121	DDFPAFAVAVMVKVVALGIFGKKCYLGD	TWNRLLDFPVIAGMLEYSLDLQNVSPSAVR	180	
DB 121	DDFPAFAVAVMVKVVALGIFGKKCYLGD	TWNRLLDFPVIAGMLEYSLDLQNVSPSAVR	180	
QY 181	TVRLRPLRAINRVP	SMRILVLLDTPMLGNVLLLCFFVFFIGVIGVQLWAGLLNR	240	
DB 181	TVRLRPLRAINRVP	SMRILVLLDTPMLGNVLLLCFFVFFIGVIGVQLWAGLLNR	240	
QY 241	CFLPENFSLPLSVDLERYQY	TENEDESPFICSQPRENMRSCRSVPTLRG	DGGGGPPCGL 300	
DB 241	CFLPENFSLPLSVDLERYQY	TENEDESPFICSQPRENMRSCRSVPTLRG	DGGGGPPCGL 300	
QY 301	DYEAYNSSNTTCVNNQY	TNCSSAGEHNPFGKAINFDNIGYAMIAIQVITL	LGWVDIM 360	
DB 301	DYEAYNSSNTTCVNNQY	TNCSSAGEHNPFGKAINFDNIGYAMIAIQVITL	LGWVDIM 360	
QY 361	YFWDHAFYNYFIYFII	IIYVGSFPMINLCVVIATQFSETKQRESQMRQVRFLSNA	420	
DB 361	YFWDHAFYNYFIYFII	IIYVGSFPMINLCVVIATQFSETKQRESQMRQVRFLSNA	420	
QY 421	STLASFSFGSCYEELLYVILKKAARRLAQV	SRAAGVRVGLSSPAPLGQGTQPS	480	
DB 421	STLASFSFGSCYEELLYVILKKAARRLAQV	SRAAGVRVGLSSPAPLGQGTQPS	480	
QY 481	SCSRSHRLSVHLLVHHHHHHH	VHLNGTILRAPASPEIQDRDANGSRRLMPPPTP	540	
DB 481	SCSRSHRLSVHLLVHHHHHHH	VHLNGTILRAPASPEIQDRDANGSRRLMPPPTP	540	
QY 541	ALSGAPPGAESVHGFYHADCHLEPVR	COAPPPSPSEASGRTVGSQVYPTVHTSPPE	600	
DB 541	ALSGAPPGAESVHGFYHADCHLEPVR	COAPPPSPSEASGRTVGSQVYPTVHTSPPE	600	
QY 601	TLKALVEVAASSGPPTL	TSLNIPPGVSSMHKLETTQSTGACQSSCKISPC	KADSG 660	
DB 601	TLKALVEVAASSGPPTL	TSLNIPPGVSSMHKLETTQSTGACQSSCKISPC	KADSG 660	
QY 661	ACGPDSCPCYCARAGAVE	LADEMPDSDSEAVYFTQDAQSDLRDPSRRQSLG	PD 720	
DB 661	ACGPDSCPCYCARAGAVE	LADEMPDSDSEAVYFTQDAQSDLRDPSRRQSLG	PD 720	
QY 721	EPSSVLAFWRLICD	FRKIVDSKYGFGIMIAILVNTLSMGIEYHQPEELTNALEISNI	780	
DB 721	EPSSVLAFWRLICD	FRKIVDSKYGFGIMIAILVNTLSMGIEYHQPEELTNALEISNI	780	

QY	781	VFTSLFALEMLKLLVY	PGFYKPNYINFDGVIVVISVWEIVGQGGGLSVLRTFLMR	840
DB	781	VFTSLFALEMLKLLVY	PGFYKPNYINFDGVIVVISVWEIVGQGGGLSVLRTFLMR	840
QY	841	VKLVRFLPALORQLV	LVLMKTDNVATFCWLLMLFIFISILGMHLFGCKFASERDGLT	900
DB	841	VKLVRFLPALORQLV	LVLMKTDNVATFCWLLMLFIFISILGMHLFGCKFASERDGLT	900
QY	901	PDRKNFDSLLWALT	VTVFQILTOEDWNKVLNGWASTSSWAALYFIALMTFGNVFLNLLV	960
DB	901	PDRKNFDSLLWALT	VTVFQILTOEDWNKVLNGWASTSSWAALYFIALMTFGNVFLNLLV	960
QY	961	AILVEGFAOEISKRE	DASQOLSCIQLPVDSDGDKANKSESEPPSPSLDGDGRKKCL	1020
DB	961	AILVEGFAOEISKRE	DASQOLSCIQLPVDSDGDKANKSESEPPSPSLDGDGRKKCL	997
QY	1021	ALVSLGEHPELRKSL	LPPLIIHTAATPMSLPKSTSTGLGEALGPASRRSSSSGASPGAA	1080
DB	998	ALVSLGEHPELRKSL	LPPLIIHTAATPMSLPKSTSTGLGEALGPASRRSSSSGASPGAA	1057
QY	1081	HEMKSPSARSSPHS	PAASWTSRRSRNSLGRAPSLKRRSPSGERRSLLSGEGESQ	1140
DB	1058	HEMKSPSARSSPHS	PAASWTSRRSRNSLGRAPSLKRRSPSGERRSLLSGEGESQ	1117
QY	1141	DEESEEERAS	PAGSDHRRHRSLEAREKSSFDLPDTLQVPLHRTASGRGSAEHQDCN	1200
DB	1118	DEESEEERAS	PAGSDHRRHRSLEAREKSSFDLPDTLQVPLHRTASGRGSAEHQDCN	1177
QY	1201	GKSASGLARALP	DDPPLDGDADDGNSLKGKERVAMIRARLPACYLDERDSWASYFP	1260
DB	1178	GKSASGLARALP	DDPPLDGDADDGNSLKGKERVAMIRARLPACYLDERDSWASYFP	1237
QY	1261	PQSRFLLCHRIITH	KMFHVLIIFLNCITTIAMERPKIDPHSAERIPLTLSNYIFTAV	1320
DB	1238	PQSRFLLCHRIITH	KMFHVLIIFLNCITTIAMERPKIDPHSAERIPLTLSNYIFTAV	1297
QY	1321	FLAEMTVKVALG	WCGEQAYLRSSNNVLDGLLVLSVIDILVSMVSDSGTKILGMLVL	1380
DB	1298	FLAEMTVKVALG	WCGEQAYLRSSNNVLDGLLVLSVIDILVSMVSDSGTKILGMLVL	1357
QY	1381	RLLRTPRLAVIS	RAOGLKLVWETLMSLKPIGNIVVICCAFFIIFGILGVQLFKGFFV	1440
DB	1358	RLLRTPRLAVIS	RAOGLKLVWETLMSLKPIGNIVVICCAFFIIFGILGVQLFKGFFV	1417
QY	1441	CQGEDTRNITKSD	CAEASVYRVRHKYNFNLGOALMSLFLVASKOGVDIMYDGLDVG	1500
DB	1418	CQGEDTRNITKSD	CAEASVYRVRHKYNFNLGOALMSLFLVASKOGVDIMYDGLDVG	1477
QY	1501	VDQOPIMNHP	WMLLYFISILLIVAFFVANFVGVVVENFHKCRHQHEEAREERKRL	1560
DB	1478	VDQOPIMNHP	WMLLYFISILLIVAFFVANFVGVVVENFHKCRHQHEEAREERKRL	1537
QY	1561	RLLEKKER	-----KAQCKPYSDYSRFRLLVHLCTSHYLDLFTITGVIGLNVVTWAME	1613
DB	1538	RLLEKKER	-----KAQCKPYSDYSRFRLLVHLCTSHYLDLFTITGVIGLNVVTWAME	1597
QY	1614	HYQOPQLDEALK	CNYIFTVIVLESVFKLVAFGPRFRFQDRWNQDLAIVLLSINGIT	1673
DB	1598	HYQOPQLDEALK	CNYIFTVIVLESVFKLVAFGPRFRFQDRWNQDLAIVLLSINGIT	1657
QY	1674	LEETEVNASIP	NTIIRIMRVLIARVLKLVMAVGMRLDVTMOALPOVGNLGLLPM	1733
DB	1658	LEETEVNASIP	NTIIRIMRVLIARVLKLVMAVGMRLDVTMOALPOVGNLGLLPM	1717
QY	1734	LLFFIFAALG	VGLFGDLECEDETHPCEGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMKDT	1793
DB	1718	LLFFIFAALG	VGLFGDLECEDETHPCEGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMKDT	1777
QY	1794	LRDCQDSTC	NTVISPVIYFVSFVLTQAQFVLNVVIVIAVLMKHLSESKKEAELEAEL	1853
DB	1778	LRDCQDSTC	NTVISPVIYFVSFVLTQAQFVLNVVIVIAVLMKHLSESKKEAELEAEL	1837

QY 1854 ELEMKTLSPOHSPGLSPPLAGVEGPDSPDPKPGALHPAAHARSASHFSLEHTWQPH 1913
 Db |||||||
 QY 1838 ELEMKTLSPOHSPGLSPPLAGVEGPDSPDPKPGALHPAAHARSASHFSLEHTWQPH 1897
 Db |||||||
 QY 1914 PTELPGPDLTVRKSGVSRTHSLPNDSYMCRHSGTAEGPLGHRGWLGPKAQSGSVLSVHS 1973
 Db |||||||
 QY 1998 PTELPGPDLTVRKSGVSRTHSLPNDSYMCRHSGTAEGPLGHRGWLGPKAQSGSVLSVHS 1957
 Db |||||||
 QY 1974 QPADTSYILQPKDAPHLLQPHSAPTWTGTPKLPPLPGSRPLAQRPLRQAARTSDLDVQ 2033
 Db |||||||
 QY 1958 QPADTSYILQPKDAPHLLQPHSAPTWTGTPKLPPLPGSRPLAQRPLRQAARTSDLDVQ 2017
 Db |||||||
 QY 2034 GLGSRDLAEVSGSPPLARAYFWGOSSTQAQHSRSHSKISKHMTTPAPCPGPERNW 2093
 Db |||||||
 QY 2018 GLGSRDLAEVSGSPPLARAYFWGOSSTQAQHSRSHSKISKHMTTPAPCPGPERNW 2077
 Db |||||||
 QY 2094 KGKPPETRSSLLELDTLSWISGDLPLPGQGEPPSPDLKKCYSEVAGSCORRPTSWLDE 2153
 Db |||||||
 QY 2078 KGKPPETRSSLLELDTLSWISGDLPLPGQGEPPSPDLKKCYSEVAGSCORRPTSWLDE 2137
 Db |||||||
 QY 2154 QRRHSIAVCLDSGQPHLGTDPNGLGQPIGGPGSRPKKLSPPSITIDPPESQGRPTP 2213
 Db |||||||
 QY 2138 QRRHSIAVCLDSGQPHLGTDPNGLGQPIGGPGSRPKKLSPPSITIDPPESQGRPTP 2197
 Db |||||||
 QY 2214 PSPGICLRRRAPSDSKDPLASGPPDSMAASPSKKDVLSSLSSDPADLDP 2266
 Db |||||||
 QY 2198 PSPGICLRRRAPSDSKDPLASGPPDSMAASPSKKDVLSSLSSDPADLDP 2250
 Db |||||||

RESULT 6

AAAY14587
 ID AAY14587 standard; protein; 2261 AA.
 XX
 AC AAY14587;
 XX
 XX 07-DEC-1999 (first entry)
 DT
 XX
 XX Human T-type voltage-gated Cc channel alpha-1-G (hCav1b).
 DE
 XX Human; T-type voltage-gated calcium channel; membrane; pore; ion;
 KW activation; current; rat; screen; drug; cardiomyopathy; epileps.
 XX
 XX Homo sapiens.
 OS
 XX WO9929847-A1.
 FN
 XX 17-JUN-1999.
 PD
 XX 30-OCT-1998; 98WO-US023161.
 PF
 XX 05-DEC-1997; 97US-00985809.
 PR
 XX (LOYO) UNIV LOYOLA CHICAGO.
 PA
 XX Perez-Reyes E, Cribbs LL;
 PI
 XX WPI; 1999-394972/33.
 DR
 XX N-PSDB; AAX83482.
 DR
 XX

PT New T-type voltage-gated calcium channels.
 XX

PS Disclosure; Page 40-49; 138pp; English.
 XX

CC This sequence represents a human T-type voltage-gated calcium (Ca)
 CC channel alpha-1-G designated hCav1b. Voltage gated channels are membrane
 CC bound glycosylated proteins formed of several subunits. The large alpha
 CC subunits form a pore in the membrane that is selective for a given ionic
 CC species. Each alpha subunit contains 4 domains (I, II, III and IV) and
 CC each domain contains 6 putative transmembrane helical segments (S1-S6). T
 CC -type Ca channels are activated at a lower voltage than L- or N-type
 CC channels. Characteristics of T-type channels include short current time,
 CC slow activation kinetics near threshold, fast inactivation kinetics and
 CC slow tail current. The sequences AAX83481-A83492 represent novel T-type
 CC

CC voltage-gated Ca channel genes from humans and rats. Each of the novel Ca
 CC -channels contains a putative IVS4 region comprising the amino acid
 CC sequence AAY14598. Cells expressing the T-type voltage-gated calcium
 CC channel proteins can be used to screen for drugs which affect calcium
 CC channels. Methods are also disclosed for treating a disease or disorder
 CC associated with a deficiency in a native T-type calcium channel nucleic
 CC acid, e.g. to treat cardiomyopathy, epilepsy, etc
 XX

SQ Sequence 2261 AA;

Query Match 98.6%; Score 11735.5; DB 2; Length 2261;
 Best Local Similarity 98.1%; Pred. No. 0;
 Matches 2241; Conservative 1; Mismatches 1; Indels 41; Gaps 2;

QY 1 MDEEDGAGAESQSPRSFMRNLDSGAGRPFGSAEKDPGSDASEAGLPYPALAPV 60
 Db |||||||
 QY 1 MDEEDGAGAESQSPRSFMRNLDSGAGRPFGSAEKDPGSDASEAGLPYPALAPV 60
 Db |||||||
 QY 61 PFYLSQDSRPRSCLRTVCNPFERISMLVTLNCVTLMGPRPCEDTACDSQRCLQAF 120
 Db |||||||
 QY 61 PFYLSQDSRPRSCLRTVCNPFERISMLVTLNCVTLMGPRPCEDTACDSQRCLQAF 120
 Db |||||||
 QY 121 DDFIFAFFAVEMVVMVALGIFGKKCYLGDWTNRDLDFVIAGMLEYSLDLQNVSFSAVR 180
 Db |||||||
 QY 121 DDFIFAFFAVEMVVMVALGIFGKKCYLGDWTNRDLDFVIAGMLEYSLDLQNVSFSAVR 180
 Db |||||||
 QY 181 TVRVLRPLRINRVPSMRILVTLLDTPMLGNVLLCFFVFFIFIGVGVQLWAGLLNR 240
 Db |||||||
 QY 181 TVRVLRPLRINRVPSMRILVTLLDTPMLGNVLLCFFVFFIFIGVGVQLWAGLLNR 240
 Db |||||||
 QY 241 CFLPENFSLPLSDLERYOTENEDESPFICSPRENGMRSCRSVPTLRGGGGPPCGL 300
 Db |||||||
 QY 241 CFLPENFSLPLSDLERYOTENEDESPFICSPRENGMRSCRSVPTLRGGGGPPCGL 300
 Db |||||||
 QY 301 DYEAYNSSNTTCVNMNYYTNCAGHNPKGAINFDNIGYAMIAIFQVITLEGWVDIM 360
 Db |||||||
 QY 301 DYEAYNSSNTTCVNMNYYTNCAGHNPKGAINFDNIGYAMIAIFQVITLEGWVDIM 360
 Db |||||||
 QY 361 YFVMDAHSFYNIYFILLIIVGSPFMINCLVVIATQFSETKQRESQMLRQVRFLSNA 420
 Db |||||||
 QY 361 YFVMDAHSFYNIYFILLIIVGSPFMINCLVVIATQFSETKQRESQMLRQVRFLSNA 420
 Db |||||||
 QY 421 STLASFSEPGSCYEELKLYVILRKAARLAQVSRAGVVRVGLSSPAPJGGGETQSS 480
 Db |||||||
 QY 421 STLASFSEPGSCYEELKLYVILRKAARLAQVSRAGVVRVGLSSPAPJGGGETQSS 480
 Db |||||||
 QY 481 SCSRSHRLSVHHLVHHHHHHHHYHLNGTILRAPRASPEIQDRDANGSRRLMLPPSTP 540
 Db |||||||
 QY 481 SCSRSHRLSVHHLVHHHHHHHHYHLNGTILRAPRASPEIQDRDANGSRRLMLPPSTP 540
 Db |||||||
 QY 541 ALSGAPPGAESVHSFYHADCHLEPVRCAQPPPPSPSEASGRTVSGKVPVTPVHTSPPE 600
 Db |||||||
 QY 541 ALSGAPPGAESVHSFYHADCHLEPVRCAQPPPPSPSEASGRTVSGKVPVTPVHTSPPE 600
 Db |||||||
 QY 601 TLKEKALVEVAASGPPPTLSLNTPGPYSSMHKLETSQSGACOSSCKISSPCLKADSG 660
 Db |||||||
 QY 601 TLKEKALVEVAASGPPPTLSLNTPGPYSSMHKLETSQSGACOSSCKISSPCLKADSG 660
 Db |||||||
 QY 661 ACGPDSQPCYCARAGAGEVELADREMPDSDSAVVEFTQDAQSHDLRPHSRQRSLGDA 720
 Db |||||||
 QY 661 ACGPDSQPCYCARAGAGEVELADREMPDSDSAVVEFTQDAQSHDLRPHSRQRSLGDA 720
 Db |||||||
 QY 721 EPSSVLAFWRLICDTFRKIVDSKYFGRGIMTIALVNTLSMGIEYHEQPEELTNALEISNI 780
 Db |||||||
 QY 721 EPSSVLAFWRLICDTFRKIVDSKYFGRGIMTIALVNTLSMGIEYHEQPEELTNALEISNI 780
 Db |||||||
 QY 781 VFTSLFALEMLKLLVGPFGYIKPNYIPGVVWISVWEIIVGQGGGLSVLRTFLMR 840
 Db |||||||
 QY 781 VFTSLFALEMLKLLVGPFGYIKPNYIPGVVWISVWEIIVGQGGGLSVLRTFLMR 840
 Db |||||||
 QY 841 VLKLVRFPLALQRLVLMKTMNDNVATFCMLMLFIFFISILGMHLFGCKFASRDGDTL 900
 Db |||||||
 QY 841 VLKLVRFPLALQRLVLMKTMNDNVATFCMLMLFIFFISILGMHLFGCKFASRDGDTL 900
 Db |||||||

QY 901 PDRKNFSLWAIWTVFQILTOBDMNKVLYNGMASTSSWAALYFIAMTFTGNVVLNLLV 960
Db 901 PDRKNFSLWAIWTVFQILTOBDMNKVLYNGMASTSSWAALYFIAMTFTGNVVLNLLV 960
QY 961 AILVEGFOAEIISKREDASQQLSCIQLPVDSCQGDANKSESEDPFSPSLDGGDRKKCL 1020
Db 961 AILVEGFOAEIISKREDASQQLSCIQLPVDSCQGDANKSESEDPFSPSLDGGDRKKCL 997
QY 1021 ALVSLGHEPELRLKLLPLLIHTAATPMSLPKSTSTGLGEALGPASRRRTSSSGSAEPGAA 1080
Db 998 ALVSLGHEPELRLKLLPLLIHTAATPMSLPKSTSTGLGEALGPASRRRTSSSGSAEPGAA 1057
QY 1081 HEMSPSPSARSPPHSPMSAASSWTSRRSSNSLGRAPSLKRRPSPGERRSLLSGEQESQ 1140
Db 1058 HEMSPSPSARSPPHSPMSAASSWTSRRSSNSLGRAPSLKRRPSPGERRSLLSGEQESQ 1117
QY 1141 DEESSEERASPAQSDHRRHGSLEERAKSSFDLPDQLVPLHRTASGRGSASEHQDCN 1200
Db 1118 DEESSEERASPAQSDHRRHGSLEERAKSSFDLPDQLVPLHRTASGRGSASEHQDCN 1177
QY 1201 GKSASGRRLARLPDDPLDGDADDDEGNLSKGERVRAMIRARLPACCLERDSWSAYIFP 1260
Db 1178 GKSASGRRLARLPDDPLDGDADDDEGNLSKGERVRAMIRARLPACCLERDSWSAYIFP 1237
QY 1261 POSRFLRLCHRIITHKMFHDHVLVIIPLNCITIAMERPKIDPHSAERIFLTLSNYIFAV 1320
Db 1238 POSRFLRLCHRIITHKMFHDHVLVIIPLNCITIAMERPKIDPHSAERIFLTLSNYIFAV 1297
QY 1321 FLAEMTVKVALGWCFCGEQAYLRSSNNVLDGLLLISVIDILSVMSVDSGKILGMLRVL 1380
Db 1298 FLAEMTVKVALGWCFCGEQAYLRSSNNVLDGLLLISVIDILSVMSVDSGKILGMLRVL 1357
QY 1381 RLRLTLRLPLVRSRAGQLKLVETLMSLKPIGNIWIICCAFFIIFGLGVQLFKGFV 1440
Db 1358 RLRLTLRLPLVRSRAGQLKLVETLMSLKPIGNIWIICCAFFIIFGLGVQLFKGFV 1417
QY 1441 CQGEDFRNTKNSDCAEASYRVRKYNFNDNLGOALMSLFLVLSKDGWVDIMYDGLDAVG 1500
Db 1418 CQGEDFRNTKNSDCAEASYRVRKYNFNDNLGOALMSLFLVLSKDGWVDIMYDGLDAVG 1477
QY 1501 VDQOPTMNNHNPWMLLYFISFLIIVAFVLMFVGVVFNHFKCRQHOHEEABRREKRL 1560
Db 1478 VDQOPTMNNHNPWMLLYFISFLIIVAFVLMFVGVVFNHFKCRQHOHEEABRREKRL 1537
QY 1561 RLLEKRR -----KACCKPYSDYSRFRLLVHHLCTSHYLDLFTGV 1602
Db 1538 RLLEKRRNMLDDVITASSGSSAASEAQCKPYSDYSRFRLLVHHLCTSHYLDLFTGV 1597
QY 1603 IGLNVVTMAEHYQOQILDEALKICNYIFTVIFVLESVKLVAFGRFRFFQDRNQDL 1662
Db 1598 IGLNVVTMAEHYQOQILDEALKICNYIFTVIFVLESVKLVAFGRFRFFQDRNQDL 1657
QY 1663 AIVLLSIMGITLBEIEVNASLPNTIIRIMVRLIRARVLKLMKAVGMRLDVTMOAL 1722
Db 1658 AIVLLSIMGITLBEIEVNASLPNTIIRIMVRLIRARVLKLMKAVGMRLDVTMOAL 1717
QY 1723 PQVGNLGLFMLFFIIFALGVLEFGDLECEHPCEGLGRHATFRNFGMAFILTFRVST 1782
Db 1718 PQVGNLGLFMLFFIIFALGVLEFGDLECEHPCEGLGRHATFRNFGMAFILTFRVST 1777
QY 1783 GDNWNGIMKOTLRDCDQESTCYNVISPPIYFVSFLTAQFVNVNVIATVLMKHLESNKE 1842
Db 1778 GDNWNGIMKOTLRDCDQESTCYNVISPPIYFVSFLTAQFVNVNVIATVLMKHLESNKE 1837
QY 1843 AKEAEAEAELEEMKLTSPHSPGLSGPFLWPGVEGSDSPKPGALHPAAHARSASH 1902
Db 1838 AKEAEAEAELEEMKLTSPHSPGLSGPFLWPGVEGSDSPKPGALHPAAHARSASH 1897
QY 1903 FSLHPTMQPHTEPLPGDILLTVKRSVSRTHSLPNDSYMCRGSTAGPLHGRGWCLPK 1962
Db 1898 FSLHPTMQPHTEPLPGDILLTVKRSVSRTHSLPNDSYMCRGSTAGPLHGRGWCLPK 1957

QY 1963 AQSGSVLSVHSQPADTSTYIILQPKDAPHLLQPHSAPTWTGTHPKLPPGRSPLAQRLLRQ 2022
Db 1958 AQSGSVLSVHSQPADTSTYIILQPKDAPHLLQPHSAPTWTGTHPKLPPGRSPLAQRLLRQ 2017
QY 2023 AAITDSDLVQGLGRREDLLAEVSGPSPPLARAYSFWGQSTQAOQHSRSHSKISKEMTP 2082
Db 2018 AAITDSDLVQGLGRREDLLAEVSGPSPPLARAYSFWGQSTQAOQHSRSHSKISKEMTP 2077
QY 2083 PAPCPGPPNMGKPPETRSLSLELDTLSWISGDLPLPGQOEPPSPRDLKKCYSVBAQS 2142
Db 2078 PAPCPGPPNMGKPPETRSLSLELDTLSWISGDLPLPGQOEPPSPRDLKKCYSVBAQS 2137
QY 2143 CORRTSWLDSQRHSIAVCLDSGSOPLHCTDPSNLGGQPLGGPSRPPKKLSPPSITI 2202
Db 2138 CORRTSWLDSQRHSIAVCLDSGSOPLHCTDPSNLGGQPLGGPSRPPKKLSPPSITI 2197
QY 2203 DPESQGRTPPSPGICLRRRAPSDSKDPLASGPPDMSMAASPPKDVLSLGLSSDPA 2262
Db 2198 DPESQGRTPPSPGICLRRRAPSDSKDPLASGPPDMSMAASPPKDVLSLGLSSDPA 2257
QY 2263 DLDP 2266
Db 2258 DLDP 2261
RESULT 7
AA14588
ID AA14588 standard; protein; 2268 AA.
XX AA14588;
XX
DT 07-DEC-1999 (first entry)
XX Human T-type voltage-gated Ca channel alpha-1-G (hCav1.1c).
DE Human; T-type voltage-gated calcium channel; membrane; pore; ion;
KW activation; current; rat; screen; drug; cardiomyopathy; epilepsy.
KW Homo sapiens.
OS
XX WO9929847-A1.
XX 17-JUN-1999.
PD 30-OCT-1998; 98WO-US023161.
XX 05-DEC-1997; 97US-00985809.
PR (LOYO) UNIV LOYOLA CHICAGO.
XX Perez-Reyes E, Cribbs LL;
XX WPI; 1999-394972/33.
DR N-PSDB; AA83483.
XX New T-type voltage-gated calcium channels.
XX Disclosure; Page 49-58; 138pp; English.
XX This sequence represents a human T-type voltage-gated calcium (Ca)
CC channel alpha-1-G designated hCav1.1c. Voltage gated channels are membrane
CC bound glycosylated proteins formed of several subunits. The large alpha
CC subunits form a pore in the membrane that is selective for a given ionic
CC species. Each alpha subunit contains 4 domains (I, II, III and IV) and
CC each domain contains 6 putative transmembrane helical segments (S1-S6). T
CC -type Ca channels are activated at a lower voltage than L- or N-type
CC channels. Characteristics of T-type channels include short current time,
CC slow activation kinetics near threshold, fast inactivation kinetics and
CC voltage-gated Ca channel genes IVS4 region comprising the amino acid
CC sequence AA14588. Cells expressing the T-type voltage-gated calcium
CC channel proteins can be used to screen for drugs which affect calcium

CC channels. Methods are also disclosed for treating a disease or disorder
CC associated with a deficiency in a native T-type calcium channel nucleic
CC acid, e.g. to treat cardiomyopathy, epilepsy, etc
XX
SQ Sequence 2268 AA;

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Query Match          98.5%; Score 11727; DB 2; Length 2268;
Best Local Similarity 97.8%; Pred. No. 0;
Matches 2240; Conservative 1; Mismatches 2; Indels 48; Gaps 2;

Qy 1 MDEEDGAGAESGQPRFMRNDLSGAGGPGGSAEKDPCGSDAEAGLPYPALAPVV 60
Db 1 MDEEDGAGAESGQPRFMRNDLSGAGGPGGSAEKDPCGSDAEAGLPYPALAPVV 60

Qy 61 FFYLSQDSRPSWCLRTVNCNPFERISMLVILLNCVTGMPRPEDACDSQRCRILQAF 120
Db 61 FFYLSQDSRPSWCLRTVNCNPFERISMLVILLNCVTGMPRPEDACDSQRCRILQAF 120

Qy 121 DDIFAPFAVEMVQWALGIFGKCYLGDFTWNRDFFIVTAGMLEYSLDQNSFSAVR 180
Db 121 DDIFAPFAVEMVQWALGIFGKCYLGDFTWNRDFFIVTAGMLEYSLDQNSFSAVR 180

Qy 181 TVRVLRPLRAINRVPSMRILVTLTDLTPMLGNVLLCCFFVFFIFGIVGVQWAGLLNR 240
Db 181 TVRVLRPLRAINRVPSMRILVTLTDLTPMLGNVLLCCFFVFFIFGIVGVQWAGLLNR 240

Qy 241 CFLPENFSLPLSVDLERYQTENEDESPFICSQPRENGMRSCSVPTLRGGGGPPCGL 300
Db 241 CFLPENFSLPLSVDLERYQTENEDESPFICSQPRENGMRSCSVPTLRGGGGPPCGL 300

Qy 301 DYEAYNSSNTTCVNNQYTCNSAGEHNPFGKAINPDNIGYNTAIPOVITLEGWDIM 360
Db 301 DYEAYNSSNTTCVNNQYTCNSAGEHNPFGKAINPDNIGYNTAIPOVITLEGWDIM 360

Qy 361 YFVMDAHSFYNYFILLIIVGSPFMNCLVATQFSETKQRESQLMRQVRFLSNA 420
Db 361 YFVMDAHSFYNYFILLIIVGSPFMNCLVATQFSETKQRESQLMRQVRFLSNA 420

Qy 421 STLASPSPGCYBELLKYLVIIRKAARRLAQVSRAGVRVGLSSPAPIGGQETQPS 480
Db 421 STLASPSPGCYBELLKYLVIIRKAARRLAQVSRAGVRVGLSSPAPIGGQETQPS 480

Qy 481 SCSHRLSVHHLVHHHHHHHHVHLGNGTLRAPRASPEIODRANGSRRLMPPSTP 540
Db 481 SCSHRLSVHHLVHHHHHHHHVHLGNGTLRAPRASPEIODRANGSRRLMPPSTP 540

Qy 541 ALSGAPPGAESVHSFYHADCHLBPVRQAPPPSPSEASGRTVSGSKVYPTVHTSPPE 600
Db 541 ALSGAPPGAESVHSFYHADCHLBPVRQAPPPSPSEASGRTVSGSKVYPTVHTSPPE 600

Qy 601 TLKESALVEVAASGPPTLTSINIPPGYPSMHKLLTQSTGACQSSCKISSPCLKADSG 660
Db 601 TLKESALVEVAASGPPTLTSINIPPGYPSMHKLLTQSTGACQSSCKISSPCLKADSG 660

Qy 661 ACPDSCPCYCARAGAVEVELADREMPDSDSAVVEFTQDAHSDLRDPHSRQBSLGDA 720
Db 661 ACPDSCPCYCARAGAVEVELADREMPDSDSAVVEFTQDAHSDLRDPHSRQBSLGDA 720

Qy 721 EPSSVLAFWRLICDTFRKIVDSKYFGRGIMTALVNTLSMGIEYHEQPEELTNALEISNI 780
Db 721 EPSSVLAFWRLICDTFRKIVDSKYFGRGIMTALVNTLSMGIEYHEQPEELTNALEISNI 780

Qy 781 VFTSLFALEMLLKLVLVYGPFGYIKNPYNI PDGVIIVISWVEIVGQGGGLSVLRTFLMR 840
Db 781 VFTSLFALEMLLKLVLVYGPFGYIKNPYNI PDGVIIVISWVEIVGQGGGLSVLRTFLMR 840

Qy 841 VLKLVRFPLALORQLVLMKTDNVAFTCMLMLFIFIPFSLIGMHLPCKCKFASERDGDTL 900
Db 841 VLKLVRFPLALORQLVLMKTDNVAFTCMLMLFIFIPFSLIGMHLPCKCKFASERDGDTL 900

Qy 901 PDRKNFDSLLWAI VTVFOILTQEDWNKVLYNGMASTSSWAALYFTALMTFCGNYVLFNLLV 960
Db 901 PDRKNFDSLLWAI VTVFOILTQEDWNKVLYNGMASTSSWAALYFTALMTFCGNYVLFNLLV 960
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Qy 961 AILVEGFOAEBSIKREDASGQLSCLQLPVDSQGGDANKSESEPDFFPSLSDGDRKKCL 1020
Db 961 AILVEGFOAE-----GDANKSESEPDFFPSLSDGDRKKCL 997

Qy 1021 ALVSLGHEPHELKSLPLIHTAATPMSLPKSTSTGLGEALGPASRTSSGSAEPGAA 1080
Db 998 ALVSLGHEPHELKSLPLIHTAATPMSLPKSTSTGLGEALGPASRTSSGSAEPGAA 1057

Qy 1081 HEMKSPPSARSSPHSPMSAASWTSRRSRNSLGRAPSLKRSPSGERRSLLSGQBSQ 1140
Db 1058 HEMKSPPSARSSPHSPMSAASWTSRRSRNSLGRAPSLKRSPSGERRSLLSGQBSQ 1117

Qy 1141 DEESSSEERASPAGSDHRRHRSGLEREAKSFDLPDLOVPLGHLRTASGRGSAHQDN 1200
Db 1118 DEESSSEERASPPGSDHRRHRSGLEREAKSFDLPDLOVPLGHLRTASGRGSAHQDN 1177

Qy 1201 GKSASGRALARALRPDDPLDGDADDGDNLSKGRVRVARIARLPACCLERDSWASYFP 1260
Db 1178 GKSASGRALARALRPDDPLDGDADDGDNLSKGRVRVARIARLPACCLERDSWASYFP 1237

Qy 1261 PQSRFRLCHRIITHKMFHDVVLVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIPTAV 1320
Db 1238 PQSRFRLCHRIITHKMFHDVVLVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIPTAV 1297

Qy 1321 FLAEMTVKVALGWCFCGEQAYLRSSWNVLDGLLVLISVIDILVMSVDSGTKILGMLRVL 1380
Db 1298 FLAEMTVKVALGWCFCGEQAYLRSSWNVLDGLLVLISVIDILVMSVDSGTKILGMLRVL 1357

Qy 1381 RLRLTLPLRVISRAQGLKLVVETLMSLSLKPIGNIIVICCAFFIIFGLIGVQLPKGKFPV 1440
Db 1358 RLRLTLPLRVISRAQGLKLVVETLMSLSLKPIGNIIVICCAFFIIFGLIGVQLPKGKFPV 1417

Qy 1441 CQGEDTNTNKSDECAEASVYRWHRKYNFNDLGOALMSLFLVASKOGWVDIMYDGLDVG 1500
Db 1418 CQGEDTNTNKSDECAEASVYRWHRKYNFNDLGOALMSLFLVASKOGWVDIMYDGLDVG 1477

Qy 1501 VDQOPIWNHNPWMLLYIFISFLLIIVAFVFLNVGVVVENFHKKRQHQBEESARRRERKL 1560
Db 1478 VDQOPIWNHNPWMLLYIFISFLLIIVAFVFLNVGVVVENFHKKRQHQBEESARRRERKL 1537

Qy 1561 RLLEKKR-----KAQCKPYYSYDSRFRPLLVHLLCTSHYL 1595
Db 1538 RLLEKKRSEKQWADMLDDVIAAGSSASASAQAQCKPYYSYDSRFRPLLVHLLCTSHYL 1597

Qy 1596 DLFTITVIGLVNVTWAMEHYQQOQILDEALKICNYIETVIEVLESVPKLVAFGRFRFFQD 1655
Db 1598 DLFTITVIGLVNVTWAMEHYQQOQILDEALKICNYIETVIEVLESVPKLVAFGRFRFFQD 1657

Qy 1656 RWNOLDLAILLSIMGITLBEIEVNASLIPNPTIIRIMRVLRIARVLKLLKMAVGMRAILL 1715
Db 1658 RWNOLDLAILLSIMGITLBEIEVNASLIPNPTIIRIMRVLRIARVLKLLKMAVGMRAILL 1717

Qy 1716 DTVMQALPOVGNLGLLPMLLFFIFAALGVELFGLECDETHPCBGLGHATFRNFGMAFL 1775
Db 1718 DTVMQALPOVGNLGLLPMLLFFIFAALGVELFGLECDETHPCBGLGHATFRNFGMAFL 1777

Qy 1776 TLFVSTGDNWNGIMKDTLRDCQESTCYNTVISPVIYFVSFVLTAQFVLVNVVIAVLMKH 1835
Db 1778 TLFVSTGDNWNGIMKDTLRDCQESTCYNTVISPVIYFVSFVLTAQFVLVNVVIAVLMKH 1837

Qy 1836 LEESNKAKEAEAELEAELEEMKTLSPQHSPLGSPFLWPGVEGPDSPSPKPGALHPAA 1895
Db 1838 LEESNKAKEAEAELEAELEEMKTLSPQHSPLGSPFLWPGVEGPDSPSPKPGALHPAA 1897

Qy 1896 HARSASHFSLHPTMQPHTELPGDILLTVRKSGVSRTHSLPNDSYMCRHSTAGEPLGH 1955
Db 1898 HARSASHFSLHPTMQPHTELPGDILLTVRKSGVSRTHSLPNDSYMCRHSTAGEPLGH 1957

Qy 1956 RGMGLPKAQSGLSVHSVHSQPADTSYIQLPKDA PHILQPHSAPTWGTIPKLPFGPSPLA 2015
Db 1958 RGMGLPKAQSGLSVHSVHSQPADTSYIQLPKDA PHILQPHSAPTWGTIPKLPFGPSPLA 2017
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Qy	2016	ORPLRQAARTDSDVQGLSGREDLLAEVSGPPLARAYFWGQSSTOAOQHSRSHK	2075
Db	2018	ORPLRQAARTDSDVQGLSGREDLLAEVSGPPLARAYFWGQSSTOAOQHSRSHK	2077
Qy	2076	ISKHMTTPAPCPGPEPNWKGPPETRSLSLELDTLSWISGDLAPPQGOEPPSPDLKKC	2135
Db	2078	ISKHMTTPAPCPGPEPNWKGPPETRSLSLELDTLSWISGDLAPPQGOEPPSPDLKKC	2137
Qy	2136	YSVEAQSCORRPTSWLDEORRHSTAVSCLDSGSOPLHGTDPNSLGGQPLGPGSRPKKL	2195
Db	2138	YSVEAQSCORRPTSWLDEORRHSTAVSCLDSGSOPLHGTDPNSLGGQPLGPGSRPKKL	2197
Qy	2196	SPPSITIDPPESQGRTPPSPGICLRRAPSDSDKPLASGPPDSMAASPDKDVLSSL	2255
Db	2198	SPPSITIDPPESQGRTPPSPGICLRRAPSDSDKPLASGPPDSMAASPDKDVLSSL	2257
Qy	2256	GLSSDPADLDP 2266	
Db	2258	GLSSDPADLDP 2268	
RESULT 8			
ID	AAB66481		
XX	AAB66481 standard; protein; 2266 AA.		
AC	AAB66481;		
DT	09-APR-2001 (first entry)		
XX	Human alpha-IG T-type calcium channel protein.		
DE	Human; antiarrhythmic; anticonvulsant; hypotensive; cardiant; nootropic;		
KW	T-type calcium channel subunit; cardiac hypertrophy; cardiac arrhythmia;		
KW	hypertension; sleep disorder; epilepsy; alpha-IG T-type calcium channel.		
OS	Homo sapiens.		
XX	WO200102561-A2.		
PN	11-JAN-2001.		
XX	04-JUL-2000; 2000WO-CA000794.		
PF	02-JUL-1999; 99US-00346794.		
XX	(NEUR-) NEUROMED TECHNOLOGIES INC.		
PA	Snutch TP, Baillie DL;		
XX	WPI; 2001-123111/13.		
DR	N-PSDB; AAF31684.		
XX	Novel T-type calcium channel alpha-1 subunit gene useful for treating		
PT	cardiac hypertrophy, cardiac arrhythmia, hypertension, sleep disorder and		
PT	epilepsy.		
XX	Example 3; Fig 6; 103pp; English.		
PS	The present sequence is given in a specification providing sequences and		
CC	partial sequences for three types of mammalian (human and rat) T-type		
CC	calcium channel subunits. An expression cassette has been generated which		
CC	comprises a nucleotide sequence encoding a T-type calcium channel alpha_1		
CC	subunit operably linked to control sequences to effect its expression.		
CC	The novel calcium channel nucleic acids and proteins are useful for		
CC	treating conditions characterised by undesirable levels of T-type calcium		
CC	channel activity such as cardiac hypertrophy, cardiac arrhythmia,		
CC	hypertension, sleep disorder and epilepsy		
XX	Sequence 2266 AA;		
SQ	Query Match 97.9%; Score 11653; DB 4; Length 2266;		
	Best Local Similarity 98.8%; Pred. No. 0;		
	Matches 2239; Conservative 7; Mismatches 20; Indels 0; Gaps 0;		

Qy	1	MDEEDGAGAESGQPRSPFMRNLDSGAGRPGPSAEKDPGSADSEAEGLPYPALAPV	60
Db	1	MDEEDGAGAESGQPRSPFMRNLDSGAGRPGPSAEKDPGSADSEAEGLPYPALAPV	60
Qy	61	FFYLSQDSRPRSWCLRTVCNPFERISMLVILLNCVTGLMFRPCEDIACDSQRCILQAF	120
Db	61	FFYLSQDSRPRSWCLRTVCNPFERISMLVILLNCVTGLMFRPCEDIACDSQRCILQAF	120
Qy	121	DDFIFAFFAVEMVWKNVALGIFGKCYLGDWTNRDLDFVIAGMLEYSLDLQNVFSAYR	180
Db	121	DDFIFAFFAVEMVWKNVALGIFGKCYLGDWTNRDLDFVIAGMLEYSLDLQNVFSAYR	180
Qy	181	TVRVLRPLRAINRVPSMRILVTLTDLTLPMLGNVLLLCFFVFFIFGIVGVQVWAGLLNR	240
Db	181	TVRVLRPLRAINRVPSMRILVTLTDLTLPMLGNVLLLCFFVFFIFGIVGVQVWAGLLNR	240
Qy	241	CFLPENFSLPLSVDLERYQTENEDESPFICQPRENGMRSCSVPTLRGDCGGGPPCGL	300
Db	241	CFLPENFSLPLSVDLERYQTENEDESPFICQPRENGMRSCSVPTLRGDCGGGPPCGL	300
Qy	301	DYEAYNSSNTTCVNNQVYTNCSAGEHNPFKGAINFDNIGYAWIAIFQVITLEGWVDIM	360
Db	301	DYEAYNSSNTTCVNNQVYTNCSAGEHNPFKGAINFDNIGYAWIAIFQVITLEGWVDIM	360
Qy	361	YFVMDAHSFYNFYIFILLIIVGSFFMINCLVVIATQFSETKQRESQLMREORVRLSNA	420
Db	361	YFVMDAHSFYNFYIFILLIIVGSFFMINCLVVIATQFSETKQRESQLMREORVRLSNA	420
Qy	421	STLASFSGSCYEELIKVLYITLKAARLQAQVRAAGVVRGLLSSPAPLGGQETQPS	480
Db	421	STLASFSGSCYEELIKVLYITLKAARLQAQVRAAGVVRGLLSSPAPLGGQETQPS	480
Qy	481	SCSRSHRRLSVHLVHHHHHHHHHHLNGTTLAPRASPEIQDRDANGSRRLMLPPSTP	540
Db	481	SCSRSHRRLSVHLVHHHHHHHHHHLNGTTLAPRASPEIQDRDANGSRRLMLPPSTP	540
Qy	541	ALSGAPPGAESVHSFYHADCHLEPVRCQAPPPRSPSEASGRVTSKGKVPVTVHTSPPE	600
Db	541	ALSGAPPGAESVHSFYHADCHLEPVRCQAPPPRSPSEASGRVTSKGKVPVTVHTSPPE	600
Qy	601	TLKEKALVEAASSGPPTLTSLNI PGPYSSMHKLLETOSTGACQSSCKISSPCLKADSG	660
Db	601	TLKEKALVEAASSGPPTLTSLNI PGPYSSMHKLLETOSTGACQSSCKISSPCLKADSG	660
Qy	661	ACGPDSCPYCARAGAGEVELADREMPDSSEAVYFTQDAQHSDLRDPHRRORSIGPDA	720
Db	661	ACGPDSCPYCARAGAGEVELADREMPDSSEAVYFTQDAQHSDLRDPHRRORSIGPDA	720
Qy	721	EPSSVLAFWRLICDTFRKIYVDSKYFGRGIMAILVNTLSMGI EYHEQPELTNALEISNI	780
Db	721	EPSSVLAFWRLICDTFRKIYVDSKYFGRGIMAILVNTLSMGI EYHEQPELTNALEISNI	780
Qy	781	VFTSLFALEMLLKLVLVYGPFGYIKNPYNI PDGVIWISVWEIVGQGGGLSVLRTFLMR	840
Db	781	VFTSLFALEMLLKLVLVYGPFGYIKNPYNI PDGVIWISVWEIVGQGGGLSVLRTFLMR	840
Qy	841	VLKLVRLPALQRLVVLVMTMDNVATFCMLMLFITFISILGMHLPGCKFASERDGTLL	900
Db	841	VLKLVRLPALQRLVVLVMTMDNVATFCMLMLFITFISILGMHLPGCKFASERDGTLL	900
Qy	901	PDRKNFSLIWAIVTVFOILTQEDNKNVYNGMASTSSWAALYFIALMTGNYVFLNLLV	960
Db	901	PDRKNFSLIWAIVTVFOILTQEDNKNVYNGMASTSSWAALYFIALMTGNYVFLNLLV	960
Qy	961	AILVEGQAEIISKREDASGQSCIQLPVDSQGGDANKSESEPPFSPSLDGDGRKKCL	1020
Db	961	AILVEGQAEIISKREDASGQSCIQLPVDSQGGDANKSESEPPFSPSLDGDGRKKCL	1020
Qy	1021	ALVSLGHPHPELRKSLPLIHTAATPMSLPKSTSTGLGALGPASRTSSSGSAEPGAA	1080
Db	1021	ALVSLGHPHPELRKSLPLIHTAATPMSLPKSTSTGLGALGPASRTSSSGSAEPGAA	1080

1081 QY HEMKSPSPASPHSPWGAASWTSSRRNSRLGRAPSLKERSPSGERSLLSGEQBSQ 1140
1081 Db HEMKSPSPASPHSPWGAASWTSSRRNSRLGRAPSLKERSPSGERSLLSGEQBSQ 1140
1141 QY DEESSSEERASPAAGSDHRRHSGSLEREAKSFDLPDTLQVPLGRLHTASGRGSAEHQDCN 1200
1141 Db DEESSSEERASPAAGSDHRRHSGSLEREAKSFDLPDTLQVPLGRLHTASGRGSAEHQDCN 1200
1201 QY GKSASGRALARALRDPDPLDGDADDNGLSKGERVRAWIRARLPACYLERSDSWASYIFP 1260
1201 Db GKSASGRALARALRDPDPLDGDADDNGLSKGERVRAWIRARLPACYLERSDSWASYIFP 1260
1261 QY POSFRLLCHRIITNKMDHVLVITIIPLNCITIAMERPKIDPHSAERIFLTLNVIYFVAV 1320
1261 Db POSFRLLCHRIITNKMDHVLVITIIPLNCITIAMERPKIDPHSAERIFLTLNVIYFVAV 1320
1321 QY FLAEMTVKVALGWCFCGQAYLRSSNNVLDGLLVLSVIDILVMSVDSGTKILGMLRVL 1380
1321 Db FLAEMTVKVALGWCFCGQAYLRSSNNVLDGLLVLSVIDILVMSVDSGTKILGMLRVL 1380
1381 QY RLLRTLRLPVRISRAQGLKLVETLMSLSKIPGINIVWICCAFFIIFGILGVQLPKGPFV 1440
1381 Db RLLRTLRLPVRISRAQGLKLVETLMSLSKIPGINIVWICCAFFIIFGILGVQLPKGPFV 1440
1441 QY COGEDTRNITNKSDCAEASYRWRHKNFDFNLGQALMSLFVLASKOGWVDIMYDGLDAVG 1500
1441 Db COGEDTRNITNKSDCAEASYRWRHKNFDFNLGQALMSLFVLASKOGWVDIMYDGLDAVG 1500
1501 QY VDQOPIMNHNPMULLYFISFLIIIVAFFVLNMFVGVVFNFKHCKRQHOEBEAREERKRL 1560
1501 Db VDQOPIMNHNPMULLYFISFLIIIVAFFVLNMFVGVVFNFKHCKRQHOEBEAREERKRL 1560
1561 QY RRLEKRRKACKXPYSDYSRFRLLVHLCTSHYLDLFTITGIVGLNVVTMAHEHYQQPQI 1620
1561 Db RRLEKRRKACKXPYSDYSRFRLLVHLCTSHYLDLFTITGIVGLNVVTMAHEHYQQPQI 1620
1621 QY LDEALKICNYITFIVFVLESFKLVAFGRFRFFQDRWNQDLAIIVLSINGITILEEVN 1680
1621 Db LDEALKICNYITFIVFVLESFKLVAFGRFRFFQDRWNQDLAIIVLSINGITILEEVN 1680
1681 QY ASLPINPTIIRIMVRLIRARLVKLLKMAVGNRALLDTVMQALPOVGNLGLLFLMLFFIFA 1740
1681 Db ASLPINPTIIRIMVRLIRARLVKLLKMAVGNRALLDTVMQALPOVGNLGLLFLMLFFIFA 1740
1741 QY ALGVELFGDLCEDETHPCEGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMKDTLRDCDQE 1800
1741 Db ALGVELFGDLCEDETHPCEGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMKDTLRDCDQE 1800
1801 QY STCVNTVISPITYFVSFVLTAQFVLVNVVIAVIMKHLEESNKEAELEAELEMKTL 1860
1801 Db STCVNTVISPITYFVSFVLTAQFVLVNVVIAVIMKHLEESNKEAELEAELEMKTL 1860
1861 QY SPQHPSPGSPPLPFGVEGSPSPSPKPCALHPAAHARSASHFSLHPTMQPHTLPGP 1920
1861 Db SPQHPSPGSPPLPFGVEGSPSPSPKPCALHPAAHARSASHFSLHPTMQPHTLPGP 1920
1921 QY DLLTVRSGVSRTHSLPNDSTMYCRHGSTAEGPLGHRGWLKPAQSGSVLSVHSQPADTSY 1980
1921 Db DLLTVRSGVSRTHSLPNDSTMYCRHGSTAEGPLGHRGWLKPAQSGSVLSVHSQPADTSY 1980
1981 QY ILQLPKDAHLLQPHASPTWTGIPKLPPGSGPLAQRLRQAAIRTDLSLVQGLGSHED 2040
1981 Db ILQLPKDAHLLQPHASPTWTGIPKLPPGSGPLAQRLRQAAIRTDLSLVQGLGSHED 2040
2041 QY LLAEVSGSPPLARAYSFWGSSSTQAQOHSRSHSKI SKHMTTPPAPCPGPEPNWKGPPET 2100
2041 Db LLAEVSGSPPLARAYSFWGSSSTQAQOHSRSHSKI SKHMTTPPAPCPGPEPNWKGPPET 2100
2101 QY RSSLELDTLSWISGDLPLPGQEQEPPSPRDLKKCYSVQAQSCORRPTSWLDEQRHSIA 2160
2101 Db RSSLELDTLSWISGDLPLPGQEQEPPSPRDLKKCYSVQAQSCORRPTSWLDEQRHSIA 2160
2161 QY VSCLDSSGQPHLGTDPNGLGGQPLGGPSRPKKLSPPSIITIDPPESQGPRTPPSGICL 2220

2161 Db VSCLDSSGQPHLGTDPNGLGGQPLGGPSRPKKLSPPSIITIDPPESQGPRTPPSGICL 2220
2221 QY RRRAPSSDSKDPGLASGPPDSMAASPSKVKDVLSSLGSSDPADLDP 2266
2221 Db RRRAPSSDSKDPGLASGPPDSMAASPSKVKDVLSSLGSSDPADLDP 2266
RESULT 9
AAY70720
ID AAY70720 standard; protein; 2428 AA.
XX
AC AAY70720;
XX
DT 18-JUL-2000 (first entry)
XX
Rat pancreatic T-type calcium channel.
DE
KW Rat; pancreatic T-type calcium channel alpha subunit; insulin;
KW pancreatic beta cell; alpha1G; low voltage activated Ca2+ channel family;
KW antidiabetic; calcium influx; L type calcium channel; NIDDM;
XX type II diabetes; non-insulin dependent diabetes mellitus.
OS Rattus sp.
XX
FH Key Location/Qualifiers
FT Region 1. .52
FT /note= "Region upstream to pancreatic T-type calcium
FT channel protein"
FT Misc-difference 4
FT /note= "Encoded by in-frame stop codon TGA"
FT Protein 53. .2428
FT /label= Pancreatic T-type calcium channel_alpha_subunit
FT /note= "This region is claimed as SEQ ID NO: 2"
FT Region 53. .86
FT /note= "Unique region that differs from amino acid
FT sequence of neuronal T-type calcium channel alpha
FT subunit (alpha1G)"
FT Region 1023. .1046
FT /label= Intracellular loop I(II-III)
FT /note= "Unique region that differs from amino acid
FT sequence of neuronal T-type calcium channel alpha
FT subunit (alpha1G)"
FT Region 1622. .1640
FT /label= Intracellular loop L(III-IV)
FT /note= "Unique region that differs from amino acid
FT sequence of neuronal T-type calcium channel alpha
FT subunit (alpha1G)"
FT Misc-difference 2341
FT /note= "Encoded by in-frame stop codon TGA"
FT Misc-difference 2371
FT /note= "Encoded by in-frame stop codon TAA"
XX WO200015845-A1.
XX
XX 23-MAR-2000.
XX
XX 26-AUG-1999; 99WO-US019675.
XX
XX 26-AUG-1998; 98US-0098004P.
XX 27-JAN-1999; 99US-0117399P.
XX
XX (SALA-) SOUTH ALABAMA MEDICAL SCI FOUND.
XX
XX Li M;
XX
XX WPI; 2000-271475/23.
XX N-PSDB; AAZ52309.
XX
XX Novel nucleic acids encoding pancreatic T-type calcium channels used for
XX regulation of T-type calcium channels and treatment of type II diabetes.
XX
XX Example 1; Page 120; 124pp; English.
PS

XX The present sequence is a protein that includes pancreatic T-type calcium
CC channel alpha subunit derived from rat insulin secreting beta cell line,
CC INS-1. The protein shows 96.3 % identity to the neuronal T-type calcium
CC channel alpha subunit (alphaIG). The T-type Ca2+ channel from INS-1
CC (alphaIG-INS) and neuronal alphaIG are alternative splice isoforms of the
CC same gene. The INS-1 isoform is also expressed in brain, neonatal heart
CC and kidney besides pancreatic beta cells. T-type Ca2+ channel belongs to
CC the family of low voltage activated Ca2+ channels. The present sequence
CC is used for treating diseases associated with abnormal expression or
CC function of T-type calcium channels. They are especially used for
CC treating type II diabetes. Modulators of pancreatic T-type Ca2+ channel
CC e.g. antisense oligonucleotides, ribozymes and inhibitors are used in
CC methods for modifying insulin secretion by pancreatic beta cells, basal
CC calcium levels, potential L type calcium channel activity, pancreatic
CC cell death, pancreatic beta cell proliferation and calcium influx through
CC L type calcium channels in cells
XX

SQ Sequence 2428 AA;
Query Match 93.3%; Score 11111; DB 3; Length 2428;
Best Local Similarity 93.3%; Pred. No. 0;
Matches 2135; Conservative 35; Mismatches 95; Indels 24; Gaps 5;
QY 1 MDEEDGAGAESGQPRSFMRNLDSGAGRGPGSAEKDPGSAADSEAGLPPALAPVV 60
DB 53 MDEEDGAGAESGQPRSFQTLNDSGAGRGQPGSTKDPGSAADSEAGLPPALAPVV 112
QY 61 FFLYSQDSRPRSWCLRTVCNPFWRISMLVILLNCVILGMPFCEDACDSQRCRILQAF 120
DB 113 FFLYSQDSRPRSWCLRTVCNPFWRISMLVILLNCVILGMPFCEDACDSQRCRILQAF 172
QY 121 DDFIFAFPAFVAVMVKVAGLIFGKCYILGDTWRNLDFPIVAGLMEYSLDLQNVSESAVR 180
DB 173 DDFIFAFPAFVAVMVKVAGLIFGKCYILGDTWRNLDFPIVAGLMEYSLDLQNVSESAVR 232
QY 181 TVRVLRPRAINRVSFMRILVLLDTLPLGNVLLLCFFVFFPIGIVGVQLMAGLLNR 240
DB 233 TVRVLRPRAINRVSFMRILVLLDTLPLGNVLLLCFFVFFPIGIVGVQLMAGLLNR 292
QY 241 CFLPENFSLPSVLDLERYQTENEDSPFICSQPRENGRSCRSVPTLRGCGGGPPCGL 300
DB 293 CFLPENFSLPSVLDLERYQTENEDSPFICSQPRENGRSCRSVPTLRGCGGGPPCGL 352
QY 301 DYEAYNSSNTTCVANNQYVWCSAGEHNPFGKAGNFDNIGYAWIAIFQVITLEGWVDM 360
DB 353 DYEAYNSSNTTCVANNQYVWCSAGEHNPFGKAGNFDNIGYAWIAIFQVITLEGWVDM 412
QY 361 YFVMDAHSFYNFYIFILLIIVGSFFMINCLVVIATQFSETKQRESQLMREQVRFLSNA 420
DB 413 YFVMDAHSFYNFYIFILLIIVGSFFMINCLVVIATQFSETKQRESQLMREQVRFLSNA 472
QY 421 STLASFSEPGSCYEELLYVILRKAARLQVSAAGVRVGLISSPAPLGGQETQSS 480
DB 473 STLASFSEPGSCYEELLYVILRKAARLQVSAAGVRVGLISSPAPLGGQETQSS 532
QY 481 SCRSRHERLVSVHLVHHHHHHHHYHLGNTLRAPRASPEIQDRDANGSRRLMLPPSP 540
DB 533 SCRSRHERLVSVHLVHHHHHHHHYHLGNTLRAPRASPEIQDRDANGSRRLMLPPSP 592
QY 541 ALSGAPPGGAESVHSFYHADCHLEPVRCAQAPPPRSPSEASGRVTGSGKVPVTHVTSPPPE 600
DB 593 TPSSGPPRGAESVHSFYHADCHLEPVRCAQAPPPRSPSEASGRVTGSGKVPVTHVTSPPPE 652
QY 601 TLKEKALVEVAASGPPPTLSNIPGYPSSMKHLLTQSTGACQSSCKISSPCLKADSG 660
DB 653 ILKDKALVEVAPSGPPTLTSNIPGYPSSMKHLLTQSTGACHSCKISSPCLKADSG 712
QY 661 ACGPDSFCPCARAGAGEVELADREMPDSDSEAVVEFTQDAQHSDLRDPHS -RRQSLGPD 719
DB 713 ACGPDSFCPCARTGAGEPESADHVMPPDSDSEAVVEFTQDAQHSDLRDPHSRRRQSLGPD 772
QY 720 AEPSSVLAFWRLICDTRFKIVDSKYFGRGIMAILVNTLSMGIEYHEQPEELTNALEISN 779

773 AEPSSVLAFWRLICDTRFKIVDSKYFGRGIMAILVNTLSMGIEYHEQPEELTNALEISN 832
QY 780 IVFTSLFALEMLLKLIVYVPGYIKPNYINFDGVIIVISVWEIVGQOGGGLSVLRTFLM 839
DB 833 IVFTSLFALEMLLKLIVYVPGYIKPNYINFDGVIIVISVWEIVGQOGGGLSVLRTFLM 892
QY 840 RVLKLVRLPALQORLVLMKTMNDVATFCMLLMFLPIFISILGMHLFGCKFASERDGT 899
DB 893 RVLKLVRLPALQORLVLMKTMNDVATFCMLLMFLPIFISILGMHLFGCKFASERDGT 952
QY 900 LPDRKNFDSLLMAIVTVFQILTQEDWNKLVNGMASTSSWAALYFIAMTGNVYVFLNLL 959
DB 953 LPDRKNFDSLLMAIVTVFQILTQEDWNKLVNGMASTSSWAALYFIAMTGNVYVFLNLL 1012
QY 960 VAILVEGQAEISKREDASGQSCIQLPVDSQGDANKSESEPPFFSPSDGDRKKC 1019
DB 1013 VAILVEGQAEISKREDASGQSCIQLPVDSQGDANKSESEPPFFSPSDGDRKKR 1072
QY 1020 LALVSLGEHPELRKSLPLIHTAATPMSLPKSTSTGLGALGAPASRRRTSSSGSAEPGA 1079
DB 1073 LALVSLGEHPELRKSLPLIHTAATPMSLPKSTSTGLGALGAPASRRRTSSSGSAEPGA 1132
QY 1080 A-HEMKSPPSARSSPHSPMSAASSWTSRSPSSNSIGRAPSLKRRSPSGERRSLISGEQGE 1138
DB 1133 AHHEMKSPPSARSSPHSPMSAASSWTSRSPSSNSIGRAPSLKRRSPSGERRSLISGEQGE 1192
QY 1139 SODERESSSEERASPAQSDHRRHGRSLEREAKSSFDLPDTLQVPGHLRTASGRSSASEHOD 1198
DB 1193 SODERESSSEERASPAQSDHRRHGRSLEREAKSSFDLPDTLQVPGHLRTASGRSSASEHOD 1252
QY 1199 CNGKSASGLARALRPDDPPLGDDADDGNNLSKGERVPAWIRARLPACYLERSDSWAVI 1258
DB 1253 CNGKSASGLARALRPDDPPLGDDADDGNNLSKGERVPAWIRARLPACYLERSDSWAVI 1312
QY 1259 FPPQSFRLLCHRIITHKMFHDVHLVILFLNCITTIAMERPKIDPHSAERIFLTLNFIPT 1318
DB 1313 FPPQSFRLLCHRIITHKMFHDVHLVILFLNCITTIAMERPKIDPHSAERIFLTLNFIPT 1372
QY 1319 AVFLAEMTVKVALGCFGEQAYLRSSMNVLGDLVLIISVIDILVSNVSDSGTKILGMLR 1378
DB 1373 AVFLAEMTVKVALGCFGEQAYLRSSMNVLGDLVLIISVIDILVSNVSDSGTKILGMLR 1432
QY 1379 VLRLRLRLPRLVIRSAQGLKLVETLMSLKPIGNIVVICCAFFIIFGLGVQLFKGKF 1438
DB 1433 VLRLRLRLPRLVIRSAQGLKLVETLMSLKPIGNIVVICCAFFIIFGLGVQLFKGKF 1492
QY 1439 FVCGEDTRNITNKSDCAEASVYRWRHKNFNDLQALMSLFLVASKDGWVDIMYDGLDA 1498
DB 1493 FVCGEDTRNITNKSDCAEASVYRWRHKNFNDLQALMSLFLVASKDGWVDIMYDGLDA 1552
QY 1499 VGVDQOPIMNHPMMLLYFISPLLIIVAFVIANFVGWVVENFHKHQHQBEEBARRREK 1558
DB 1553 VGVDQOPIMNHPMMLLYFISPLLIIVAFVIANFVGWVVENFHKHQHQBEEBARRREK 1612
QY 1559 RLRLLEKRR-----KAQCKPYSDYSRFRLLVHHLCTSHYLDLFI 1600
DB 1613 RLRLLEKRRMLDDVIVASGSSASASEAQCKPYSDYSRFRLLVHHLCTSHYLDLFI 1672
QY 1601 GVIGLVVTVMAHEHYQQPILDEALKICNVIPTVIVLESVKLVAFGRFRFFQDRWNOL 1660
DB 1673 GVIGLVVTVMAHEHYQQPILDEALKICNVIPTVIVLESVKLVAFGRFRFFQDRWNOL 1732
QY 1661 DIAIVLLSINGITILEEVNASLPINPTIIRIMVLRIRARVLLKLMKAVGNRALLDVTM 1720
DB 1733 DIAIVLLSINGITILEEVNASLPINPTIIRIMVLRIRARVLLKLMKAVGNRALLDVTM 1792
QY 1721 ALPOVNGLGLLFLMLIFFIFAAALGVLEFGLDECDTHPCGELGRHATFRNFGMAFLTFRV 1780
DB 1793 ALPOVNGLGLLFLMLIFFIFAAALGVLEFGLDECDTHPCGELGRHATFRNFGMAFLTFRV 1852
QY 1781 STGDNNWNGIMKOTLDDCQESTCYNTVTSPIYFVSFVLTAQFVLNVVIVAVLMKHEESN 1840

Db 1853 STGDWNGIMKDTLRDCQESTCYNTVISPFIYFVSFVLTAQFVLNVNVIAMKHLERN 1912
 Qy 1841 KEAKEAELEAELEEMKTLSPQHSPLGSPFLWPGVGPSPDPSPKPGALHPAAHARSA 1900
 Db 1913 KEAKEAELEAELEEMKTLSPQHSPLGSPFLWPGVGVNSPDPSPKPGAPHTTAHIGAA 1972
 Qy 1901 SHFSLHPTMOPHTPELP--GPDLTVRKSGVSRTHSLPNDSYMCRHGSTAEGPLGHRG 1957
 Db 1973 SGFSLHPTMVPHEVEVPVLPGLDVLTVRKSGVSRTHSLPNDSYMCRHGSTAEGPLGHRG 2032
 Qy 1958 WGLPKAQSGSVLSVHSPADTSYILQLPKDAPHLLQPHSAPTWGTIPKLPPLPGSPPLAQR 2017
 Db 2033 WGLPKAQSGSVLSVHSPADTSYILQLPKDAPHLLQPHSAPTWGTIPKLPPLPGSPPLAQR 2092
 Qy 2018 PLRQAAIRTSLOVQGLSGREDLLAEVSGSPPLARAYSTWQSGSTQAQHSRSHSKIS 2077
 Db 2093 PLRQAAIRTSLOVQGLSGREDLLAEVSGSPPLARAYSTWQSGSTQAQHSRSHSKIS 2152
 Qy 2078 KHMTPPAPCPGEPNMGKPPETRSSLELDTLSWISGDLPPGQOEPPSPRDLKKCY 2137
 Db 2153 KHIRLPAPCPGLEFSWAKDPPETRSSLELDTLSWISGDLPPGQOEPPSPRDLKKCY 2211
 Qy 2138 YEAQSCRRPTSWLDEQRRHSIAVSCLDGSGQPHLGTDPNLSGQPLGPGSRPKKLSL 2197
 Db 2212 VETQSCRRPGSWLDEQRRHSIAVSCLDGSGQPHLGTDPNLSGQPLGPGSRPKKLSL 2271
 Qy 2198 PSITIDPESQGPRTPPSPGICLRRRAPSSDSKOPLAGPPDPMAAASPSPKDVLSGL 2257
 Db 2272 PSITIDPESQGPRTPPSPGICLRRRAPSSDSKOPLAGPPDPMAAASPSPKDVLSGL 2331
 Qy 2258 SSDPADLDP 2266
 Db 2332 SSDPDMDP 2340

RESULT 10

AA14593
 ID AA14593 standard; protein; 2247 AA.
 AC AA14593;
 XX
 DT 07-DEC-1999 (first entry)
 XX
 DE Rat T-type voltage-gated Ca channel alpha-1-G (rCavTid).
 XX
 KW Human; T-type voltage-gated calcium channel; membrane; pore; ion;
 KW activation; current; rat; screen; drug; cardiomyopathy; epilepsy.
 XX
 OS Rattus sp.
 XX
 FN W09929847-A1.
 XX
 PD 17-JUN-1999.
 XX
 PF 30-OCT-1998; 98WO-US023161.
 XX
 PR 05-DEC-1997; 97US-00985809.
 XX
 PA (LOYO) UNIV LOYOLA CHICAGO.
 XX
 PI Perez-Reyes E, Cribbs LL;
 XX
 DR WPI; 1999-394972/33.
 DR N-ESDB; AAX83488.
 XX
 PT New T-type voltage-gated calcium channels.
 XX
 PS Disclosure; Page 94-103; 138pp; English.

This sequence represents a rat T-type voltage-gated calcium (Ca) channel alpha-1-G designated rCavTid. Voltage gated channels are membrane bound glycosylated proteins formed of several subunits. The large alpha subunits form a pore in the membrane that is selective for a given ionic

CC species. Each alpha subunit contains 4 domains (I, II, III and IV) and
 CC each domain contains 6 putative transmembrane helical segments (S1-S6). T
 CC -type Ca channels are activated at a lower voltage than L- or N-type
 CC channels. Characteristics of T-type channels include short current time,
 CC slow activation kinetics near threshold, fast inactivation kinetics and
 CC slow tail current. The sequences AAX83481-X83492 represent novel T-type
 CC voltage-gated Ca channel genes from humans and rats. Each of the novel Ca
 CC channels contains a putative IVS4 region comprising the amino acid
 CC sequence AAY14598. Cells expressing the T-type voltage-gated calcium
 CC channel proteins can be used to screen for drugs which affect calcium
 CC channels. Methods are also disclosed for treating a disease or disorder
 CC associated with a deficiency in a native T-type calcium channel nucleic
 CC acid, e.g. to treat cardiomyopathy, epilepsy, etc

XX Sequence 2247 AA;

Query Match 92.1%; Score 10962.5; DB 2; Length 2247;
 Best Local Similarity 92.8%; Pred. No. 0;
 Matches 2108; Conservative 33; Mismatches 101; Indels 29; Gaps 5;
 Qy 1 MDEEDGAGABESGQPSRSMRLNDLSGAGRGPGSABKDPGSADSEAGLPYPALAPV 60
 Db 1 MDEEDGAGABESGQPSRSMRLNDLSGAGRGPGSABKDPGSADSEAGLPYPALAPV 60
 Qy 61 FFYLSQDSRPSRSCWCLRTVCNPFERISMLVLLNCVTLGMPERPCEDIAQDRCRILQAF 120
 Db 61 FFYLSQDSRPSRSCWCLRTVCNPFERISMLVLLNCVTLGMPERPCEDIAQDRCRILQAF 120
 Qy 121 DDFIFAFVAVMVVMVALGIFGKKCYLGTWNRDLDFIVTAGMLEYSLDLQNVSFSAVR 180
 Db 121 DDFIFAFVAVMVVMVALGIFGKKCYLGTWNRDLDFIVTAGMLEYSLDLQNVSFSAVR 180
 Qy 181 TVRVLRLPRLAINRVPSMRILVTLTLLDPLMGNVLLLCFFVFFIFGIVGVQLWAGLLRNR 240
 Db 181 TVRVLRLPRLAINRVPSMRILVTLTLLDPLMGNVLLLCFFVFFIFGIVGVQLWAGLLRNR 240
 Qy 241 CFLPENFSLPLSDLEPYOTENEDESPFICSPRENGMRSCRSVPTLRGGGGPPCGL 300
 Db 241 CFLPENFSLPLSDLEPYOTENEDESPFICSPRENGMRSCRSVPTLRGGGGPPCGL 300
 Qy 301 DYEAYNSSNTTCVNMNQYTNCSAGEHNPFGAINFDNIGYAMIAIFQVITLEGWVIM 360
 Db 301 DYEAYNSSNTTCVNMNQYTNCSAGEHNPFGAINFDNIGYAMIAIFQVITLEGWVIM 360
 Qy 361 YFVMDAHSFYNIYFILLIIVGSPFMNLCVLTATQFSETKQRESQMLRQVRFLSNA 420
 Db 361 YFVMDAHSFYNIYFILLIIVGSPFMNLCVLTATQFSETKQRESQMLRQVRFLSNA 420
 Qy 421 STLASFSEPGSCYEELKLYVILRKAARLAQVSRAGVVRVGLLSSPAPLGQGTQPS 480
 Db 421 STLASFSEPGSCYEELKLYVILRKAARLAQVSRAGVVRVGLLSSPAPLGQGTQPS 480
 Qy 481 SCRSRRLSVHLLVHHHHHHHHYHLNGTGLAPRASPEIQDRDANGSRRLMPPSTP 540
 Db 481 SCRSRRLSVHLLVHHHHHHHHYHLNGTGLAPRASPEIQDRDANGSRRLMPPSTP 540
 Qy 541 ALSCAPPGABSVHSFYHADCHLEPVRCPAPPPSPSEASGRTVSGKVYPTVHTSPPE 600
 Db 541 ALSCAPPGABSVHSFYHADCHLEPVRCPAPPPSPSEASGRTVSGKVYPTVHTSPPE 600
 Qy 601 TLKEKALVEVNAASSGPTLTSLNIPGPGYSMMHKLLETQSTGACOSSCKISSPCLKADSG 660
 Db 601 TLKEKALVEVNAASSGPTLTSLNIPGPGYSMMHKLLETQSTGACOSSCKISSPCLKADSG 660
 Qy 661 ACPDSCPCYCARAGAGVELADREMPDSDSAVYFTQDAQSHDLRDPHS--RRORSLGPD 719
 Db 661 ACPDSCPCYCARAGAGVELADREMPDSDSAVYFTQDAQSHDLRDPHS--RRORSLGPD 719
 Qy 720 ABPSSVLAFLWRLICDTFRKIVDSKYFGRGIMAILVNTLSMGIYHPOEELTNALEISN 779
 Db 720 ABPSSVLAFLWRLICDTFRKIVDSKYFGRGIMAILVNTLSMGIYHPOEELTNALEISN 779
 Qy 780 IVFTSLFALEMLLKLIVYGFPGYIKNPYNIPDGVIVVISVWEIVGQGGGLSVLRTFLM 839

[illegible]

Db 1958 LSVHSQPADTSCILQLPKDHYLLQPHGAPTWGAIPKLPBPPGSRPLAQRPLRQAAIRTD 2017
QY 2029 SLVQGLGSRDILLAEVSGSPPLARAYSEWGOSSTQAOQHRSRSHKISKHMTTPAPCPG 2088
Db 2018 SLVQGLGSRDILLAEVSGSPPLARAYSEWGOSSTQAOQHRSRSHKISKHMTTPAPCPG 2077
QY 2089 PEPNMGKPPETRSSLELDELTELWISGDLPLPGQEEPPSPDLKCYVSEVQSCORRT 2148
Db 2078 LEPWAKDPPETRSSLELDELTELWISGDLPLPGQEEPPSPDLKCYVSEVQSCORRT 2136
QY 2149 SWLDEQRHRSIAVCLSGSGPHGLTDPNGLGQPLGGGSRPKKLSPPSIIDPPESQ 2208
Db 2137 FWLDEQRHRSIAVCLSGSGPHGLTDPNGLGQPLGGGSRPKKLSPPSIIDPPESQ 2196
QY 2209 GPRTPPGICLRRRAPSSDKPLASGPPDPSMAASPPKDVLSLGLSSDPADLDP 2266
Db 2197 GSRPPCSPGVCLRRRAPASDSKDPVSPDLSTAAASPPKDVLSLGLSSDPADLDP 2254

RESULT 12
AAY14591
ID AAY14591 standard; protein; 2265 AA.

XX AAY14591;
AC AAY14591;
DT 07-DEC-1999 (first entry)

DE Rat T-type voltage-gated Ca channel alpha-1-G (rCav1b).

XX Human; T-type voltage-gated calcium channel; membrane; pore; ion;
KW activation; current; rat; screen; drug; cardiomyopathy; epilepsy.

XX Rattus sp.

XX WO929847-A1.

XX 17-JUN-1999.

XX 30-OCT-1998; 98WO-US023161.

XX 05-DEC-1997; 97US-00985809.

XX (LOYO) UNIV LOYOLA CHICAGO.

XX Perez-Reyes E, Cribbs LL;

XX WPI; 1999-394972/33.

XX N-PSDB; AAX83486.

XX New T-type voltage-gated calcium channels.

XX Disclosure; Page 76-85; 138pp; English.

XX This sequence represents a rat T-type voltage-gated calcium (Ca) channel
XX alpha-1-G designated rCav1b. Voltage gated channels are membrane bound
XX glycosylated proteins formed of several subunits. The large alpha
XX subunits form a pore in the membrane that is selective for a given ionic
XX species. Each alpha subunit contains 4 domains (I, II, III and IV) and
XX each domain contains 6 putative transmembrane helical segments (S1-S6). T
XX -type Ca channels are activated at a lower voltage than L- or N-type
XX channels. Characteristics of T-type channels include short current time,
XX slow activation kinetics near threshold, fast inactivation kinetics and
XX slow tail current. The sequences AAX83481-X83492 represent novel T-type
XX voltage-gated Ca channel genes from humans and rats. Each of the novel Ca
XX channels contains a putative IVS4 region comprising the amino acid
XX sequence AAY14598. Cells expressing the T-type voltage-gated calcium
XX channel proteins can be used to screen for drugs which affect calcium
XX channels. Methods are also disclosed for treating a disease or disorder
XX associated with a deficiency in a native T-type calcium channel nucleic
XX acid, e.g. to treat cardiomyopathy, epilepsy, etc

XX Sequence 2265 AA;

XX SQ

Query Match 91.9%; Score 10939.5; DB 2; Length 2265;
Best Local Similarity 92.0%; Pred. No. 0;
Matches 2107; Conservative 34; Mismatches 101; Indels 47; Gaps 6;
QY 1 MDEEDGAGABESGQPPSRFRLNDLSGAGRPFGSGAEKDPGSADEAEGLPYPALAPV 60
Db 1 MDEEDGAGABESGQPPSRFRLNDLSGAGRPFGSGAEKDPGSADEAEGLPYPALAPV 60
QY 61 FFLYSQSRPSRSCWCLRTVCPNPFERISMLVILLNCVTLGMFRPCEDIACQSQRILQAF 120
Db 61 FFLYSQSRPSRSCWCLRTVCPNPFERISMLVILLNCVTLGMFRPCEDIACQSQRILQAF 120
QY 121 DDFIFAPFAVEMVVMVALGIFGKKCYLGDWTNRLDFFIAGLWLESLDQNVSPSAVR 180
Db 121 DDFIFAPFAVEMVVMVALGIFGKKCYLGDWTNRLDFFIAGLWLESLDQNVSPSAVR 180
QY 181 TVRVLRPLRAINRVPSPMRILVTLTLLDTPMLGNVLLLCFFVFFIFGIVGQWAGLNR 240
Db 181 TVRVLRPLRAINRVPSPMRILVTLTLLDTPMLGNVLLLCFFVFFIFGIVGQWAGLNR 240
QY 241 CFLPENFSLPLSVDLERYOTENEDSPFICSQPRENGMRSCRSVPTLRGGGGPPCGL 300
Db 241 CFLPENFSLPLSVDLERYOTENEDSPFICSQPRENGMRSCRSVPTLRGGGGPPCGL 300
QY 301 DYEAYNSSNTTCVNNQYTYNCSAGEHPKGAINDNIGVAMTAFQVITLGGWVDM 360
Db 301 DYEAYNSSNTTCVNNQYTYNCSAGEHPKGAINDNIGVAMTAFQVITLGGWVDM 360
QY 361 YFVMDAHSFYNIYFILLIIVGFFMNLCLVVIATQFSETKQRESQMRQVRLSNA 420
Db 361 YFVMDAHSFYNIYFILLIIVGFFMNLCLVVIATQFSETKQRESQMRQVRLSNA 420
QY 421 STLASFEPGSCYEELLYLVILKAAARLAQVRAAGVRLGLSSPAPLGGQGTQPS 480
Db 421 STLASFEPGSCYEELLYLVILKAAARLAQVRAAGVRLGLSSPAPLGGQGTQPS 480
QY 481 SCRSRRLSVHLLVHHHHHHHHVHLNGTTLRPRASPEIQDRDANGSRRLMLPPSTP 540
Db 481 SCRSRRLSVHLLVHHHHHHHHVHLNGTTLRPRASPEIQDRDANGSRRLMLPPSTP 540
QY 541 ALSGAPPGGAESVHSFYHADCHLEPVRCQAPPPSPSEASGRTVSGKYVPTVHTSPPE 600
Db 541 TPGGPPRGAESVHSFYHADCHLEPVRCQAPPPSPSEASGRTVSGKYVPTVHTSPPE 600
QY 601 TLXKALVEVAASGPPTLTSLNIPGPYSSMHKLLETQSTGACQSSCKISSPCSKADSG 660
Db 601 ILKDXALVEVAPSPGPPTLTSLNIPGPYSSMHKLLETQSTGACQSSCKISSPCSKADSG 660
QY 661 ACGPDCPCYCARAGAGEVELADREMPDSSEAVYETQDAQHSDLRDPHS-RRQRSIGPD 719
Db 661 ACGPDCPCYCARAGAGEVELADREMPDSSEAVYETQDAQHSDLRDPHS-RRQRSIGPD 719
QY 720 AEPSSVLAFWRLICDTRFKIVDSKYFGRGIMIALVNTLSMGIEYHEQPELTNALEISN 779
Db 721 AEPSSVLAFWRLICDTRFKIVDSKYFGRGIMIALVNTLSMGIEYHEQPELTNALEISN 780
QY 780 IVFTSLFALEMLKLLVYGPYKPNYIFDGVIVVISVWEIVGQGGSLVLRFLM 839
Db 781 IVFTSLFALEMLKLLVYGPYKPNYIFDGVIVVISVWEIVGQGGSLVLRFLM 840
QY 840 RVLKLVRLPALQOLVVMKTMNVATFCMLMLFIFISILGMHLFGCKFASERDGT 899
Db 841 RVLKLVRLPALQOLVVMKTMNVATFCMLMLFIFISILGMHLFGCKFASERDGT 900
QY 900 LPDRKNFSLMAIVTVFQILTQEDWNKLVYNGMASTSSWAALYFIALMTFGNVLNLL 959
Db 901 LPDRKNFSLMAIVTVFQILTQEDWNKLVYNGMASTSSWAALYFIALMTFGNVLNLL 960
QY 960 VAILVEGFQAEISIKREDASGOLSCIQLPVDQSGDANKSEPEFSPSDGDRKKC 1019
Db 961 VAILVEGFQAEISIKREDASGOLSCIQLPVDQSGDANKSEPEFSPSDGDRKKC 997
QY 1020 LALVSLGHEPRLKSLPLLIHTAATPMSLPKSTSTGLGEALGPASRRRTSSSGSAEPGA 1079

Db 998 LALVALGHAELKSLPLLIHTAATPMSPKSSSTGVGALGSGRRTSSSGAEPGA 1057
Qy 1080 A-HWKSPSPARSPHSPWASASWTSSRRNSLGRAPSLKRSPSGERRSLLSGEGOE 1138
Db 1058 AHHEWKCPSPARSPHSPWASASWTSSRRNSLGRAPSLKRSPSGERRSLLSGEGOE 1117
Qy 1139 SODEEESSEERASPDGHDHGRSLEREAKSSFDLPTLQVPGHRTASGRSASEHOD 1198
Db 1118 SODEEESSEEDRASPDGHDHGRSLEREAKSSFDLPTLQVPGHRTASGRSASEHOD 1177
Qy 1199 CNKGSASGLARALRPDPPLDGDADDDEGNLSKGERVRAMTRARLPACYLERSWSAYI 1258
Db 1178 CNKGSASGLARTLTDDPQLDGDADDDEGNLSKGERIQAWRSRLPACCRERSWSAYI 1237
Qy 1259 FPPOSFRLCHRIITHKQFHVVLVIFLNCITIAMERPKIDPHSAERIFLTLSNYIFT 1318
Db 1238 FPPOSFRLCHRIITHKQFHVVLVIFLNCITIAMERPKIDPHSAERIFLTLSNYIFT 1297
Qy 1319 AVFLAEMTVKVALGWCFCGEQAYLRSSWNVLGDLVLISVIDILVMSVDSGTKILGMLR 1378
Db 1298 AVFLAEMTVKVALGWCFCGEQAYLRSSWNVLGDLVLISVIDILVMSVDSGTKILGMLR 1357
Qy 1379 VLRLRLRLRVRISRAOGLKLVETLMSSLKPIGNIWVICAPFIIFGILGVOLFKGKF 1438
Db 1358 VLRLRLRLRVRISRAOGLKLVETLMSSLKPIGNIWVICAPFIIFGILGVOLFKGKF 1417
Qy 1439 FVCGEDTRNITNKSDCAEASYRVRHKYNFDNLGOALMSLFLVASKDGVVDIMYDGLDA 1498
Db 1418 FVCGEDTRNITNKSDCAEASYRVRHKYNFDNLGOALMSLFLVASKDGVVDIMYDGLDA 1477
Qy 1499 VGVDQOPIIMNPNWMLLYFISFLIVAFVPLMFGVVVNFHFKCRHQHOOEERREK 1558
Db 1478 VGVDQOPIIMNPNWMLLYFISFLIVAFVPLMFGVVVNFHFKCRHQHOOEERREK 1537
Qy 1559 RLRLLEKKRR-----KAOCKPYSDYSRFRLLVHHLCTSHYLDLFT 1600
Db 1538 RLRLLEKKRNLMLDDVTASGSSASAASEAOCKPYSDYSRFRLLVHHLCTSHYLDLFT 1597
Qy 1601 GVLGLNVVTMAEHYQQOILDEALKICNYIFTVFVLESFVKLVAFGRFRFPQDRWNQL 1660
Db 1598 GVLGLNVVTMAEHYQQOILDEALKICNYIFTVFVLESFVKLVAFGRFRFPQDRWNQL 1657
Qy 1661 DLAIVLISIMGITLSEIEVNSLSPINPTIIRIMVLRIRARVLKLLKMAVGRALLDTMQ 1720
Db 1658 DLAIVLISIMGITLSEIEVNSLSPINPTIIRIMVLRIRARVLKLLKMAVGRALLDTMQ 1717
Qy 1721 ALPOVGNLGLLFMLLFFIFALGVLFGLDCEDETHPCGEGLRHATFRNFGMAFLTFRV 1780
Db 1718 ALPOVGNLGLLFMLLFFIFALGVLFGLDCEDETHPCGEGLRHATFRNFGMAFLTFRV 1777
Qy 1781 STGDNWNGIMKDTLRDCDOESTCYNTVISPITYFVSFVLTAQFVLNVNVIAMKHEESN 1840
Db 1778 STGDNWNGIMKDTLRDCDOESTCYNTVISPITYFVSFVLTAQFVLNVNVIAMKHEESN 1837
Qy 1841 KEAKEEAELAELEEMKTLSPQHSPLGSPFLPGVEGPPSPSPKPGALHPAARSA 1900
Db 1838 KEAKEEAELAELEEMKTLSPQHSPLGSPFLPGVEGPPSPSPKPGAPHTTAHTGAA 1897
Qy 1901 SHFSLHPTMOPHTPLP---GPDLITVRKGVSRTHSLPNDSYMCRHGSTAEGPLGHRG 1957
Db 1898 SGFSLHPTMOPHTPLP---GPDLITVRKGVSRTHSLPNDSYMCRHGSTAEGPLGHRG 1957
Qy 1958 WGLPKAOGSVLSVHSQPADTSYILQLPKDAPHLLQPHSAFTWGTIPKLPFGPSPLAQ 2017
Db 1958 WGLPKAOGSVLSVHSQPADTSCILQLPKDVHLLQPHGAPTWGAIKLPFPGRSPLAQ 2017
Qy 2018 PLRQAAIRTRDSLDVQGLSGRDLLEAVSGSPPLARAYSTWGSSTQAOQHSRSHKIS 2077
Db 2018 PLRQAAIRTRDSLDVQGLSGRDLLEAVSGSPPLARAYSTWGSSTQAOQHSRSHKIS 2077
Qy 2078 KHMTPPAPCPGPEPWGKGPETRSSLELDTLSWISGDLPLPCGQEEPPSPDRDLKCY 2137

Db 2078 KHIRLPAPCGLPESWAKOPPETRSSLELDTLSWISGDLPLPCGQEEPPSPDRDLKCY 2136
Qy 2138 VEAQSCORRPTSWLDEQRHSHIAVCLDSGQPHLGTDPNLGGQPLGGPSRPPKKULSP 2197
Db 2137 VETQSCRRRPGFWLDEQRHSHIAVCLDSGQPHLGTDPNLGGQPLGGPSRPPKKULSP 2196
Qy 2198 PSITIDPESOGPTPTSPSGICLRRRASPSSDKPLASGPPDSMAASPSPKDVLSLSG 2257
Db 2197 PSISIDPESOGSPRPPSPGVCLRRRAPASDKPVSPLDSTAAASPSPKDVLSLSG 2256
Qy 2258 SSDPADLDP 2266
Db 2257 SSDPTDMDP 2265
RESULT 13
AAV14592
ID AAV14592 standard; protein; 2272 AA.
XX AC AAV14592;
XX DT 07-DEC-1999 (first entry)
XX Rat T-type voltage-gated Ca channel alpha-1-G (rCavTic).
DE Human; T-type voltage-gated calcium channel; membrane; pore; ion;
KW activation; current; rat; screen; drug; cardiomyopathy; epilepsy.
XX Rattus sp.
XX WO9929847-A1.
XX PD 17-JUN-1999.
XX PF 30-OCT-1998; 98WO-US023161.
XX PR 05-DEC-1997; 97US-00985809.
XX PA (LOYO) UNIV LOYOLA CHICAGO.
XX Perez-Reyes E, Cribbs LL;
PI WPI; 1999-394972/33.
XX N-PSDB; AAX83487.
PT New T-type voltage-gated calcium channels.
XX Disclosure; Page 85-94; 138pp; English..
XX This sequence represents a rat T-type voltage-gated calcium (Ca) channel
alpha-1-G designated rCavTic. Voltage gated channels are membrane bound
glycosylated proteins formed of several subunits. The large alpha
subunits form a pore in the membrane that is selective for a given ionic
species. Each alpha subunit contains 4 domains (I, II, III and IV) and
each domain contains 6 putative transmembrane helical segments (S1-S6). T
-type Ca channels are activated at a lower voltage than L- or N-type
channels. Characteristics of T-type channels include short current time,
slow activation kinetics near threshold, fast inactivation kinetics and
slow tail current. The sequences AAX83481-X83492 represent novel T-type
voltage-gated Ca channel genes from humans and rats. Each of the novel Ca
-channels contains a putative IVS4 region comprising the amino acid
sequence AAY14598. Cells expressing the T-type voltage-gated calcium
channel proteins can be used to screen for drugs which affect calcium
channels. Methods are also disclosed for treating a disease or disorder
associated with a deficiency in a native T-type calcium channel nucleic
acid, e.g. to treat cardiomyopathy, epilepsy, etc
XX Sequence 2272 AA;
Query Match 91.8%; Score 10925; DB 2; Length 2272;
Best Local Similarity 91.7%; Pred. No. 0;
Matches 2106; Conservative 33; Mismatches 103; Indels 54; Gaps 6;

QY 1 MDEEDGAGAEBSGQPRSFMRINDLSAGGRPGSAEKDPCGSADSEABGLPYPALAPV 60
Db 1 MDEEDGAGAEBSGQPRSFMRINDLSAGGRPGSAEKDPCGSADSEABGLPYPALAPV 60
QY 61 FFYLSQSRPSWCLRVNCPWPERISMLVILLNCVTLGMFRPCEDICADSORCILQAF 120
Db 61 FFYLSQSRPSWCLRVNCPWPERISMLVILLNCVTLGMFRPCEDICADSORCILQAF 120
QY 121 DDFIFAFVEMVVMVALGIFGKKCVLGTWRLDFFVIAGMLYSIDLQNVSAVR 180
Db 121 DDFIFAFVEMVVMVALGIFGKKCVLGTWRLDFFVIAGMLYSIDLQNVSAVR 180
QY 181 TVRVLRLPRAINRVPSPMRILVLLDTPMLGNVLLCFVFFIFGIVGQVLWAGLLRNR 240
Db 181 TVRVLRLPRAINRVPSPMRILVLLDTPMLGNVLLCFVFFIFGIVGQVLWAGLLRNR 240
QY 241 CFLPENFSLPLSVDLERYQTEDESPFICQPRENGMRSRVPTRLRGDGGGPPCGL 300
Db 241 CFLPENFSLPLSVDLERYQTEDESPFICQPRENGMRSRVPTRLRGDGGGPPCGL 300
QY 301 DYEATNSSNTTCVNMNOYITNCAGAHNPKGAINFDNIGYAMIAIFQVITLEGWDIM 360
Db 301 DYEATNSSNTTCVNMNOYITNCAGAHNPKGAINFDNIGYAMIAIFQVITLEGWDIM 360
QY 361 YFVMDAHSFYNFIFILLIIVGSPFMNLCUWVATOPSETKQRESQIMREQVRFLSNA 420
Db 361 YFVMDAHSFYNFIFILLIIVGSPFMNLCUWVATOPSETKQRESQIMREQVRFLSNA 420
QY 421 STLASFSEPGCYEBELLKVLVILKAAARLQVSRAGVRVGLSSPAPIGGQETQPS 480
Db 421 STLASFSEPGCYEBELLKVLVILKAAARLQVSRAGVRVGLSSPAPIGGQETQPS 480
QY 481 SCRSRRRLSVHLLVHHHHHHHYYLNGTLRAPASPEIQDRDANGSRRLMLPPSP 540
Db 481 SCRSRRRLSVHLLVHHHHHHHYYLNGTLRAPASPEIQDRDANGSRRLMLPPSP 540
QY 541 AUSGAPPGAEBSVHSFYHADCHLEPVRCOAPPRSPSEASGRTVSGKVYPTVHTSPPE 600
Db 541 TPSSGPPRGAESVHSFYHADCHLEPVRCOAPPRSPSEASGRTVSGKVYPTVHTSPPE 600
QY 601 TLKEALVEVAASGPGPTLTSNIPPGYSSMHKLETOSTCACOSSCKISPPCLKADSG 660
Db 601 ILKDKALVEVAPSPGPTLTSNIPPGYSSMHKLETOSTCACOSSCKISPPCLKADSG 660
QY 661 ACPDSCPCYCARAGAEVELADREMPDSSEAVYFTQADSHDLRDHPS-RRORSGLPD 719
Db 661 ACPDSCPCYCARAGAEVELADREMPDSSEAVYFTQADSHDLRDHPS-RRORSGLPD 720
QY 720 AEPSSVLAFWRLICDTRKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPEELTNALEISN 779
Db 720 AEPSSVLAFWRLICDTRKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPEELTNALEISN 780
QY 780 IVFTSLFALEMLKLALVYGFYIKNPYNIFDGVIVVISWEIVGOGGGLSVLRTFLM 839
Db 780 IVFTSLFALEMLKLALVYGFYIKNPYNIFDGVIVVISWEIVGOGGGLSVLRTFLM 840
QY 840 RVLKLVRLPALQQLVLMKTMNDVATFCMLLMFIFIFSLGMHLFGCKFASERDGT 899
Db 840 RVLKLVRLPALQQLVLMKTMNDVATFCMLLMFIFIFSLGMHLFGCKFASERDGT 900
QY 900 LPDRKNFDSLWAIIVTFQILTOEDWNKVLNGMASTSSWAALYFTALMTFGNVFLNLL 959
Db 900 LPDRKNFDSLWAIIVTFQILTOEDWNKVLNGMASTSSWAALYFTALMTFGNVFLNLL 960
QY 960 VAILVEGQAEIISKREDASQLSQILPVDSCQGDANKSESEDPFSPSLDGDGRKKC 1019
Db 960 VAILVEGQAEIISKREDASQLSQILPVDSCQGDANKSESEDPFSPSLDGDGRKKC 997
QY 1020 LALVSLGHEPRLKSLPLIHTAATPMGLPKSTISGLGALGPASRRRTSSGSAEPGA 1079
Db 998 LALVALGAEHLKSLPLIHTAATPMGLPKSTISGLGALGPASRRRTSSGSAEPGA 1057
QY 1080 A-HEMKSPPSARSSPWSAASSWTSRRSSRNSLGRAPSLKRRSPSGRRSLLSGEGQE 1138

Db 1058 AHHEMKCPPARSPSPWSAASSWTSRRSSRNSLGRAPSLKRRSPSGRRSLLSGEGQE 1117
QY 1139 SQDEESESERASPAAGSDHRRHGSGLERAKSSFDPDLTQVPLGRLHTASGRGSAHEQD 1198
Db 1118 SQDEESESERASPAAGSDHRRHGSGLERAKSSFDPDLTQVPLGRLHTASGRGSAHEQD 1177
QY 1199 CNGKSASGRRLARALRPDDPPLDGDADDDEGNLSKGBRVRARLAPACYLERSDSWAI 1258
Db 1178 CNGKSASGRRLARALRPDDPPLDGDADDDEGNLSKGBRVRARLAPACYLERSDSWAI 1237
QY 1259 PPQOSRFRLLCHRIITHKMFHDVVLVIIIFLNCITIAMERPKIDPHSNERIFLTLNVIPT 1318
Db 1238 PPQOSRFRLLCHRIITHKMFHDVVLVIIIFLNCITIAMERPKIDPHSNERIFLTLNVIPT 1297
QY 1319 AVFLAEMTVKVALGWCFCGEQAYLRSSWNVLDDLVLISVIDIIVSVSDSGTKILGMLR 1378
Db 1298 AVFLAEMTVKVALGWCFCGEQAYLRSSWNVLDDLVLISVIDIIVSVSDSGTKILGMLR 1357
QY 1379 VLRLTLRLPLRVISRAQGLKLVVETLMSSLKPIGNIVVICCAFFIIFGILGVOLFKGK 1438
Db 1358 VLRLTLRLPLRVISRAQGLKLVVETLMSSLKPIGNIVVICCAFFIIFGILGVOLFKGK 1417
QY 1439 FVCOGEDTRNITNKSDCAEASVVRVVRHKNYFNDLGQALMSLFLVLSKDGWDIMYDGLDA 1498
Db 1418 FVCOGEDTRNITNKSDCAEASVVRVVRHKNYFNDLGQALMSLFLVLSKDGWDIMYDGLDA 1477
QY 1499 VGVDOOPTIMNHPMMLLYFISFLIVAFVLMVGVVVENFHKRQHOEERARRREK 1558
Db 1478 VGVDOOPTIMNHPMMLLYFISFLIVAFVLMVGVVVENFHKRQHOEERARRREK 1537
QY 1559 RLRLLEKKRR-----KAOCKPYSDYSRFRLLVHHLCTSH 1593
Db 1538 RLRLLEKKRR-----KAOCKPYSDYSRFRLLVHHLCTSH 1597
QY 1594 YLDLFTTIGVIGLVNVTMAHEHYQQOQILDEALKICNYITVIFVLESFVKLVAFGRFRFF 1653
Db 1598 YLDLFTTIGVIGLVNVTMAHEHYQQOQILDEALKICNYITVIFVLESFVKLVAFGRFRFF 1657
QY 1654 QDRWNQILDALVLLSINGITLLEEIVNLSLNPITIRIMRVLRIARVLKLLKMAVGMA 1713
Db 1658 QDRWNQILDALVLLSINGITLLEEIVNLSLNPITIRIMRVLRIARVLKLLKMAVGMA 1717
QY 1714 LLDTWQALPOVGNLGLLFFMILLFFIPAAALGVLEFGDECDTHPCBGLGRHATFRNFGMA 1773
Db 1718 LLDTWQALPOVGNLGLLFFMILLFFIPAAALGVLEFGDECDTHPCBGLGRHATFRNFGMA 1777
QY 1774 FLTLFRVSTGDNNGIMKOTLRDCQDESTCYNTVISPIYFVSFVLTAQFVLVNVVIAVLM 1833
Db 1778 FLTLFRVSTGDNNGIMKOTLRDCQDESTCYNTVISPIYFVSFVLTAQFVLVNVVIAVLM 1837
QY 1834 KHLSESKAEKEAELEAELEEMKTLSPHSPGLSPFLWPGVEGPDSPSPKPGALHP 1893
Db 1838 KHLSESKAEKEAELEAELEEMKTLSPHSPGLSPFLWPGVEGPDSPSPKPGALHP 1897
QY 1894 AAHARSASHESLEHTPQPHTELP---GPDLLTVKSGVSRTHSLPNDSMCRHGSTAE 1950
Db 1898 TAHIKAASGFSLEHTPQPHTELP---GPDLLTVKSGVSRTHSLPNDSMCRHGSTAE 1957
QY 1951 GPLGHRGGLPKAOGSVLSVHSPADTSTYLOPKDAPHLLOPHSAPTWTGTIKLPDPPG 2010
Db 1958 RSLGHRGGLPKAOGSVLSVHSPADTSTYLOPKDAPHLLOPHSAPTWTGTIKLPDPPG 2017
QY 2011 RSPLAQRPLRQAARTDSDVQGLGSRDILLAEVSGSPPLARAYFWGSSSTQAQOHS 2070
Db 2018 RSPLAQRPLRQAARTDSDVQGLGSRDILLAEVSGSPPLARAYFWGSSSTQAQOHS 2077
QY 2071 RSHKISKHMTFPPAPCPGPEPNWKGPPETRSSLSLELOTELTSWISGDLPLPGQGEPPSPR 2130
Db 2078 GIKQSVKSHIRLAPCPGLEFSWAKDPPETRSSLSLELOTELTSWISGDLPLPGQGEPPSPR 2136
QY 2131 DLKCKYCVBAQSCORRPTSWLDEQRHSHIAVSCLDGSGOHLGTDTPSNLGGQPLGGGSR 2190

Db	2137	DLKNCYSVETQSCRRRGFWLDEQRHRSIAVCLDSGQFRLCPSPSSLGQPLGGPGR	2199
Qy	2191	PKKKLSPSPSITIDPPESQGPRTPEPGICLRRAPSSDSKDPLASGPPDSMAASPSPKKD	2250
Db	2197	PKKKLSPSPSITIDPPESQGSRRPSPGVCLLRRAPASDSKDPSSVSLDSTAASPSPKKD	2256
Qy	2251	VLSLSGLSSDPADLDP	2266
Db	2257	TLSSLSGLSSDPTDMDP	2272
RESULT 14			
AAB66475			
ID	AAB66475 standard; protein; 2287 AA.		
XX	AAB66475;		
XX	09-APR-2001 (first entry)		
XX	Rat alpha-IG calcium channel protein.		
DE	XX		
DE	XX		
KW	Rat; expressed sequence tag; EST; antiarrhythmic; anticonvulsant;		
KW	hypotensive; cardiant; nootropic; T-type calcium channel subunit;		
KW	cardiac hypertrophy; cardiac arrhythmia; hypertension; sleep disorder;		
KW	epilepsy; alpha-IG calcium channel.		
XX	XX		
OS	Rattus sp.		
XX	XX		
PN	WO200102561-A2.		
XX	XX		
PD	11-JAN-2001.		
XX	XX		
PF	04-JUL-2000; 2000WO-CR000794.		
XX	XX		
PR	02-JUL-1999; 99US-00346794.		
XX	XX		
PA	(NEUR-) NEUROMED TECHNOLOGIES INC.		
XX	XX		
PI	Snutch TP, Baillie DL;		
XX	XX		
DR	WPI; 2001-123111/13.		
DR	N-PSDB; AAF31677.		
XX	XX		
PT	Novel T-type calcium channel alpha-1 subunit gene useful for treating		
PT	cardiac hypertrophy, cardiac arrhythmia, hypertension, sleep disorder and		
PT	epilepsy.		
XX	XX		
PS	Disclosure; Page 63-72; 103pp; English.		
XX	XX		
CC	The present sequence is given in a specification providing sequences and		
CC	partial sequences for three types of mammalian (human and rat) T-type		
CC	calcium channel subunits. An expression cassette has been generated which		
CC	comprises a nucleotide sequence encoding a T-type calcium channel alpha_1		
CC	subunit operably linked to control sequences to effect its expression.		
CC	The novel calcium channel nucleic acids and proteins are useful for		
CC	treating conditions characterised by undesirable levels of T-type calcium		
CC	channel activity such as cardiac hypertrophy, cardiac arrhythmia,		
CC	hypertension, sleep disorder and epilepsy		
XX	XX		
XX	Sequence 2287 AA;		
Query Match 90.5%; Score 10774; DB 4; Length 2287;			
Best Local Similarity 92.3%; Pred. No. 0;			
Matches 2075; Conservative 33; Mismatches 105; Indels 36; Gaps 6;			
Qy	30	GRPGSGAEKDPGSADSEAGLPYPALAPVVFYLSQDSRPSWCLRTVCNPFERISML	89
Db	62	GAAGAGSTEDPGSADSEAGLPYPALAPVVFYLSQDSRPSWCLRTVCNPFERVSML	121
Qy	90	VILLNCVTGLMFRPCEDIACDSORCILOAFDDFIFAFFAVENVKVALGIFGKCYLG	149
Db	122	VILLNCVTGLMFRPCEDIACDSORCILOAFDDFIFAFFAVENVKVALGIFGKCYLG	181

```
Db 1239 GNLSKGERIQAWVSRLPACCRDSSAVIFPPQSRFLLCRTHIIRKMFHDLVVLVIF 1298
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Db 1839 QFVLNVNVIAVLMKHLEESKEAEAELEAELEAELEAELEAELEAELEAELEAELEAELE 1898
Qy 1881 DSPSPKPGALHPAAHARSASHFSLHPTMOPHTLP - - - GPDLTLVRKSGVSRTHSLP 1937
Db 1899 NSTDSPKPGAPHTTAHGAAGSFSLEHPTMVHPPEEVVPLGPDLLTVRKSGVSRTHSLP 1958
Qy 1938 NDSYMCRRHGSTAEGPLGHRGWLKPAQSGSVLSVHSQPADTSYIOLPKDAPHILLOHSA 1997
Db 1959 NDSYMCRRHGSTAEGPLGHRGWLKPAQSGSVLSVHSQPADTSYIOLPKDAPHILLOHSA 2018
Qy 1998 PTWGTIPKLPKPPGSRPLAQRPLRQAARTDSDVQGLGSRDILLAEVSGSPPLARAYS 2057
Db 2019 PTWGAIPKLPKPPGSRPLAQRPLRQAARTDSDVQGLGSRDILLAEVSGSPPLARAYS 2078
Qy 2058 FWGSSSTQAQHSRSHSKISKIMTTPAPCPGPEPNWGWGPPETRSLSLELDTLSWISGDL 2117
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Db 2258 LDSTAASPPKVDLSGLSDPADLDP 2286
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AAU00474
ID AAU00474 standard; protein; 1207 AA.
XX
AC AAU00474;
XX
DT 18-JUL-2001 (first entry)
XX
Human T-type calcium channel CACNA1G protein.
DE
KW Human; T-type calcium channel; CACNA1G; cytosine methylation; CpG island;
KW cellular proliferative disorder; colorectal cancer; age related disease;
KW apolipoprotein B; APOB; caudal type homeobox transcription factor 2;
KW CDX2; epidermal growth factor receptor; EGFR; fibrillin-1; FBNI; MINT31;
KW G protein-coupled receptor 37; GPR37; heat shock 70KD protein 6; HSP70B;
KW HSPA6; RasGAP-related protein; IQGAP2; proteinase-activated receptor 2;
KW PAR2; paired-like homeodomain transcription factor 2; PITX2; klotho; KL;
KW patched A; patched B; PTCHA; PTCHB; syndecan 1; syndecan 4; SDC1; SDC4;
KW chromosome 17.
XX
OS Homo sapiens.
XX
PN WC200119845-A1.
XX
PD 22-MAR-2001.
XX
PF 14-SEP-2000; 2000WO-US025479.
XX
PR 15-SEP-1999; 99US-00398522.
XX
PA (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
XX
PI Issa J;
XX
WPI; 2001-244777/25.
XX
N-PSDB; AAS01624.
XX
New nucleic acid molecule for use as a marker for screening cancer,
comprises the coding region for a T-type calcium channel and regulatory
sequences associated with the channel.
XX
Claim 9; Fig 3B; 125pp; English.
```

The present sequence representing a novel human T-type calcium channel CACNA1G maps to chromosome 17. The methylation state of specific regions within CpG islands associated with the CACNA1G gene correlate with several cancerous phenotypes involving various tissue and cell types. Since aberrant methylation of normally unmethylated CpG islands is often observed in immortalised and transformed cells, CACNA1G is implicated in cellular proliferative disorders e.g. leukaemia, colorectal, lung, breast and other cancers. The nucleic acid coding for CACNA1G is useful as a marker for screening cancer and age related diseases. A diagnostic kit containing primers (AAS01574-AAS01623) for amplification of a CpG polynucleotide sequence (AAS01627-AAS01676), can be used for detecting aberrant methylation. The CpG island sequences (AAS01677-AAS01692) are selected from genes encoding CACNA1G, apolipoprotein B (APOB), caudal type homeobox transcription factor 2 (CDX2), epidermal growth factor receptor (EGFR), fibrillin-1 (FBNI), G protein-coupled receptor 37 (GPR37), heat shock 70KD protein 6 (HSP70B; HSPA6), RasGAP-related protein (IQGAP2), klotho (KL), proteinase-activated receptor 2 (PAR2), paired-like homeodomain transcription factor 2 (PITX2), patched A and B (PTCHA; PTCHB) and syndecan 1 and 4 (SDC1; SDC4) or a MINT 31 sequence

Sequence 1207 AA;

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Best Local Similarity 99.1%; Pred. No. 0;
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Db 1 MDEEDGAGAEESQPRSFMRNLDSLGGAGRPGSGAEKDPGSADEAGLPYPALAPV 60
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Db 61 FFYLSQDSRPSWCLRTVCNPFERRISMLVILLNCVTIGMPPCEDIACDSORCIILOAF 120
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Db 121 DDIFAFPAFVAVMVKQVALGIFGKKCYLGDWTNRDLDFIIVAGMLEYSLDLQNVSFSAVR 180
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Db 241 CFLPENFSLPLSVDLERYQTENEDESPFICISQPRENGMRCRSVPTLRGGGGPPCGL 300
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Search completed: April 13, 2005, 16:34:38
Job time : 256 secs

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Db 1178 GKSASGRLARALRPDDPPLDGGDDADDEGNL 1207

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 13, 2005, 16:30:32 ; Search time 57 Seconds
(without alignments)
2967.628 Million cell updates/sec

Title: US-09-611-257A-37
Perfect score: 11904
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 6: /cgn2_6/ptodata/1/iaa/backfiles.pap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	11241	94.4	2220	4	US-09-949-016-9730
3	6315.5	53.1	1207	4	US-09-398-522-52
4	6211	52.2	2353	3	US-08-984-709A-50
5	5492.5	46.1	2175	3	US-09-404-650-2
6	5492.5	46.1	2175	4	US-09-935-541-2
7	5484	46.1	2188	3	US-09-404-650-4
8	5484	46.1	2188	4	US-09-935-541-4
9	5366	45.1	1835	3	US-09-404-650-5
10	5366	45.1	1835	4	US-09-935-541-5
11	1750.5	14.7	2343	3	US-09-268-163-4
12	1749	14.7	2337	3	US-08-713-118-2
13	1749	14.7	2337	3	US-09-452-007-2
14	1748.5	14.7	2339	1	US-08-455-543A-47
15	1748.5	14.7	2339	2	US-08-223-305C-47
16	1746.5	14.7	2339	3	US-09-268-163-6
17	1743	14.6	2237	1	US-08-455-543A-48
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19	1741	14.6	2237	3	US-09-268-163-8
20	1722	14.5	2336	3	US-09-268-163-10
21	1632.5	13.7	1873	1	US-08-435-675B-4
22	1622.5	13.6	1873	1	US-08-336-257A-7
23	1619.5	13.6	1984	3	US-08-836-325-10
24	1619.5	13.6	1984	4	US-09-457-571-10
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29	1615.5	13.6	1989	4	US-09-457-571-12	Sequence 12, Appl
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33	1601	13.4	1977	4	US-09-495-714C-4	Sequence 4, Appl
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39	1587	13.3	2016	4	US-09-896-994-2	Sequence 2, Appl
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41	1586	13.3	1969	3	US-09-457-571-16	Sequence 16, Appl
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43	1586	13.3	2016	4	US-09-840-125-4	Sequence 4, Appl
44	1583	13.3	1977	4	US-09-976-594-757	Sequence 757, App
45	1583	13.3	1977	4	US-09-919-039-367	Sequence 367, App

ALIGNMENTS

RESULT 1
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; Sequence 5, Application US/09426998
; Patent No. 6358706
; GENERAL INFORMATION:
; APPLICANT: DUBIN, ADRIENNE E.
; APPLICANT: PYATI, JAVASHREE
; APPLICANT: ZHU, JESSICA Y
; APPLICANT: ERLANDER, MARK G
; APPLICANT: GALINDO, JOSE E
; TITLE OF INVENTION: DNA ENCODING HUMAN ALPHAIG T-TYPE CALCIUM
; FILE REFERENCE: ORT-1057
; CURRENT APPLICATION NUMBER: US/09/426,998
; CURRENT FILING DATE: 1999-10-26
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PATENTIN VER. 2.0
; SEQ ID NO 5
; LENGTH: 2273
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-426-998-5

Query Match	99.7%	Score 11862.5;	DB 3;	Length 2273;
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			Indels	7;
			Gaps	1;
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QY 1614 HYQOQILDEALKICNYIFTVIFVLESVKLVAFGRRFQDRWNOLDLAIVLISMGIT 1673
DB 1621 HYQOQILDEALKICNYIFTVIFVLESVKLVAFGRRFQDRWNOLDLAIVLISMGIP 1680
QY 1674 LESIEVNASIPINPTIIRIMRVLIARVLKLMVGMRAALLDTVMQALPOVGNLGLLPM 1733
DB 1681 LEQIEVNASIPINPTIIRIMRVLIARVLKLMVGMRAALLDTVMQALPOVGNLGLLPM 1740
QY 1734 LLFFIFAAALGVLEFGDLECDETHPCBGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMKOT 1793
DB 1741 LLFFIFAAALGVLEFGDLECDETHPCBGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMKOT 1800
QY 1794 LRDCDQESTCINTVISPFIYFVSFVLTAQFVLVNVVIAVLMKHLSEENKEAKEAELEAEL 1853
DB 1801 LRDCDQESTCINTVISPFIYFVSFVLTAQFVLVNVVIAVLMKHLSEENKEAKEAELEAEL 1860
QY 1854 ELEMKTLSPOPHSPLSGPFLWPGVEGPDSPDPSKPGALHPAAHARSASHSFSLHPTMQPH 1913
DB 1861 ELEMKTLSPOPHSPLSGPFLWPGVEGPDSPDPSKPGALHPAAHARSASHSFSLHPTMQPH 1920
QY 1914 PTELPGPDLTLVRKSGVSRTHSLPNDSYMCRHSGSTAEGPLGHRGWGLPKAQSGSVLSVHS 1973
DB 1921 PTELPGPDLTLVRKSGVSRTHSLPNDSYMCRHSGSTAEGPLGHRGWGLPKAQSGSVLSVHS 1980
QY 1974 OPADTSVILQIPKADPHLOPHSAPTWTGTPKPPGSRPLAORPLRQRAIIRTSLSDVQ 2033
DB 1981 QPADTSVILQIPKADPHLOPHSAPTWTGTPKPPGSRPLAORPLRQRAIIRTSLSDVQ 2040
QY 2034 GLSREDLLAEVSGSPPLARAYSFWGQSTQQAQHSRSHSKISXKMTTPPAPCPGPEPNW 2093
DB 2041 GLSREDLLAEVSGSPPLARAYSFWGQSTQQAQHSRSHSKISXKMTTPPAPCPGPEPNW 2100
QY 2094 GKGPETRSLELDTLSWISGDLPPGGOEPPSPDLKKCYSVBAQSCORRPTSWLDE 2153
DB 2101 GKGPETRSLELDTLSWISGDLPPGGOEPPSPDLKKCYSVBAQSCORRPTSWLDE 2160
QY 2154 QRHSIAVSCLDGSGQPHLGTDPNLGGQPLGGPSRPPKLLGPPSITIDPPESQGRTP 2213
DB 2161 QRHSIAVSCLDGSGQPHLGTDPNLGGQPLGGPSRPPKLLGPPSITIDPPESQGRTP 2220
QY 2214 PSPGICLRRRAPSDSDXDPPLASGPPDMSAASPDKDVLSSLGSLSSDPADLDP 2266
DB 2221 PSPGICLRRRAPSDSDXDPPLASGPPDMSAASPDKDVLSSLGSLSSDPADLDP 2273

RESULT 2

US-09-949-016-9730
; Sequence 9730, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL004307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498

;; PRIOR FILING DATE: 2000-09-08
;; NUMBER OF SEQ ID NOS: 207012
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 9730
;; LENGTH: 2220
;; TYPE: PRT
;; ORGANISM: Human
US-09-949-016-9730

Query Match 94.4%; Score 11241; DB 4; Length 2220;
Best Local Similarity 95.1%; Pred. No. 0;
Matches 2162; Conservative 1; Mismatches 1; Indels 110; Gaps 4;

Qy	1	MDEEDGAGAESGQPRSMRLNDLSGAGRGPGSAEKDPGSADSEAGLPYPALAPVV	60
Db	49	MDEEDGAGAESGQPRSMRLNDLSGAGRGPGSAEKDPGSADSEAGLPYPALAPVV	108
Qy	61	FFYLSQDSRRPSWCLRTVWNP-WFERISMLVILLNCVTLMGFRPCEDTACDSQCRILQA	119
Db	109	FFYLSQDSRRPSWCLRTVWNP-WFERISMLVILLNCVTLMGFRPCEDTACDSQCRILQA	168
Qy	120	FDDFIPAFPAFVEMVVMKVALGPGKCKYLGDTWNRDLFFIAGMLEYSLDLQNVFSAV	179
Db	169	FDDFIPAFPAFVEMVVMKVALGPGKCKYLGDTWNRDLFFIAGMLEYSLDLQNVFSAV	228
Qy	180	RTVRVLRPLRAINRVPSNRILVTLTLLDTPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRN	239
Db	229	RTVRVLRPLRAINRVPSNRILVTLTLLDTPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRN	288
Qy	240	RCFLPENFSLPSVDLERYOTENEDSPFICSQPRENGMSCRSVPTLRGDDGGGPPCG	299
Db	289	RCFLPENFSLPSVDLERYOTENEDSPFICSQPRENGMSCRSVPTLRGDDGGGPPCG	348
Qy	300	LDYEAYNSSNTTCVNMNYYTNCAGAHNPFKGAINDFNIGYAWIAIFQVITILEGWDI	359
Db	349	LDYEAYNSSNTTCVNMNYYTNCAGAHNPFKGAINDFNIGYAWIAIFQVITILEGWDI	408
Qy	360	MYFWDAAHSFNFIYFILLIIVGFFMINCLVIAIATQFSTKQESQJMQREQVRFLSN	419
Db	409	MYFWDAAHSFNFIYFILLIIVGFFMINCLVIAIATQFSTKQESQJMQREQVRFLSN	468
Qy	420	ASTLASFEGSCGYEELLYVILTKAARLAQVSRAGRVGLLSPPALGGOETQPS	479
Db	469	ASTLASFEGSCGYEELLYVILTKAARLAQVSRAGRVGLLSPPALGGOETQPS	528
Qy	480	SSCSRRRLSVHLLVHHHHHHHHYHLNGTTLRAPASPEIQDRDANGSRRLMLPPST	539
Db	529	SSCSRRRLSVHLLVHHHHHHHHYHLNGTTLRAPASPEIQDRDANGSRRLMLPPST	588
Qy	540	PALSGAPPGGAESVHSFYHADCHLEPVRCQAPPSPRSPSEASGRVTGSGKVPTVHTSPPP	599
Db	589	PALSGAPPGGAESVHSFYHADCHLEPVRCQAPPSPRSPSEASGRVTGSGKVPTVHTSPPP	648
Qy	600	ETLKEKALVEAASGPPTLTSLNIPGPGYSMMHKLLETQSTGACQSCCKTSSPCLKADS	659
Db	649	ETLKEKALVEAASGPPTLTSLNIPGPGYSMMHKLLETQSTGACQSCCKTSSPCLKADS	708
Qy	660	GACGPDSCPCYCARAGAGEVELADREMPDSDSEAVVEFTQDAQHSDLRDPHRSRQRLGPD	719
Db	709	GACGPDSCPCYCARAGAGEVELADREMPDSDSEAVVEFTQDAQHSDLRDPHRSRQRLGPD	768
Qy	720	AEPSVLAFWRLICDTFRKIVDSKYFGRGIMAILVNTLSMGIEYHEQPEBELTNALEISN	779
Db	769	AEPSVLAFWRLICDTFRKIVDSKYFGRGIMAILVNTLSMGIEYHEQPEBELTNALEISN	828
Qy	780	IVFTSLFALEMLLKVYGPYIKNPYNIIDGIVLVISWEIYVCOQGGGLSVLRTFLM	839
Db	829	IVFTSLFALEMLLKVYGPYIKNPYNIIDGIVLVISWEIYVCOQGGGLSVLRTFLM	888
Qy	840	RVLKLVRLPALQRLQVLMKTMNDVATFCMLLMLEFIIFSLGMLHFGCKFASERDGT	899
Db	889	RVLKLVRLPALQRLQVLMKTMNDVATFCMLLMLEFIIFSLGMLHFGCKFASERDGT	948

Qy	900	LPDRKNFDSLLWAIVTVFOILLTOEDMKNVLYNGMASTSSWAALYFIALMTFGNYVLFNLL	959
Db	949	LPDRKNFDSLLWAIVTVFOILLTOEDMKNVLYNGMASTSSWAALYFIALMTFGNYVLFNLL	1008
Qy	960	VAILVEGFOAEISKREDASQOLSCIQLPVDSQGDANKSESEDPFSPSDGCDRKKC	1019
Db	1009	VAILVEGFOAE-----GDKANSSESDPFSPSDGCDRKKC	1045
Qy	1020	LALVSLGEHPELRKSLPLPLIHTAATPMSLPKSTSTGLGALGPASRRTSSSGSAEPGA	1079
Db	1046	LALVSLGEHPELRKSLPLPLIHTAATPMSLPKSTSTGLGALGPASRRTSSSGSAEPGA	1105
Qy	1080	AHEMKSPSASRSPHSWASASSTWTSRRSSNSIAGRAPSLKRRSPSGRRSILLSGEGQES	1139
Db	1106	AHEMKSPSASRSPHSWASASSTWTSRRSSNSIAGRAPSLKRRSPSGRRSILLSGEGQES	1165
Qy	1140	QDESESEERASAPAGDHRHGRSLEAKSSFDLPDTLQVPGHLRTASGRGSAEHQDC	1199
Db	1166	QDESESEERASAPAGDHRHGRSLEAKSSFDLPDTLQVPGHLRTASGRGSAEHQDC	1225
Qy	1200	NGKSASGLRALAPDPDPPDGDADDDEGNLSKGERVRAMIRARLPACYLBERDSWAIYF	1259
Db	1226	NGKSASGLRALAPDPDPPDGDADDDEGNLSKGERVRAMIRARLPACYLBERDSWAIYF	1285
Qy	1260	PQOSRFRLLCHRIITHKMEHVVLIIFLNCITITAMERPKIDPHSAERIILTLSNYIFTA	1319
Db	1286	PQOSRFRLLCHRIITHKMEHVVLIIFLNCITITAMERPKIDPHSAERIILTLSNYIFTA	1345
Qy	1320	VFLAEMTVKVALGWCFCGEQAYLRSSNVLDGLLVLISVIDILVSMVSDSGTKILGMLRV	1379
Db	1346	VFLAEMTVKVALGWCFCGEQAYLRSSNVLDGLLVLISVIDILVSMVSDSGTKILGMLRV	1405
Qy	1380	LRLRLTLRLRVISRAQGLKLVETLMSLKPIGNIVVICAPFIIIGILGVQLPKGKFF	1439
Db	1406	LRLRLTLRLRVISRAQGLKLVETLMSLKPIGNIVVICAPFIIIGILGVQLPKGKFF	1465
Qy	1440	VCQGEDTNTKSDCAEASVWRVYRHKYFNEDNLGOALMSFLVLSKOGVMDIMYDGLDAV	1499
Db	1466	VCQGEDTNTKSDCAEASVWRVYRHKYFNEDNLGOALMSFLVLSKOGVMDIMYDGLDAV	1525
Qy	1500	GVDOQPTMNNPMMLLYFISPLLIIVAFVLMNFGVVVNFHFKCRHQHQBEEARREBEKR	1559
Db	1526	GVDOQPTMNNPMMLLYFISPLLIIVAFVLMNFGVVVNFHFKCRHQHQBEEARREBEKR	1585
Qy	1560	LRLLEKRR-----KAQCKPYYSRFRPLLVHHLCTSHYLDLFTGTGVLNVVTWAM	1612
Db	1586	LRLLEKRRSKEKQMAEQAQCKPYYSRFRPLLVHHLCTSHYLDLFTGTGVLNVVTWAM	1645
Qy	1613	EHYQOQILDEALKICNYIFTVIFVLSVFKLVAFGRFRFFQDRWNQDLALVLLSIMG	1672
Db	1646	EHYQOQILDEALKICNYIFTVIFVLSVFKLVAFGRFRFFQDRWNQDLALVLLSIMG	1705
Qy	1673	TLBIEVNASLPINPITIRIMRVLRIRARVLLKLMVGMRLALDTVMQALPQVGNLGLLF	1732
Db	1706	TLBIEVNASLPINPITIRIMRVLRIRARVLLKLMVGMRLALDTVMQALPQVGNLGLLF	1765
Qy	1733	MLLFFIIFAAALGVELFGDLECDETHPCBGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMKD	1792
Db	1766	MLLFFIIFAAALGVELFGDLECDETHPCBGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMKD	1825
Qy	1793	TLRDCQESTCYNTVISPIFYVSFLTAQFVLNVVITAVLMKHEESNKEAKEAELEAE	1852
Db	1826	TLRDCQESTCYNTVISPIFYVSFLTAQFVLNVVITAVLMKHEESNKEAKEAELEAE	1885
Qy	1853	LEBMTKLSPOPSPGLSGPFLWPGVEGSDSPSKPGALHPAAHARSASHFSLBHTMQP	1912
Db	1886	LEBMTKLSPOPSPGLSGPFLWPGVEGSDSPSKPGALHPAAHARSASHFSLBHTMQP	1945
Qy	1913	HPTLPCPDLLTVKRSVSRTHSLPNDSYMCRHSGSTAEGPLGHRGWGLPKAQSGSVLSVH	1972
Db	1946	HPTLPCPDLLTVKRSVSRTHSLPNDSYMCRHSGSTAEGPLGHRGWGLPKAQSGSVLSVH	2005
Qy	1973	SQPADTSYIQLPKDAPHLLQPHSAPTWGTTPKLPFGPSRSPLAQRPLRQAIRTDSDLDV	2032

; COUNTRY: US
 ; ZIP: 92037
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSEQ Version 1.5
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/984,709A
 ; FILING DATE: 02-DEC-1997
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Seidman, Stephanie L.
 ; REGISTRATION NUMBER: 33,779
 ; REFERENCE/DOCKET NUMBER: 24735-9815 (formerly 6362-9815)
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (619) 450-8400
 ; TELEFAX: (619) 587-5360
 ; INFORMATION FOR SEQ ID NO: 50:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 2353 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; HYPOTHEICAL: NO
 ; ANTI-SENSE: NO
 ; FRAGMENT TYPE: internal
 ; ORIGINAL SOURCE:
 ; US-08-984-709A-50

Query Match 52.2%; Score 6211; DB 3; Length 2353;
 Best Local Similarity 56.6%; Pred. No. 0;
 Matches 1365; Conservative 214; Mismatches 523; Indels 310; Gaps 60;

Qy	7	GAGAEESQOP-RSFWRLNDLSGAGRPGPGSAEKDPSGADSEAGLRYPALAPVVFYLS	65
Db	27	GASPEPCAPGREARGSEL-GVPSSEP-RAERGAELGADEBQRPYPALAAVVFYCLG	84
Qy	66	QDSRPSRCLRTVCNPFERISMLVILLNCVTGLMFRFCEDACDSQRCILQAFDDIF	125
Db	85	QTTSPRSCLRLVCNPFERISMLVILLNCVTGLMFRFCEDVEGSERCNILEAFDAFIP	144
Qy	126	APFAVEMVVKVVALGIFGKKCYLGDWNRLDFFIVIAGLMYSYLDLQNVFSVARTVRVL	185
Db	145	APFAVEMVVKVVALGIFGKKCYLGDWNRLDFFIVIAGLMYSYLDLQNVFSVARTVRVL	204
Qy	186	RPLRAINRVPMSRILVTLTLLDPLMGLNVLLCFVFFIFIGIVGVLWAGLNRCLPE	245
Db	205	RPLRAINRVPMSRILVTLTLLDPLMGLNVLLCFVFFIFIGIVGVLWAGLNRCLFDS	264
Qy	246	NFSLPLSD-LERYQTENEDESPFCISQPRENGMRCSRVP---TLRGDGGGPPCGLD	301
Db	265	AFVRNNNLTLFRLPYVQTEGEENFPICSSRRDNGMKCKSHIPGRREL----MPCTLG	318
Qy	302	YEAYN-----SSNTTCVNNQYVNCSGAENHPFKGANPDNIGHAVTAIQVITL	354
Db	319	WEAYTQPAQGVGAARNACINQYVNCVSGDGNPHNGAINFDNIGYAVTAIQVITL	378
Qy	355	GWVDMYVMDAHSFYNYFIYILLIIVGSPFMNLCVVIATQFSETKQRESQLMREORV	414
Db	379	GWVDMYVMDAHSFYNYFIYILLIIVGSPFMNLCVVIATQFSETKQRESQLMREORA	438
Qy	415	RFLNASTLASFPGSCYEELLYVYLKKAARRLAQVRAAGVRYGLLSSPAPLGQ	474
Db	439	RHLNNDSTLASFPGSCYEELLYVYGHIFKVKERSRLRYARQSRWRKVKVDSAVQGO	498
Qy	475	ETQSSSSCSRRH-RLSVHLV-HHHHHHHHHYHNGTLPRAASPIQDRDANGSRRL	532
Db	499	--GPHRRORRAGRHTASVHLVYTHHHHHHHHHYHSHGSPRRPGPEGACD-----TRLV	551
Qy	533	MLPPSPPALSGAPPGGAESVHSFVHADCHLE--PVRCAQPPPRSPSEASGR-TVGSKV	589

Db	552	RAGAPPPSPGPGPPDAESVHSYHADCHIEGPOERARVAHAATAAASLRLATGLGTM	611
Qy	590	-YPTV-----HTSP-----PPBTLKEKALVEVAASSGPTLTSLNIPPGPY	629
Db	612	NYPTILPSGVSGKSTSPGPKGWAGPGPT-----GGHGPLSLNS---PDY	657
Qy	630	SSMHKLLETQSTGACQS-----SKLSSPCLKADSGACGPDSCPCYCARA-GAGEVELA	681
Db	658	EKIPHVVEHGLGQAPHLGSLVPCPLSP--PAGTLTCLKSCPCYCTRALEDPEGELS	715
Qy	682	DREMPDSSEAVYEFOTAOAHSDLRDP-----HSRRORSGLPDAEPSSV	725
Db	716	GSESGSDSGRGVYEFQDVHRGDRNDPTRPRATDTPGPGSGPORRAQQAAPCEPGMW	775
Qy	726	LAFWRLICDTPRKIVDSKYFORGIMAILVNTLSMGIBYHPOBELTVALISNIVFTSL	785
Db	776	GRLVWTFSGKLRRIVDSKYFSRGIMAILVNTLSMGVEYHPOBELTVALISNIVFTSM	835
Qy	786	FALEMLLKLAVYGPYIKENYINFDGVIVISWEIVGQGGGLSVLTRLMLRVKLIV	845
Db	836	FALEMLLKLACGPGLYIRNPYNIFDGIIVISWEIVGQADGGLSVLTRLMLRVKLIV	895
Qy	846	RFLPALORQLVLMKTMNDVATFQMLLMFIFISILGMHLFGCKFASERD-GDTLPDRK	904
Db	896	RFLPALRRQLVVMKTMNDVATFQMLLMFIFISILGMHLFGCKFSLKTDGTVDRK	955
Qy	905	NFDSLMLAIVTVFOILTQEDWNKVLVNGMASTSWAALFYIALMTFGYVLFNLVAILV	964
Db	956	NFDSLMLAIVTVFOILTQEDWNVVLVNGMASTSWAALFYVALMTFGYVLFNLVAILV	1015
Qy	965	EGFOAEISKREDASGQLSCIQLPVDGSGGDKANSESEPFDFSPSLDGD-----GD	1015
Db	1016	EGFOAE-----GDANRSDTDEKTSVHFEEFHKLRLOTTTE	1052
Qy	1016	RKCLALVSLGHEPELRKSLPLLIHTAATPMSLPKSTSTGLGALGPASRRRTSSGSA	1075
Db	1053	LKMCSLAVTPNGHLEGSLSPPLIMCTAATPMTPKSSPFLDPAAPSLPDRRGSSSGD	1112
Qy	1076	EPGAHEMKSPPSARSPSPHSPMSAASWTSSRRNSLRAPSLKRRSPSGERRSLSGE	1135
Db	1113	PP--LGDKPPASLURSPCAPWPGSGAWSRRSSWSLGRAPSLKRRQCCGERESLSGE	1170
Qy	1136	GOESQDESESESEERASPA--GSDHRHSGSLERAKSPDLPTL-----QVPLH---	1184
Db	1171	KGSTDDDE--AEDGRAAPGRPRATFLRRABSLDPRLPALPPTKCRDRDQGWALPSDF	1228
Qy	1185	--RTASGRGSAEHDGNGKSGASGRALARALPDDPPLDGDADDDEGNLSKGERVRAWIRA	1242
Db	1229	FLRDSHREDAAELDDSEDCCLRLHKVLEPYK-----QWCRS	1268
Qy	1243	RLPACYLERDSWSAYIFPPQSRPRLCHRIITHKHFDHVLVLIIFLNCITIAMERPKIDP	1302
Db	1269	-----REAWALYLFSPQNRPRVSCQVITHKMFHVLVLIIFLNCVITIALERPDIDP	1320
Qy	1303	HSABRIELTISNYIIFTAVFLAEMTVKVALGWCGEQYALSSWNVLGILLVLSVIDIL	1362
Db	1321	GSTERVELSVSNYIFTAIFVAEMVVKVVALGSLGSEHAYLOSSWNVLGILLVLSVIDIV	1380
Qy	1363	VSMVSDSGTKILGMLRVLRLLRLRLRVRISRAQGLKLVVETLMSLKPIGNIVVICAF	1422
Db	1381	VAMASAGAKILGVLRLRLRLRLRVRISRAQGLKLVVETLISLSPIGNIVVICAF	1440
Qy	1423	FIIFGILGVQLFKGKFFVQCGEDTRNTNKSDCBAESYRWYRHKYFNDFNLGOALMSLFLV	1482
Db	1441	FIIFGILGVQLFKGKFFVQCGEDTRNTNKSQAACRAAHYRWYRKYFNDFNLGOALMSLFLV	1500
Qy	1483	ASKDGWVDIMYDGLDVGVDQOPIWNNHPWMLLIFFISFLLIIVAFVFLNMFGVVVENPHK	1542
Db	1501	SSKDGWVIMYDGLDVGVDQOQVQNNHPWMLLIFFISFLLIIVAFVFLNMFGVVVENPHK	1560
Qy	1543	CRQHOEEERARRRERKRLRLLEKKRR-----KAQCKPYSDYSRFRLLVHHLCTSHYLD	1596
Db	1561	CRQHOEEERARRRERKRLRLLEKKRR-----KAQCKPYSDYSRFRLLVHHLCTSHYLD	1620

		Query Match	46.1%;	Score 5492.5;	DB 3;	Length 2175;		
		Best Local Similarity	51.3%;	Pred. No. 0;				
		Mismatches 1233;	Conservative 214;	Mismatches 508;	Indels 447;	Gaps 55;		
QY	31	RPGPSAEKDPGSADEAEG-----	LPYPALAPVVFYLLSQDSRPSRSCWLCRTVNCNPFERI	86				
DB	25	QFGRSPSSPGLPELDGADPHVPHDPAIAFFCLRQTTSRPNWCIMKVPWFECV	84					
QY	87	SMVLINCVTLGMPRCPEDACDSORCILQAFDFIFAPFAVMVVMVAVGALGFGKCC	146					
DB	85	SMVLINCVTLGMPYQCDMDCLSDRCKILQVDFDFIFPAMENVLXWALGIFGKCC	144					
QY	147	YLGDTWNRLLDFIVTAGMLEYSLDLQNVFSFSAVRVRLPLRAINRVPSMRLVTLTLLD	206					
DB	145	YLGDTWNRLLDFIVMAGVVEYSLDLQNLNSAIRTVRVLPLKAINRVPSMRLVTLTLLD	204					
QY	207	TLPMGLNVLCCFFVFFIFGIVGVQLWAGLLNRCFLPENFSLPLSVDLERYOTENED	266					
DB	205	TLPMGLNVLCCFFVFFIFGIIIGVQLWAGLLNRCFLPENFIOGDVALPPYIQEED	264					
QY	267	SPFICQSPRENGMRCRSVPTLRGDGGGPPCGL-----	DYEAIVSSSNTT--	CVNNNQ	318			
DB	265	MPFICSLGSDGIMGCHIEIPLPEKEQ-----	GRECLSKDDVYDFGAGRQDLNASGLCVNNR	321				
QY	319	YITNCISAGENPKGAINFDNIGYAWIAI	FOVITLEGWVDIMYFVMDAHSFYNYFIILL	378				
DB	322	YINVCRTGSANPHKGAINFDNIGYAWIVIFOVITLEGWVEIMYFVMDAHSFYNYFIILL	381					
QY	379	IIVGSPFMNLCUVIATOPSETKQBSOLMEORVFLSNASTLASFPGSCYBELLK	438					
DB	382	IIVGSPFMNLCUVIATOPSETKQREHRLMLEQRYLS--SSTVASTAEPCDCEVEIFQ	440					
QY	439	YLVYILKARLRQAQVSRAGVRVGLSSPAPLGQGTQPSSSCSRSHRLSLVHLVHHH	498					
DB	441	YVCHILKAKR-----	RALGLYALQSRQALG-----			468		
QY	499	HHHHHHYHNGTLAPRASPEIQDRDANGSRRLMLPPSTPALSGAPGGAESVHSFYH	558					
DB	469	-----	PEAPA--PAKPGP-----	H	480			
QY	559	ADCHLEPVRQAPPPSPSEASGRVTGSGKVVYFVHTSPPEETLKEKALVEVAASSGPPT	618					
DB	481	AK---EPHYQLCPQHSPLDAPHTL---	VQIPATL-----	511				
QY	619	LTSNLNPPGYSSMHKLLTQSTGACQSCCKISSPCLKADSGACGPDSCPYCAR---	672					
DB	512	-----	ASDPASCPCCQHQEDGRPP	529				
QY	673	AGAGEVELADREMPDSDSEAVYFTQDAHQHSLDRPHSRQRSLGDAEPSSVL-----	726					
DB	530	SGLGSTD--SGQEGSGSGSSAGGE--	DEADGAGARSEDGASSELGKEEEEEQADGAVWL	586				
QY	727	--AFWRLICDTFRKIVDSKYFGRGIMAILVNTLSMGIEYHEQPEELTNALEISNIYVTS	784					
DB	587	CGDVWRETRAKLRGIVDSKYFNRMIMAILVNTVSMGIEHHEQPEELTNALEISNIYVTS	646					
QY	785	LFALEMLIKLVYGPFGYIKNPYNIFDGVIVISVWEIVGQGGGLSVLRTFLRLVRLKL	844					
DB	647	MFALEMLIKLVYGPFGYIKNPYNIFDGVIVISVWEIVGQGGGLSVLRTFLRLVRLKL	706					
QY	845	VRFLPALORQLVTLKMTMDNVATFCMLLMFLFIFSLGMLHFGCKEASERD--GDTLPDR	903					
DB	707	VRFLPALORQLVTLKMTMDNVATFCMLLMFLFIFSLGMLHFGCKEASERD--GDTLPDR	766					
QY	904	KNFDSLLWAIIVTVFQILTQEDNKNVLYNGMASTSSWALYFIALMTGNYVFLNLLVAIL	963					
DB	767	KNFDSLLWAIIVTVFQILTQEDNKNVLYNGMASTSSWALYFIALMTGNYVFLNLLVAIL	826					
QY	964	VEGFOAEISKREDAAGQSLQIQLPVDGQDANKSESEPFPSPS-----	LDGD	1013				
DB	827	VEGFOAE-----	GDANRSYDEDEQSSSNIIEFPKLEGLDSS	863				

QY	1597	LFTITGVIGLVNVTWAMEHYQOQOILDBALKICNYIFTVIFVLBSVFKLVAFGRFRFFQDR	1656	
DB	1621	LFTITFIICVNVITWMEHYNQKSLDEALKYCNVFTIVFVFEAALKLVAFGRFRFFQDR	1680	
QY	1657	WNQDLAIVLISINGITLIEIEVNASLPINPTIIRIMVLRIRARVILKLMKAVGMRRALLD	1716	
DB	1681	WNQDLAIVLISLNGITLIEIEVNASLPINPTIIRIMVLRIRARVILKLMKATGMRRALLD	1740	
QY	1717	TVMOALPOVGNLGLLFWLLFFIPALGVLFGLDECDDETHPCBGLGRHATFRNFGMAFLT	1776	
DB	1741	TVMOALPOVGNLGLLFWLLFFIPALGVLFGLRCESEDNPCBGLSRHATFRNFGMAFLT	1800	
QY	1777	LFRVSTGDNWNGIMKOTLDC---DQBSTCYNTVISPIYFVSFVLAQFVLNVVIAVLM	1833	
DB	1801	LFRVSTGDNWNGIMKOTLRECSREKCHLSYLPALSPVYFVTFVLAQFVLNVVIAVLM	1860	
QY	1834	KHLEESNKEAEAEAELEMLEKTLSPQHSPLGSPFLWPGVEGPDSP--DSPKPCA	1890	
DB	1861	KHLEESNKEAREDAELDAEIELEM-----AQPGSARRVDAORP--	1899	
QY	1891	LHPAAHARSASHFSLHPTMOPHTLPG---PDLLTVRKSGVSRTHSLPNDSYMCRHG	1946	
DB	1900	-----PLQESPGARDAPNLV-ARKVSVSRMLSLPNDSYMFPRV	1937	
QY	1947	STAEGP-----LHHRGWLKPAQSGSVLSVHSQPADTSYIQLPKDAPHLLQPHSA	1997	
DB	1938	VPASAPHRPLQEVEMETYGATP---LGSVASVHSPFAESCASLQIP-----LAVSSPA	1989	
QY	1998	PTWGTIPKLPDPG--RSLAORPLRROAAIIRTDLSLDVQGLSREDLL--AEVSGPSP--P	2051	
DB	1990	RSGEPLHALSPRGATARSPLSRLLCRQBAVHTDSLEK-IDSPRDLTPAEPGEKTPVPR	2048	
QY	2052	LARAYFWG--QSSSTAQOHSRHSKISKHMTTPAP--CPGPEPNWKGPPETRSLSLELDT	2108	
DB	2049	VTQGSLSQSPSPRPAASVTRKHT--FGQCHVSSRPAAPGGE-----EAEASDPADE	2099	
QY	2109	ELSWITSGDLPL-----FGQGEPP--SPRDLKKCYVEAQSCORRPTSWLDEQRHSI	2159	
DB	2100	EVSHITSSACWQPTAEPHGPPEASVAGGERDLRLYSVDAQGLDKP--GRADEQWRPSA	2158	
QY	2160	AVSCLDSGQPHGLDTPSNLQGPGLGPGSRPKKLSPPSITIDPP--ESQGPRTTSPSP--	2216	
DB	2159	ELSGEPGEAKWGPZ-----AEP--ALGARRKKQWSPPCISVEPPAEDGSRAPSAEG	2211	
QY	2217	GICLRRRAPSDSK-----DPLASGPPDSMAASPPKDVLSLSGLSS	2259	
DB	2212	GSTTLRRRTTSCATPHRESLEPTEGSGAGDPAKGRWGQA---SCRAEHLTVPSFAP	2268	
QY	2260	DPADL-----DP	2266	
DB	2269	EPLDLGVPSGDP	2280	

RESULT 5
US-09-404-650-2
; Sequence 2, Application US/09404650
; Patent No. 6309858
; GENERAL INFORMATION:
; APPLICANT: Dietrich, Paul S.
; APPLICANT: McGivern, Joseph G.
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
; TITLE OF INVENTION: AND USES
; FILE REFERENCE: R0043B-REG sequence listing
; CURRENT APPLICATION NUMBER: US/09/404,650
; CURRENT FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 2175
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-404-650-2

QY 379 IIVGSPMINCLVVIATQSETKQRESQLMREORVFLSNASTLASFSRPGCYELLK 438
Db 382 IIVGSPMINCLVVIATQSETKQREHRLMLEQORYLS--SSTVASYPGOCYEEIFQ 440
QY 439 YLVVILKAAARLQAQVRAAGVRGLSSPAPLGGQETQPSSSCSRSHRRLSVHHLVHHH 498
Db 441 YVCHILKAKR-----RALGLYQALQSRQALG----- 468
QY 499 HHHHHHVLNGTLRAPRASPEIQDRDANGSRRLMLPPSTPALSGAPPGGARSVHSFYH 558
Db 469 -----PEAPA--PAKPGP-----H 480
QY 559 ADCHLEPVRCQAPPRSPSEASGRTVSGKYVPVHTSPPELTKERALKVEVAASSGPPT 618
Db 481 AK--EPHYQLCPQHSPLDTPHTL-----VQPIPATL----- 511
QY 619 LTSLNIPGPYSSMHKLETOSTGACQSSCKISSPCLKADSGACGPPSCPYCAR----- 672
Db 512 -----ASDPASCPCQCHDGRRP 529
QY 673 AGAGEVELADREMPDSDSEAVYFTQDAQHSDLRDPHRRORSIGPDAEPSSVL----- 726
Db 530 SGLASTD--SGOEGSGSGSAGGE--DEADGGGARSSEGDGASSELGKEEBEEQADGAVWL 586
QY 727 --AFWRLICDTFRKIVDSKYFGRGIMIAIIVNTLSMGIEYHEQPEELTNALIEINIVFTS 784
Db 587 GCDVWRETRAKRLGLVDSKYFNAGIMAILVNTVSMGIEHEQPEELTNILEICNVVFTS 646
QY 785 LFALEMLKLALVYGPFGYKPNYINFDGVIVVIVSWEIVGQGGGLSVLRTFRMLRVKL 844
Db 647 MFALEMLKLAAFGFLDYLRPNYINFDGIIIVSWEIVGQADGGLSVLRTFRLLRVKL 706
QY 845 VRFLPALOROLVLMKTDNVAFCMLMLFIFLSILGMLFCKKASERD--GDTLPDR 903
Db 707 VRFPALREROLVLMKTDNVAFCMLMLFIFLSILGMLFCKKFLRTDGTVPDR 766
QY 904 KNFDSLLWAIIVTFOILTQEDWNKVLVNGMASTSSWAALYFIALMTFGNYVFLNLLVAIL 963
Db 767 KNFDSLLWAIIVTFOILTQEDWNVYVNGMASTSPWASLYFVALMTFGNYVFLNLLVAIL 826
QY 964 VEGFOAEISKEDASGQSLCQLPVDSCGGDANKSESEPPFFSPS-----LDGD 1013
Db 827 VEGFOAE-----GDANRSYDEQSSNIEEFKLOEGLDSS 863
QY 1014 GDRKCLALVSLGEHPELRKSLPLLIITHAATPMSLPKSTSTGLGEALGPASRRT----- 1069
Db 864 GDFKLCPIPMTPNGH-----LDP-----SLPLGHLGPAGAGAPRLSLQPD 906
QY 1070 -----SSSGSAEPGAAHEMKPPPGARSPPHSPWASASWTSRRSRNSRLGRAPSLK 1120
Db 907 PMLVALGSRKSSVMSLGRMSYDQRLSSSRSSYYGFWGRSAWASRRSSWN-----SLK 960
QY 1121 RSPSGERSLSLGE--GOESQDEESSEE--FRASPAGSDH-----RRHG 1162
Db 961 HKPPSAEHSLSAERGGARVCEVAADGPPRAAPLTPHAAHIIHGPHLAHRHRRHRR 1020
QY 1163 SLERAKSSFDLPDLOVPLHRTASGR--GSASEHQDCNGKASGRALARALRPDPPLD 1220
Db 1021 TSLDNRSDVDLAELVPAVGAHPRAAWRAAGPAGHEDCNGRWPISAKDVFTKMGDRGR 1080
QY 1221 GDADDEGNLSKGERVRAWIRARLPACYLERDSWASAYIPPOSFRLLCHRIITHMFDH 1280
Db 1081 GED--EBEIDYTLCFVRVKMIDVYKPDWCEVREDWSVYLFSPENRFRVLCQTIIAHKLFDY 1139
QY 1281 VLVVILFLNCITITAMERPKIDPHSAERIFLTISNYIFTAVFLAEMTKVVALGCWCFGEQA 1340
Db 1140 VLVAFILNCITITALERQPQIEAGSTERIFLTISNYIFTAVFGEMTLKVVSILGLVGEQA 1199
QY 1341 YLRSSNNVLDGLVLIVSIDIIVMSVSDSGTKILGMLRVLRLLRTRPLRVISRAQGLKL 1400
Db 1200 YLRSSNNVLDGLVLFVFSIDIIVVLSASAGAKILGVLRLRLTRPLRVISRAPGLKL 1259

QY 1401 VVETLSSSLKPIGNIIVVICCAFFIIFGILGVOLFPGKFFVCOGEDTRNITNKSDCAESY 1460
Db 1260 VVETLSSSLKPIGNIIVVICCAFFIIFGILGVOLFPGKFFVCOGEDTRNITNRSDCAANY 1319
QY 1461 RWVRHKYNFDNLGOALMSLFLVSLASDGVDMYDGLDVGVDQOQIMNHNPMWLLYFISF 1520
Db 1320 RWVHKYNFDNLGOALMSLFLVSLASDGVDMYDGLDVGVDQOQIMNHNPMWLLYFISF 1379
QY 1521 LLIIVAFVLMNMFVVVENFHKCRQHOEEERREKELRLEKRRKRAQCKPYYSDYS 1580
Db 1380 LLIIVAFVLMNMFVVVENFHKCRQHOEEERREKELRLEKRRKRAQRLPYVATYC 1439
QY 1581 RPELLVHLCSTHYLDLFTIGVILNVTWMEHVQOPOILDEALKICNYITVIVPLS 1640
Db 1440 HTELLIHSCTHYLDLFTITICLNVVWTSLEHYNQPTSLTALKYCNYMETTIVLEA 1499
QY 1641 VFKLAVFGRFRFQDRNQLDLAIVLLSITWLTBIEIVNASIPINPTIIRIMRVLIAR 1700
Db 1500 VLKLVAFGLRRFPKDRWNQDLAIVLLSITWLTBIEIVNASIPINPTIIRIMRVLIAR 1559
QY 1701 VLKLVAVMVRALLDTVMQALPQVGNLGLLMLFFIFAALGVELFGLDECDETHPCBG 1760
Db 1560 VLKLVAVMVRALLDTVMQALPQVGNLGLLMLFFIFAALGVELFGLVCNDEPCBG 1619
QY 1761 LGHATFRNFGMAFLITFLVSTGDNWNGIMKOTLRDC--DOESTCYNTV--ISPIYVSFV 1817
Db 1620 MSRHATFRNFGMAFLITFVSTGDNWNGIMKOTLRDCTHDSRCLSLFOVSLYFVSFV 1679
QY 1818 LTAQFVLNVVIAVLMKHEESNKEAEAEAELELEM--KTLSPQHPSPGLSPFLWPG 1876
Db 1680 LTAQFVLNVVIAVLMKHLDDSNKEAQEDAEMAELEMAHGLGPGRLPTGSPGA--PG 1738
QY 1877 VEGDPSD-----SPKPGAL-----HPAHA----- 1897
Db 1739 -RGPGAGGGGTGEGLCRRCYSPAQDSLEGELTIIDNLGSIFFHYSSPAGCKCHDK 1797
QY 1898 -----RSAS-----HFSLEHPTMQP-----HPTELPGDPLLTVRKSG-- 1929
Db 1798 QEVOLAEATEAFSLNSRSSSILIGDLDLSDPTACPPGRKDSKGELDPPEPMVGLDGE 1857
QY 1930 ---VSRTHSLPN--DSYMCRHGSTAEGPLGHRGMLPKAQSGSVLSVHSQPADTSYILQLP 1985
Db 1858 FFLPSSSTAVSPDENFLCEMEEIPFNPV--RSW--LKHDSSQAPPSPFSPDASSPLPMP 1913
QY 1986 KDAPH-----LLQPHSAPTWTIIPKLPPG-----RSLAQRPLRQAAIRTDSDVQ 2034
Db 1914 AEFPHPAVSASQKPEKGTGTGLPKALQGSWASLRSPRVNCTLRQATGSDTSLD--- 1970
QY 2035 LGSREDLLAEVSGSPPLARAYFWGOSSTQAQGHRSKSHSKI SKHMTTPPAPCPGEPENWG 2094
Db 1971 -----ASPSSAGSLQTTLEDLSLSDSPRA-----LGPPAPAGPRAGLS 2012
QY 2095 KGPPETRSSLDELTELWSIGDLLPPGQBEPSPDLKKCYVSAOSCORRPTSWLDEQ 2154
Db 2013 ---PAARRLSL-----RGRGLFSLRLGRA-----HQ 2036
QY 2155 RRHSIAVCLDSQPHLGTDPN---LGGOPLGCGSRPKKLSPPSIT---IDPPESQ 2208
Db 2037 RSHSGGS--TSPGTHDSMDPDSDEERGAGGAGGAGSEHSETLSSLSLSLFCPPP--- 2092
QY 2209 GPRTPPGPGICLRRRAPSSDS---KDFLASGPPDPSMAASPSPKKOVLISLGSSSDPA 2264
Db 2093 ---PPAPGLTPARKFSSTSLAAGPRPHAAALHGLARSPSWAAD-----RSKDPGR 2143
QY 2265 DP 2266
Db 2144 AP 2145

RESULT 7
US-09-404-650-4
; Sequence 4, Application US/09404650
; Patent No. 6309858

GENERAL INFORMATION:

; APPLICANT: Dietrich, Paul S.
 ; APPLICANT: McGivern, Joseph G.
 ; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
 ; FILE OF INVENTION: AND USES
 ; CURRENT APPLICATION: R0043B-REG sequence listing
 ; CURRENT FILING DATE: 1999-09-23
 ; NUMBER OF SEQ ID NOS: 12
 ; SOFTWARE: Patent in Ver. 2.0
 ; SEQ ID NO 4
 ; LENGTH: 2188
 ; TYPE: PRN
 ; ORGANISM: Homo sapiens
 ; US-09-404-650-4

Query Match 46.1%; Score 5484; DB 3; Length 2188;
 Best Local Similarity 51.1%; Pred. No. 0;
 Matches 1234; Conservative 212; Mismatches 509; Indels 460; Gaps 56;

Qy	31	RPFGSABKPGSADSEAG-----LPYPALAPVVFYLSQSRPSRSCLRVTVCNPFERI	86
Db	25	QPGSPSPSPGPEELDGADPHVPHDPLAPIAFFCLRTTSPRNWCIKMVCNPFECV	84
Qy	87	SMVLILNCVTLGMRPCDIACDSQRCRIILQAFDDFIFAFVEMVVMVALGIKGC	146
Db	85	SMVLILNCVTLGMRPCDDMDCKILQVDFDIFIFAMEMVLMVALGIFGKCC	144
Qy	147	YLGTWNRDLFFIAGLMLEYSLDQNVFSFSAVRTVRVLRPLRINRVPSMRILVLLD	206
Db	145	YLGTWNRDLFFIAGLMLEYSLDQNVFSFSAVRTVRVLRPLRINRVPSMRILVLLD	204
Qy	207	TLPLMGNVLLCFVFFIFIGVQVMAGLNRNCFDENFSLPSLDLRYQTEDE	266
Db	205	TLPLMGNVLLCFVFFIFIGVQVMAGLNRNCFDENFSLPSLDLRYQTEDE	264
Qy	267	SPFTCSQPRENGMRSRVPVTLRGDGGGPGGL-----DYEAYNSSNTT--CVNWNQ	318
Db	265	MPFTCSJSGDNGMGCHEIPPLKQ---GRECCSKDDVDYDFGAGRODLNAGSLCVNWR	321
Qy	319	YNTCSAGEHNPFGAINFDNIGYAWIAIFQVITLEGVVDIMYFMDAHSFYNTIFILL	378
Db	322	YNNVCRGTSANPHKGAINFDNIGYAWIIFQVITLEGVVEIMYVMDAHSFYNTIFILL	381
Qy	379	IIVGSPFMINCLVVIATQFSETKQSRQMRQVRPLSNASTLASPEGSCYBELLK	438
Db	382	IIVGSPFMINCLVVIATQFSETKQSRQMRQVRPLSNASTLASPEGSCYBELLK	440
Qy	439	YLVLILKAARLAQVSRAGVRVGLLSSPAPLGGQETQPSSCSRSHRLSVHLLVHH	498
Db	441	YVCHILRAKAR-----RALGLYQALQSRQALG-----	468
Qy	499	HHHHHHYHLNGTLRAPRASPEIQDRDANGSRRLMLPPSPALSGAPPGGAEVSHSYH	558
Db	469	-----PEAPA--PAKGP-----H	480
Qy	559	ADCHLEPVRQAPPPRSPSEASRTVGSKYVPTVHTSPPTLKEKALVEVAASSGPPT	618
Db	481	AK---EPRHYQLCPQHSPLDATPHTL-----VQPIPATL-----	511
Qy	619	LTSLNIPGPYSMMHKLLETQSTGACQSSCKISSPCLKADSGACGPPSCPYCAR	672
Db	512	-----ASDPASCPCQCHEDGRPP	529
Qy	673	AGAGEVELADREMPDSSEAVYFTQDAQHSDLDRPHSRQRSLGPDAPSSVL-----	726
Db	530	SGLGSTD--SGEGSGSGSAGGE--DEADGAGASSEDGASSELKKEEERQADGAWL	586
Qy	727	--AFWRLICDTRKIVDSKYFGRGIMTIALVNTLSMGIEYHEQPEELTNALEISNIVFTS	784
Db	587	CGDVWRRETRAKLIGVDSKYFNRRGIMMAILVNTVSMGIEHHEQPEELTNALEISNIVFTS	646
Qy	785	LFALEMLLKLLVYGFPGYIKNPYINFDGVIIVISVWEIVGQGGGLSVLRTFLMRVLKL	844

Db	647	MFALEMILKKAAGLDFYLRNPYNIFDSIIIVISWEIVGQDGLSVLRTFLMRVLKL	706
Qy	845	VRFLPALQRLVLMKTMNDNVATFCMLMLFIFFSILGMLHFGCKFASERD--GDTLPDR	903
Db	707	VRFPALRRQLVLMKTMNDNVATFCMLMLFIFFSILGMLHFGCKFSLRTDGTGTPDR	766
Qy	904	KNFDSLLWAIIVTVFQILTOEDWNKVLNGMASTSSWAALYFIALMTFGYVLFNLLVAIL	963
Db	767	KNFDSLLWAIIVTVFQILTOEDWNVLYNGMASTSPWASLYFVALMTFGYVLFNLLVAIL	826
Qy	964	VEGFOABEISKREDASGLSCIQLPVDSQGDANKSESEPDPFSPS-----LDGD	1013
Db	827	VEGFOABE-----GDARNSYDEBQSSNSNIEEPFKLQBGLOSS	863
Qy	1014	GDRKCLALVSLGHPHKLKSLPLLIHTAATPMSLPKSTSTGLGEALGPASRRT----	1069
Db	864	GDPKCLPIPTMPNGH-----LDP-----SLPLGGHLGPAGAAGPAPRLSLQPD	906
Qy	1070	-----SSSGSABEPGAHEMKSPPSARSPPSHPSAASWTSSRRSSRLGRAPSLK	1120
Db	907	PMLVALGRSKSSVMSLGRMSYDQSLSSSRSSSYTGPWGRSAWASRRSSWN-----	960
Qy	1121	RRSPSGERRSILSGE--GOESQDEESSEE--ERASPAGSDH-----RRHG	1162
Db	961	HKPESAHEHLSAERGCGARVCVAADGPPRAAPLHTPHAHIIHGPHLAHRHRHRR	1020
Qy	1163	SLEREAKSSFDPLTQVPGHLRTASGR--GSASEHODCNKGSASGRLARALRDPDPLD	1220
Db	1021	TLSLDNRDSVDLAELVPAVGAHPRAAWRAAGAPGHEDCNGRMPSIAKDVTKMGDRGR	1080
Qy	1221	GDDADDSEGNLSKGRVRAWIRARLPACVLERDSSWAIYIPPOSRPRLICHRITTHMFDH	1280
Db	1081	GED--EEBIDYTLCPFRKMDVYKPDWCCEVEDSVYLFSPENRFRVLCOTIIAHKLFDY	1139
Qy	1281	VLVIIFLNCITIAWERPKDIPHSARFELTSLNVIPTAVLAEMTVKVALGWCFCGQA	1340
Db	1140	VLAFIFLNCITIAERPPQTEAGSTERIFLTVSNYIIFTAIFVGMTLKVSLGLYFGQA	1199
Qy	1341	YLSSMNVLGDLVLIIVDILVMSVDSGTGKILGLMLRVLRLRLTLRLRIVISRAQGLKL	1400
Db	1200	YLSSMNVLGDLVLFVFSIIDIVSLASAGGAKILGLVLRVLRLLTLRLRIVISRAQGLKL	1259
Qy	1401	VVETLMSLKPIGNIVVICAPFIIFGLVQLPKGPFVCOGEDTRNITNKSDCABASY	1460
Db	1260	WETLISLKPIGNIVVICAPFIIFGLVQLPKGPFVCHGLVDTRNITNRSDCMAAY	1319
Qy	1461	RWVRHKYNFNLGQALMSLVASKGQVDMYDGLDAGVDQDQPIVNNHNPMLLYFTSF	1520
Db	1320	RWVHKYNFNLGQALMSLVASKGQVDMYDGLDAGVDQDQPVNHNPMMLLYFTSF	1379
Qy	1521	LLIVAFVLMNVGVVVENFHKHQHQBEEAREERREKRLRLEKRRKAKQCKPYYSYS	1580
Db	1380	LLIVSFFVLMNVGVVVENFHKHQHQBEEAREERREKRLRLEKRRKAKQRLPYATYC	1439
Qy	1581	RFRLLVHLCTSHYLDIFITGVIGLVNVTWAMEHYQQPILDEALKICNYITFTVIFLES	1640
Db	1440	HTRLIHSMTCTSHYLDIFITFIIICLVNVTWMSLEHYNQPTSLTALKYCNVFTVIFLEA	1499
Qy	1641	VFKLVAFGRFFRQDRWNOLDLAIVLASIMGITLLEEVNASLPINPTIIRIMVLRAR	1700
Db	1500	VKLVAFLGRFFRQDRWNOLDLAIVLSVMGITLLEIEINAAIPINPTIIRIMVLRAR	1559
Qy	1701	VLKLLKMAVGMRALDVTVMQALPOVGNLGLLFLMLFFIFALGVELFGDLCEDETHPCEG	1760
Db	1560	VLKLLKMATGNRALDVTVMQALPOVGNLGLLFLMLFFIYALGVELFGKLCNDENPCEG	1619
Qy	1761	LGRHATPRNGMAFLTFRVSTGDNWNGIMKDTLRDC--DQSTCYNTV--ISPIYFTSVFV	1817
Db	1620	MSRHATPRNGMAFLTFQVSTGDNWNGIMKDTLRDCTHDSRCLSSIQFVSPLYFSFV	1679
Qy	1818	LTAQFVLNVVIAVLMKGLSESKAEAEAEAELEAELEEM-KTSLSPQHSPLGSPFLWPG	1876

Db 1680 LTAQFVLINVVAVLMKHLDDSNKEAQEDAEADAELEMAHGLGPGPRLPTGSPGA-PG 1738
Qy 1877 VEGPD-----SP-----DSPKPGALH-- 1892
Db 1739 -RGFGAGGGDTBGLCRRCYSPAENMLDSVSLIIKDSLEGELTIIDNLGSGIFPHY 1797
Qy 1893 --PAA-----HARSAS-----HFSLEHTMQP-----HPTFLP 1918
Db 1798 SSPAGCKCHDKQEOVLAEAFSLNSDRSSILLGDDLSLEDDPTACPPGRKDSKGELD 1857
Qy 1919 GPDLLTVRKSG-----VSRTHSLPN-DSYMRHSGSTAEGPLHGRGMLPKAQSGSVLSVH 1972
Db 1858 PPEMRVGLGECFFPLSSSTAVSDPENFLCEMEEIPEFNV--RSW--LKHDSSQAPSP 1913
Qy 1973 SQPADTSYIQLPKDAPH-----LQPHSAPTWGTITPKPPPG-----RSPLAQRLRR 2021
Db 1914 FSPDASSBLLPMAPEFFHAPVASQKGEKGTGTLPKIALQGSWASLSPRVNCTLLR 1973
Qy 2022 QAAITRDSLDVQGLGSRDLDLAEVSGSPPLARAYSFWGQSSTOQQHSHRSKISHMT 2081
Db 1974 QATGSDTSLD-----ASPSSAGSIQTTLEDLSLTDSFRA-- 2012
Qy 2082 PPAPCGPEPNWKGPPETRSLELDTLSWISGDLPLPPGQOEPPSPRDLKKCYVEAQ 2141
Db 2013 PPAPAGFPAGLS--PAARRLSL-----RGRGLFSLRGLRA- 2047
Qy 2142 SCORRPTSWLDEQRHSTAVSCLSGSPHLGTDPSN---LGQPLGPGSPRKKLSPP 2198
Db 2048 -----HORSHSGGS-TSPGCTHDSMDPSDEBGRGAGGGAGSEHSETLSL 2095
Qy 2199 SIT---IDPESQGRTPPSGICLRRAPSSDS---KDPLASGPPDSMAASPSPKDV 2251
Db 2096 SLTSLFCPPP-----PPAPGLTPARKFSSSTSLAAPGRHAALAHGLARSFSAAD- 2148
Qy 2252 LSLGLSGSDPADLDP 2266
Db 2149 -----RSKDPGGRAP 2158

RESULT 8
US-09-935-541-4
; Sequence 4, Application US/09935541
; Patent No. 6589787
; GENERAL INFORMATION:
; APPLICANT: Dietrich, Paul S.
; APPLICANT: McGovern, Joseph G.
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
; FILE REFERENCE: R0043B-REG sequence listing
; CURRENT APPLICATION NUMBER: US/09/935,541
; CURRENT FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: 09/404,650
; PRIOR FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 2188
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-935-541-4

Query Match 46.1%; Score 5484; DB 4; Length 2188;
Best Local Similarity 51.1%; Pred. No. 0;
Matches 1234; Conservative 212; Mismatches 509; Indels 460; Gaps 56;

Qy 31 RPEGGAEKDPSGADSEAG-----LPYALAPVVFYLLSODSRPSRWCLRTVCNWFERRI 86
Db 25 QCPGRSPSPSPGLEBFLDGADPHVPHDLAPIAFLCRLQTTSPRNWCIMKVCNPFECV 84
Qy 87 SMLVILLNCVTLMGFRPCEDDIACDQRCRILQAFDDFIFAFVAVENVMVQALGIFGKKC 146
Db 85 SMLVILLNCVTLMGFRPCDDMCLSDRCKILQVDFDFIIFFAMENVLSKVALGIFGKKC 144

Qy 147 YLGDWTNRLLDFIVLVIAGMLEYSLDLQNVSFSAVTRVRLPLRAINRVPSMRILVTLLLD 206
Db 145 YLGDWTNRLLDFIVVAGVVEYSLDLQNVLSAIRTVRLPLKAINRVPSMRILVNLLD 204
Qy 207 TLPMLGNVLLLCFFVFFIFIGVQVLMAGLNRNCFLPENFSLPLSDVRLERYOTENED 266
Db 205 TLPMLGNVLLLCFFVFFIFIGVQVLMAGLNRNCFLEENFTIQGDVALPPYQPEEDDE 264
Qy 267 SPFICSQPRENGWRCRSVPTLRGDDGPPCGL-----DYEAYNSSNTT--CVWNQ 318
Db 265 MPFICSLSDNGIMGHEIPLKEQ---GRECLSKDDYDFGAGRODLNAGSLCVWNWR 321
Qy 319 YTNCSAGHNPFKGAINFNDNIGYAMIAIFOVITILEGWVDIMYFVMDAHSFYNYFILL 378
Db 322 YNVNCHTGSANPHKGAINFDNIGYAMIVIFOVITILEGWVEIMYVYMDAHSFYNYFILL 381
Qy 379 IIVGSFFMINCLVVIATOFSETKQESOLMEORVFLSNASTLASPEPCSCYEELK 438
Db 382 IIVGSFFMINCLVVIATOFSETKQEHRLMLEQORLYLS-SSTVASYAEPGDCYEEIFQ 440
Qy 439 YLVYIILKKAARLQAQVSRAGVRVGLLSPAPLGGQETQPSSSCSRSHRRLSVHLLVHH 498
Db 441 YVCHILRKAKR-----RALGLYQALQSRQALG----- 468
Qy 499 HHHHHYHLNGTLPAPRASPEIQDRDANGSRRLMLPPFSTPALSCAPPGGAESVHSFYH 558
Db 469 -----PEAPA--PAKFGP-----H 480
Qy 559 ADCHLEPRVCOAPPPSPSEASGRVTSKGYVTVHTSPPETLKEKALVEVAASGPPT 618
Db 481 AK---EPRHYQLCFQSHPLDATHTL-----VQIPATL----- 511
Qy 619 LTSINIPPGPYSSMHKLLETQSTGACQSSCKISSPCLKADSGACGPDSCPYPYCAR----- 672
Db 512 -----ASDPASCPCCQHGDRP 529
Qy 673 AGAGEVELADREMPDSDSEAVYEFTODAQHSDLRDPSRRQRSLGDPAPSSVL----- 726
Db 530 SGLGSTD-SQGGSGSGSSAGGE--DEADGDGARSSEDDGASSSELGKEEEDGAGAVWL 586
Qy 727 --AFWRLICDTFRKIVDSKYFGRGIMAILVNTLSMGIEYHQEPEELTNALEISNVFTS 784
Db 587 CGDVNRETRAKLRGIVDSKYFNKGMWAILVNTVSMGIEHQEPEELTNALEISNVFTS 646
Qy 785 LFALEMLLKLAVYPPGYIKNPNYINFDGVIWISVWEIVQCGGGLSVLTFPLMRVXL 844
Db 647 MFALEMLKLAAGFLGFDYLRNPNYINFDIIVISWEIVQADGGLSVLTFPLLRVLKL 706
Qy 845 VRFLPALORQVLMKTMNDNVATFCMLLMFIFIFISILGMHLFGCKPASERD-GDTLPDR 903
Db 707 VRFPALRRQLVLMKTMNDNVATFCMLLMFIFIFISILGMHIFGCKESLTDGDTVPDR 766
Qy 904 KNFDSLLWAVTVFQILTOEDMNKLVNMGMASTSSWAALYFIALMTFGNVVLFNLLVAIL 963
Db 767 KNFDSLLWAVTVFQILTOEDMNKLVNMGMASTSPWASLYFVALMTFGNVVLFNLLVAIL 826
Qy 964 VEGFOABEISKREDASGQLSCIQLPVDSDGDKANKSESEDFPSPS-----LDGD 1013
Db 827 VEGFOAE-----GDANRSYDQDQSSSNTTEEFKXQLEGDSS 863
Qy 1014 GDRKKCLALVSLGHPHRLKSLPLPIIHTAATMSLPKSTSTGLGALPASPRT----- 1069
Db 864 GDPKLCPIPMTPNGH-----LDP-----SLPLGHLGAGAGAPRLSLQPD 906
Qy 1070 -----SSSGSAEFGAAHEMKSPPSARSPPSPWASASSWTSSRRSSNLSGRASLKL 1120
Db 907 PMLVALGSRKSSVMSLGRMSYDQSLSSRSYSGPMPGRSAWASRRSSWN-----SLK 960
Qy 1121 RRSPPGERSLLSGE-GQESODEESSEE--ERASPAQSDH-----RHRG 1162
Db 961 HKPFSAEHLSLSAERGCGARVCEVADEGPPRAPLHTPHAHIHGHGPHLAHRHRHR 1020
Qy 1163 SLEREAKSSFDLPDTLQVPLHRTASGR--GSASEHQDCNGKSASGRALARALRPPDPPLD 1220

[illegible]

Qy	1633	TVTVFVLESVPKLVAFGRFRFPQDWRNOLDLAI	VLLSIMGTTTLEIEIVNASLPINPTIIRI	1699
Db	1486	TTTVFLEAVLKVAFGURFRFPQDWRNOLDLAI	VLLSVMGITTEIEINAAIPINPTIIRI	1545
Qy	1693	MRVLRARVLKLLKMAVGRALLDTVMQALPQV	GNLGLLFMLLFFIFAALGVELFGDLEC	1752
Db	1546	MRVLRARVLKLLKMATGMRAALLDTVVQALPQV	GNLGLLFMLLFFIVAALGVELFGKLVC	1605
Qy	1753	DETHPCEGLGRHATFRNFGMAFTLTPRVSTGDN	WNWNGIMKDTLRDC--DOESTCYNTV--IS	1809
Db	1606	NDENPCEGMSRHATFENFGMAFTLTPQVSTGDN	WNWNGIMKDTLRDCTHDETKTSSUQFVS	1665
Qy	1810	PIYFVSFVLTAQFVLNVNVTAVLMKHLAESNKEA	KEAELELELEM-KTLSPQPHSPL	1868
Db	1666	PLYFVSFVLTAQFVLNVVAVLMKLUDDSKAQAED	AEADAELEMAHGLGPCP----	1721
Qy	1869	GSPPFLWPGVEGDPSPSPKPGALHPAAHARSAS	HSFSLHEFTWQPHFTLPGPDLLTV---	1925
Db	1722	-----GPCFG-----	PCPCPCPCPCAGPRLPTSSPG	1747
Qy	1926	---RKSGVSRTHSLPNDSYNCRH	1945	
Db	1748	APGRGGGAGAGG-DTESHLCRH	1769	
RESULT 10				
US-09-935-541-5				
; Sequence 5, Application US/09935541				
; Patent No. 6589787				
; GENERAL INFORMATION:				
; APPLICANT: Dietrich, Paul S.				
; APPLICANT: McGivern, Joseph G.				
; TITLE OR INVENTION: T-TYPE CALCITRIUM CHANNEL VARIANTS: COMPOSITIONS THEREOF;				

RESULT 10
US-09-935-541-5
; Sequence 5, Application US/09935541
; Patent No. 6589787
; GENERAL INFORMATION:
; APPLICANT: Dietrich, Paul S.
; APPLICANT: McGivern, Joseph G.
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF.
; TITLE OF INVENTION: AND USES
; FILE REFERENCE: R0043B-REG sequence listing
; CURRENT APPLICATION NUMBER: US/09/935,541
; CURRENT FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: 09/404,650
; PRIOR FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 1835
; TYPE: PRT
; ORGANISM: Rattus sp.
US-09-935-541-5

Query Match	45.1%	Score 5366;	DB 4;	Length 1835;
Best Local Similarity	56.8%;	Pred. No. 0;		
Matches 1138; Conservative	183;	Mismatches 346;	Indels 336;	Gaps 38;
QY	27	GAGRPGPSAEKDPGSANDSAEG----	LPALAPVVFVFLSODSRPSRCLRTVCNWP	82
DB	19	GITEQPGSRPPSPGLEEPLGTPDVPHPDLAPVAFF	CLRQTTSRNCICIKMVCNWP	78
QY	83	FERTSMLVILLNCVTGLMFRCEBDCDSQR	CRILIQAPDDFIFAFFAVEMVMKVALGIF	142
DB	79	FECVSMVLVILLNCVTGLMYPQCDDECLSDRCKILQ	LOVDDFIFIFFAMEWMLKVALGIF	138
QY	143	GKKCYLGTWNRLLDFFIVIAGMFLYSLDLQNVSP	AVRTVRLAPRLAIRNPVPSNRILVT	202
DB	139	GKKCYLGTWNRLLDFFIVMAGMVEYSLDLQNLIN	SAIRTVRLAPRLKAINRVPSNRILVN	198
QY	203	LLLDLPLMGLNVLLCCFPVFIFGIVGVLWAGLL	RNRCFLPENFSLPLSDLERYQTE	262
DB	199	LLLDLPLMGLNVLLCCFPVFIFGIVGVLWAGLL	RNRCFLPENFTIIGDVALPPYQPE	258
QY	263	NEDSPFICSPQPRENGMCRSCSVPTLRDGGGGP	CGGL-----DYEAYNSSNTT--CV	314
DB	259	EDDENPFICSLTGDNGIMGCHEIPLPKEQ---	GRECCLSKDDVYDFGAGRODLNASGLCV	315
QY	315	NNNQYITNCSEAHNPFGKAINFDNIGVANI	TAIPQVITLGEWWDIMYFMDAHSFNFTY	374

Db 316 NNRYNVCRTGNANPHGAINFNINIGAGIVFQVITLEGVEMLYVMDAHSEYFIY 375
Qy 375 FILLIIVGSFMINCLVVIATQFSETKORSEQLMREQVRFLSNASTLASFSEPGCYE 434
Db 376 FILLIIVGSFMINCLVVIATQFSETKORSEQLMREQVRFLSNASTLASFSEPGCYE 434
Qy 435 ELLKXVVLKKAARLQAQVRAAGVRVGLLSSPAPLGGQETQPSSSCSRRRLSVHL 494
Db 435 EIFOVYCHILRAKRALGLYOALQNR 461
Qy 495 VHHHHHHHHVHLGNTLRAPRASPEIQORDANGSRRLMLPPPSPALSGAPPGAGSVH 554
Db 462 -----RQWG-----PGTPA--PAKGP----- 477
Qy 555 SFYHADCHLEVRQAPPSPSEASGRVSGKYVPTVHTSPPPETLKEKALVEVAASS 614
Db 478 ---HAK---EPShCKLCPRHSPLO-----PTPHTLVQP----- 504
Qy 615 GPPTILSLNIPPGPYSSMHKLLLEQTQSGACQSSCKISSPCLKAUSGACGPDSCPYCAR-- 672
Db 505 -----ISAILASD-----PSSCPHCQHEA 523
Qy 673 ---AGAGEVELADREMPDSEAVYFTQDAQSHDLRDPHSRRORSGLGPAESPSSVLA- 727
Db 524 GRRPSGLSTD-SQEGSGSGSAEABANGD-----LOSSEDGSSDLCKEEBEDGNA 578
Qy 728 ---FWRLICDTFRKIDVSKYFGRGIMTALVNTLSMGIEYHEQPEELTNALEISNIVFT 783
Db 579 LCGDWMRETRKLRGIDVSKYFNRGIMAILVNTVSMGIEHHEQPEELTNALEISNIVFT 638
Qy 784 SLFALEMLLKLIVGPGFYIKNPYNI FDCVIVIVISWEIVGQGGGLSVLFTFLMRVLK 843
Db 639 SMPALEMLTKAALFDFLRPNYNI FDSIIIVISWEIVGQADGGLSVLFTFLMRVLK 698
Qy 844 LVRLPALOROLVLMKTMNDVAFMCLMLFIFISILGHMHLFCCKPASEBD-GDTLPD 902
Db 699 LVRFWAPALRRQLVLMKTMNDVAFMCLMLFIFISILGHMHLFCCKPASEBD-GDTLPD 758
Qy 903 RKNFDSLLWAIIVTFQILTOEDWNKVLNGMASTSSWAALYFIALMTFGNYVLFNLLVAI 962
Db 759 RKNFDSLLWAIIVTFQILTOEDWNKVLNGMASTSSWAALYFIALMTFGNYVLFNLLVAI 818
Qy 963 LVGEFOABEIEKREDASQQLCIQLPVDOSQGDANKSEBDFPSPS-----LDG 1012
Db 819 LVGEFOABEIEKREDASQQLCIQLPVDOSQGDANKSEBDFPSPS-----LDG 855
Qy 1013 DGRKKCLALVSLGHPBLRKSLLPLLIHTAATPMSLPKSTSTGLGALGPA-SRRTSS 1071
Db 856 SRDLKLCPIWTPNGH-----LDP-----SLP-----LGAHLGPAWTMGTP 892
Qy 1072 SGSAEPG-----AAHEMKSPSPSARSPHSWASASWTSRSTRSSNSL 1113
Db 893 RLSLQPDVPLVALDSKSSVMSLGRWSYDQSLSSRSSYYPGWRSGTWSARSSWN-- 950
Qy 1114 GRASLKRSPSGERRSLLSGEQSDOE-ESSEEE---RASPAGSDH----- 1158
Db 951 ---SLKHKPPSAHESLISGEGGSCVRACEGAREEAPTPTAPLHAPHAAHHAHGHPLA 1006
Qy 1159 ---RHGRSLREAKSFPDPTLQVCPGLHRTAS--GRGSASEHODCNKGSARLARAL 1212
Db 1007 HRHRHRTLSLDRSDVLDGELVPVVGAAHRAWRGAGAPGHEDCNMRPNIAKOVFT 1066
Qy 1213 RPDDPPLDGDDADDEGNLSKGERVRAWIRALPACLYBERDSWSAYIFPPQSRFLLCHRI 1272
Db 1067 KMDDRRDRGED-EEEDYTLFRVRKMDIVYKPDKCEVREDWSVYLFSPENKFRILCOTI 1125
Qy 1273 ITHKMFHVLVLIPLNCITIAMERPKIDPHASERIFLTLNYYITAVFLAEMTKVVAL 1332
Db 1126 IAHKLFYVVLAFIPLNCITIALERPOIEAGSTERIFLTVSNYITAITFVGEMTLKVWSL 1185
Qy 1333 GWCFFEQAYLRSSNNVLDGLVLISVIDILYSWYSDSGTKILGMLRVLRALRLPLRVI 1392

Db 1186 GLYFGEQAYLRSSNNVLDGLVLISVIDIVSVASAGAKILGVLRVLRLLRLPLRVI 1245
Qy 1393 SRAQGLKLVETLSSSLKPIGNIVVCCAFIIFGILGVQLFKGFKFVQOQSDTNRITNK 1452
Db 1246 SRAQGLKLVETLSSSLKPIGNIVVCCAFIIFGILGVQLFKGFKFVQOQSDTNRITNR 1305
Qy 1453 SDCAEASRVVRHKYKFNGLGOALMSLFLVLTASKDGVMDIMYDGLDAGVDOOPIMNHPW 1512
Db 1306 SDCVAANRVVRHKKYKFNGLGOALMSLFLVLTASKDGVMDIMYDGLDAGVDOOPIMNHPW 1365
Qy 1513 MLLYFISFLLIVAFVFLNMVGVVVENFHKCRQHEEAEARRRERKRRLRLEKKERKAQC 1572
Db 1366 MLLYFISFLLIVAFVFLNMVGVVVENFHKCRQHEEAEARRRERKRRLRLEKKERKAQC 1425
Qy 1573 KPYTSDYSRFRLLVHLLCTSHYDLFTIGVTLNVVWAMBYOQOQLDBALKICNYIF 1632
Db 1426 LPYTATYCPTRLIIHSMCTSHYDLFTIGVTLNVVWAMBYOQOQLDBALKICNYIF 1485
Qy 1633 TVIFVLESVFKLVAPGRRRFFQDRWNOLDLAIVLLSITMGITLRETEVNASLPINPTIIRI 1692
Db 1486 TTVFVLEAVLKLAVAFGRURRFFKDRWNOLDLAIVLLSITMGITLRETEVNASLPINPTIIRI 1545
Qy 1693 MRVLRIRARVLRKLVAVGMRRALLDTVMQALPQVGNLGLLFFMLFFIFAAALGVLEFGDLEC 1752
Db 1546 MRVLRIRARVLRKLVAVGMRRALLDTVMQALPQVGNLGLLFFMLFFIFAAALGVLEFGDLEC 1605
Qy 1753 DETHPCBGLGHATFRNFGMAFLTLFRVSTGDNWNGIMKOTLRDC-DOESTCYNTV--IS 1809
Db 1606 NDENPCBMSRHATFENFGMAFLTLFRVSTGDNWNGIMKOTLRDC-DOESTCYNTV--IS 1665
Qy 1810 PIYFVSFVLTAQFVLNVVAVTAMKHEESKEAEAEAEAELEEM-KTLSPOPHSPL 1868
Db 1666 PIYFVSFVLTAQFVLNVVAVTAMKHEESKEAEAEAEAELEEM-KTLSPOPHSPL 1721
Qy 1869 GSPFLWPGVEGPDSPDKPGALHAAHARSASHFSLEHPTMQPHTELPDPLTLTV--- 1925
Db 1722 -----GPCFG-----PCPCPCPCACGPRLTSSPG 1747
Qy 1926 ---RKSGVSRTHSLPNDSSYMCRRH 1945
Db 1748 APGRSGGAGAGG-DTSHSLCRH 1769

RESULT 11

US-09-268-163-4
; Sequence 4, Application US/09268163B
; Patent No. 6353091
; GENERAL INFORMATION:
; APPLICANT: Lipscombe, Diane
; APPLICANT: Schorge, Stephanie
; TITLE OF INVENTION: HUMAN N-TYPE CALCIUM CHANNEL ISOFORM AND USES THEREOF
; FILE REFERENCE: B1055/7000
; CURRENT APPLICATION NUMBER: US/09/268,163B
; CURRENT FILING DATE: 1999-03-12
; EARLIER APPLICATION NUMBER: US 60/077,901
; EARLIER FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 2343
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-268-163-4

Query Match 14.7%; Score 1750.5; DB 3; Length 2343;
Best Local Similarity 24.2%; Pred. No. 2.6e-133;
Matches 639; Conservative 363; Mismatches 827; Indels 815; Gaps 84;
Qy 27 GAGGCGPGSABKDPGSDASAEGLPYPALAPVVF-----FYLSQDSRP 70
Db 25 GAGGAGGPGGGLQGQGVLYKQSIQAQARTMALYNPIPVKQNCFTVNRSLVFSEDNV 84
Qy 71 RSWCLRTVCNPFWRISMLVILLNCVILGMPRPCEADCSQRCLIQAFDD---FIFAP 127

85 RYAKRITTEPPFMYMILATIANCIVAL-----BOHLPDGDKTIPMSERLDDTEPIFIGI 140
 128 FAVMVVWVWALG-IFGKCYGLDTWNRDLFFIVIAQMLEYS---LDLQNVSPSAVRTVR 183
 141 PCFAGIKIALGFVFKHGSVLRGNWVMDVVVLTGILATAGTDFDLR-----TLRAVR 195
 184 VLRLPRAINRVPWRILVLTLLDTPMLGNVLLLCFFVFFIFGIVGVQWAGLLRRCFL 243
 196 VLRLKLVSGIPSLQVVLKSMKAMVPLLOGLLFFAILMFAILGLEFYMGKPHKACF- 254
 244 PENFSLPLSLDLERYQYOTENEDESPFICSPRENGMESCRSVPTLRGDCGGGPPCGLDYE 303
 255 -----PNSTDAE-----PV-----GDFPCGKEAP 273
 304 AYNSSNTTCVNMQYITNCAGBNPFGKAINFDNIGYAMIAIFQVITILEGWVDIMYFV 363
 274 ARLCEDTEC---REYMP-----GPNFGITNFDNILFAITVFQCIITMEGWTDILYNT 323
 364 MD-AHSFTNFIYFILLIIVGFFMNLCLVIAQFSETKORES-----OLMREORVRF 416
 324 NDAAGTWNWLYFIPLIIGSFFMLNLVGLSGEFAKERERVENRRAFLKLRQOOIE- 382
 417 LSNASTLASFEPGSCYBELKLYVILRKAARLAQVSRAGVRVGLLSPAPLGGQET 476
 383 -----RELNGYLEWIPKAEVWMLAEDRNA-----BEK 410
 477 QPSSCSRSRRRLSVHVLVHHHHHHHHHNGTILRAPRASPEIQDODANGSRRLMLPP 536
 411 SPLDLKRAATKKSNDLIH-----AEEGEDRFAD----- 440
 537 PSTPALSGAPCGAESVHSFYHADCHLEPVRQAPPPRSPSEASGRTVSGKVYPTVHTS 596
 441 ----- 440
 597 PPPETLKEKALVEVAASGPPTLSLTPPGPYSSMHKLETSQACQSKISSPCLK 656
 441 -----LCAVGSPPAR 450
 657 AUSGACGDPSCYCARAGAGEVELADREMPDSDSEAVVEFTQDAQHSLDRPHSRQRSL 716
 451 ASLKSGETESSYFR-----KEKMF----- 473
 717 GPDAESSVLAFWRLICDTRKIVDSKYVGRGIMAILVNTLSMGIEYHEQPEELTNALE 776
 474 -----FIRWVKAQSYVWVLCVVALNTLCVAMVHYNQPRRLTTY 515
 777 ISNIVFTSLFALEMLKLVLVPGFYKPNYNIFDGVIVVISWELVGO-----QGGGLS 831
 516 FAEFVFLGLFTMSLKMVGLGRSYFRSFCDFGVIVGVFVFWAAIKPGSSFGIS 575
 832 VLRTFELMVLVRLPALQRLVLMKTDNVTAFMCLMLFIFISILGMHIFGCKF 891
 576 VLRAULRLRIKVKTKVSSRLNLVSLNSMKSIIISLFLFLFVFWALLGQWFGGOF 635
 892 ASERDGDITLDRKNFDSLWAIIVTFQILTOEDWKNVLYNGM-----ASTSSWALYFIA 946
 636 NFODETPT---TNEDTFPAALITVFQILTGEDWNAVYHVGIESQGVSKGMFSFYFIV 691
 947 LMTFGNYVLNLLVALIVEGF-QAEISK-----REDASQO-----LSCIQ 986
 692 LTLFGNYTLNVLTAIVDNLANAQLTKDEEEMEEAANKUALQKAEVAEVPMSAAN 751
 987 LPVDSOGGDKSESPDFPSLDGDRKKCLALVSLGE-----HPELRK 1033
 752 ISTAARQONSAKARSVWEQASQLRLQNLRASCEALYSEMDPEERLPATTRHRLPDMKT 811
 1034 SLPLPLIHTAATMSLP-----KSTSTGLGEALGPASR-----RTSSSG----- 1073
 812 HLDRPLVGLRGARGFVGKARPEAAEAPEGVDPDRHRRHDXDKTPAAGDQDRAEA 871
 1074 ---SAPGA-----AHMKSPPSARS-----SPH-----SPWSAASSW 1103

872 PKAESGEPGAREPRHRSHSKAAAGPPARESRGRGPGEGGRRHRRSGPEEAARE 931
 1104 TSR-RSSNSLGRASLSKRSFSGERRSLLSGEGESQDEBESSEE-----ERASP- 1153
 932 PRHRAHRH---ODPSKECAGAKGERRAHRGPGPAGPREAESGEPARRHARHKAQPA 988
 1154 -----AGSDHRHRSLEAREKSSFDLPDTLOVPGUHLRTASGRG 1191
 989 HEAVEKETTEKATEKEAEIVEADKEKELRNHQPREPHCDLETSCTVTVPMMHTLPSTCL 1048
 1192 SASEHODCNKGSASGLARALRPDP-----PLDGDADDENL-----SKGE 1234
 1049 QKVEEPEADQNRNVRMSQPPDENTIVHVPMLTGPLGEATVPSGNVLESQAEGK 1108
 1235 R-----VRAMTRARLPACYLERDSWSAYIPPPQSRFRLLCHRIITHKMFHVVLVIF 1287
 1109 KEVEADDVMSGRPIVPS-----SMFCLSPNLLRRFCHYIVTMRYFEFWILVIA 1161
 1288 LNCITTAMERPKNIDPHSAERIFLTSNYIFTAVFLAEMTVKVALWCFCGEQAYLSSWN 1347
 1162 LSSIALAEDP-VRTDPSRNNALKYLDYFTGTFTPEWIKMIDGLLLHGPAYFRDLWN 1220
 1348 VLDGLAVLSVIDI-LVSMVSDSGTKILGMLRVLRLRLRPLRVISRAQGLKLVVETLM 1406
 1221 ILDFIVVSGALVAFAPSSFVGGSKGDKINTIKSLRVLRLPKTKIKLPKLVAFDCVV 1280
 1407 SSLKPIGNIVVICAPFIIFGILGVQFKGPFVCOGE-----DTRN--ITNKSACA 1458
 1281 NSLKNVILIVTMLFMFIFAVIAVQLFKGFKFYCDESKELERDCRGYLDYEKEVEEA 1340
 1459 SYR-WVRHKYNFNLCQALMSLFLVASKGQVDIMYDGLDVGVDQOQPMNHNPMMLLVF 1517
 1341 QPRQWKYDHYDNVLMWALLTLFTVSTGEGWMLKHSVDATYEEOGPSPGMYMELISFY 1400
 1518 ISFLLVAPFLVAMFVGVVWVNEPHKCRQHEBEARERRERKRLRLEKERRKA-----QC 1572
 1401 VTFVVFPPFVNI FVALIITF-----QEQGDVWSE-----CSLEKNERACIDFAISA 1450
 1573 KPY--XSDYSR--FRLLVHHLCTSHYLDLFTITVIGLVNVTWAMEHYQOQIIDEALKIC 1628
 1451 KPLTRYMPQNRQSFQYKTYTFFVSPFPFEYFIMAMIALNTVLMKMFYDAPYFELMLKCL 1510
 1629 NYLFTVFLVLESFVKLVAFCFRFRFFODRNOLDLAIVLLSIMGITILEE1-EVNASLPINP 1687
 1511 NIVFTSMFSECVLKIIIFAGVLYFRDANVDFVTVLGSITDILVETIAETN-----NF 1565
 1688 TIIRMEVLRARIKLLKMAVGNRRALLDTVMQALPOVGNLGLLMLLFFIFAALGVFLF 1747
 1566 INLSFLRFRARLILKLRQGYTIRILLWTFVQSFKALPYVCLLIAMLFFIYAIIGQVF 1625
 1748 GDLECDETHPCGGLGRHATERNFGMAFLTLFRVSTGNNWNGIMKDTLRD--CQOE--STC 1803
 1626 GNIALDDD--TSINRNNFRTPLOQLMLLFRSATGEAWHEIMLSCLSNQACDEQANATE 1682
 1804 YNTVISPIYVSFVLTQAQFVLNVNVIAMV-----KHLEE----- 1838
 1683 CGSDFAFYFVSFIFLCSFLMLNLFVAVIMDNFEYLRDSSILGPHLDEFIRVWAEYDP 1742
 1839 ----- 1838
 1743 AACGRISYNDMFEMLKHMSPLGLGKPCARVAYKRLVRNMMPISNEDMTVHTSTLMAL 1802
 1839 -----SKEAKEAEAELEEMKTLSPQSPHSPGLSPFPPLWPGVEGSDSP 1886
 1803 IRTALEIKLAPAGTKQOCDAELRKEISVVWANL-PQKTLDLLVP-----PHKPEDEM 1853
 1887 KPGALHPA-----AHARSASHFSLHPTM-----QHPTELPGPD 1921
 1854 TVGVYVAAIMTFDFYKQNTKTRDQWQAPGGLSQMGPVSLFPHPLKATLEOTQPAVLGAR 1913
 1922 LITVKSQSVTHSLPNDNSYMCRHGTAEGPLGHRGWLKPAQSGSVLSVHSQADTSYI 1981
 1914 VFLRQKSTSLSN-----GGAIQNESGIGESV-----SWG 1944

Db 739 KEVAEVSMPGAANISIAAQQNSAKARVMEQASQLRLQNLASCBALYSEMDPEERLR 798
Qy 1025 ---LGEHPELRKSLPLIHTAATPMSLP-----KSTGTGLGEALGPASR----- 1067
Db 799 FATTHRRPDMKTHLRPLVVELGDCARGPVGKARPEAAEAPGVDPPRRHRRDKD 858
Qy 1068 RTSSSG-----SAPPGA-----AHEMKSPPGARS-----SPH----- 1094
Db 859 KTPAAGQODRAEAPKASGGPGAREPRHRSHUSKEAAGPPEARSERGPGPEGGRH 918
Qy 1095 ---SPMSAASSWTSR-RSRNSLGRAPSLKRRSPGERSLLSGEQESQDEESSEE- 1148
Db 919 HRRGSPREAEERPRHRAHH---QDPSKECAGKERRARRHGGPRAGPREAESGEEP 975
Qy 1149 ---ERASP-----ACSDHHRGSLERAKSFDLPDIL 1178
Db 976 ARHRARHKAQPAHEAVEKETTEKEATEKEABIVEADKEKEKELRNHQPREHCDLTSGTV 1035
Qy 1179 QVPGHLRTASGRGSASEHODCNKGSASGLARALRPPDP-----PLDGDADD 1226
Db 1036 TVGPMHTLPSTCLOKVEQEDADNQRNVTMGSPDPNTIVHIVMLTGPGEATVVP 1095
Qy 1227 EGNL-----SKGER-----VRAMIRARLPACYLERSWSAYIPPOSRPRLCHRIIT 1274
Db 1096 SGNVDLESQAGKKEVEADDVMRSGPRPIVYS-----SMFCLSPNTLLRRECHYIVT 1148
Qy 1335 CFGEQAYLRSSWNVDGLLVLISIDILVSMV-SDSGTKILGMLRLRLRLTLRLRVIS 1393
Db 1208 LLHGAFTYRLDNLNDL-----FIVSGALVAFAPSGSKGDINTIKSLRVLRLPLKTIK 1263
Qy 1394 RAQGLKLVETLMSSLKPIGNIVVICCAFFIIFGILGVOLFKGFVFCQGE-----DTR 1447
Db 1264 RLPLKAVFDCVNSLKNVLNLIIVYMLFMFIFAVIAVQLFKGFYFCTDESKELRDCR 1323
Qy 1448 N-ITNKSDCAEASVR-WVRKYNFDNLGOALMSLFVLASKDQGVNDIMYDGLDVGVDQO 1504
Db 1324 GOYLDEKEEVAQPRQKKYDFHYDNLVALLTLFTVSTGEGPMVLKHSVDATEYEQ 1383
Qy 1505 PIMHNPWMLYFISFLILVAFVLMFVGVVVENFHKRQHEEBAARRREKRLRLE 1564
Db 1384 PSPGYRMELSIPIVYVYVFPFVFNIFVALIITF-----QEQGDKVME-----CSLE 1433
Qy 1565 KKRKA-----OCKPY--YSDYSR--FRLVHHLCTSHYDLFTGTGLVNVMTAMEHY 1615
Db 1434 KNERACIDPAISAKPLTRYMPQNRQSFQKXTWTFVVSPPFEYFMAMIALNTVLMKFX 1493
Qy 1616 QQPQILDEALKICNVIFTVIFVLESVFKLVAFGRFRFFQDRWNQDLDAIVLLSINGITL 1675
Db 1494 DAPYELMKCLNIVFTSMFSWECVLKIIAFGLVNLFRDANNVDFVTVLGSIITLVT 1553
Qy 1676 EIEVNASUPINTIIRIMVRLIARVLLKLVAGNMLALDVTMOALPOVGNLGLFMLL 1735
Db 1554 EIANNF---IN---LSFLRLFAARLIKLRQGYTIRILLMTFVQSFKALPVVCLLIAML 1607
Qy 1736 FTIFAALVELFGDLECDETHCEGIGHATFRNGMAFLTFRVSTGDNWNGIMKDTLR 1795
Db 1608 FFYIALIGNQVFNALDODD---TSINRNNFTFLQALMLLFRSATGEAWHEIMLSCLS 1664
Qy 1796 D-CQOE--STCYNTVISPIYFVSFVLTAQVLNVNVAIVL-----KHL 1836
Db 1665 NQACDEQANATECGSDFAFYFVSPIFLCSFLMLNLFVAVIMDNFEYLTRDSSILGPHHL 1724
Qy 1837 EE----- 1838
Db 1725 DEFIRVWBYDPAACGRISYNDMFEMLMKMSPLGLKKPCPARVAYKRLVRNMNPISED 1784
Qy 1839 ---SNKEAKEBAEAELEAELEEMKTLSPQHPSPGLSPFTW 1874
Db 1785 MIVHTSTLMALIRTALEIKLAPAGTKQHQCDALRKEISVVWANL-PQKTLDLLVP--- 1840

Qy 1875 PGVEGSDSPDKPGALHPA-----AHARSASHFSLEHPTM--- 1910
Db 1841 -----PHKEDMTVKVYAALMIFDYKQNKTRDQMQAAPGGLSQMGVSLFHLPLKATL 1895
Qy 1911 -QPHTELPDPLLVKRGVSRTHSLPNDSYNCRHGSTAEGLHGRGWLKPAQSGSVL 1969
Db 1896 EQTPAVLRGARVFLRKSTSLSN-----GGAIONQESGIKE 1933
Qy 1970 SVHSQPADTSYIILPKDAPHLLQP-----HSAPWTGTIPKLPPPGSRSLAQRLRRQAA 2024
Db 1934 SV-----SWGTQRTQDAPHEARPPLEKCHTEI-----PVGRSGALAVDVQMOSI 1978
Qy 2025 IR-----TDSLVDQGLSREDLLAEVSGP---SPPLARAYSWFQSQSTQAOQHRSYS 2074
Db 1979 TRRGPDGEQPGLESQGRAASMPRLAAETQPVTDASPMKRSI-----STLAQRPRTGTHL 2032
Qy 2075 KISKHMTTPAPCPG-----PEPNWKGPPETRSLSLELDTELSWISGDL 2117
Db 2033 CST---TPDRPPPSQASSHHHRRHRRDRRQRSLKQRP---SLGADMDGAPSSAVGPG 2086
Qy 2118 LPPGGOEPPSPRDLKKCYSVBAQSCQRR-PTSWLDEQRHRSIAVSLDSG----- 2167
Db 2087 LPEG---EGPTGCRERRRQRSSRQSRQSPSSSEKQRF---YSCDRFGGREGPPKPKP 2141
Qy 2168 ---SQPHLGTPD-----SNLGGQPL-----GGPGRPKKLLSP-PSITI 2202
Db 2142 SLSSHPTSPTAGQEPGPHQPGSGSVNGSPLLSTSGASTFCRGGRRLQPTPLTPRPSITY 2201
Qy 2203 ---DPPESQGRPT--PP-SPG-----ICLRRAPSSDKDPLASGPPDSMAASP 2245
Db 2202 KTANSPFIHPAGAQTSILPAPSPGRRLSRGLSEHNALLQRPDLS---QPLAPG----- 2249
Qy 2246 SPKKDVLSSLGSSDP 2261
Db 2250 -----SRIGSDP 2256

RESULT 13

US-09-452-007-2
; Sequence 2, Application US/09452007
; Patent No. 6140485
; GENERAL INFORMATION:
; APPLICANT: Franco, Rodrigo
; APPLICANT: Sun Chen, Ai Ru
; APPLICANT: Suey, David J.
; TITLE OF INVENTION: NUCLEIC ACID ENCODING HUMAN NEURONAL
; TITLE OF INVENTION: CALCIUM CHANNEL SUBUNITS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173-4799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/452,007
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/713,118
; FILING DATE: 16-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mata, Elizabeth W.
; REGISTRATION NUMBER: 38,236
; REFERENCE/DOCKET NUMBER: ACC96-01
; TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-861-6240

TELEFAX: 617-861-9540

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 2337 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-452-007-2

Query Match 14.7%; Score 1749; DB 3; Length 2337;
Best Local Similarity 24.3%; Pred. No. 3.5e-133;
Matches 645; Conservative 359; Mismatches 832; Indels 820; Gaps 86;

Qy 14 GQPSFMRNLNDLSAGGRRPGSGAEKPGSDADSBAEGLPYPALAPVVF-----61
Db 13 GPGGGERARG-GGAGGAGGPGGGLQPGQVLYKQSIQAQARTWALNPVPKNCFTV 71
Qy 62 ----PYLSQDSRPSWCLRTVCNPFERISMLVILLNCVTILGMRPCEDIACQRCRIL 117
Db 72 NRSUFVSEDNVVRKYAKRITETWPPFEYMIATIANCIVLAL----BOHLPDGDGKTPTS 127
Qy 118 QAFDD---FIFAFVAVENVRKVALG-IFGKKCYLGDWTNRLLDFFVIAGMLEYS---LD 170
Db 128 ERLDDTEFYFICFEAGIKIILGFVPHKGSYLKNGWNVMDFWVLGTILATAGTDFD 187
Qy 171 LONVSFAVTRVRLPRAINRVPMSRILVTLTLLDPLMGNVLLCFFVFFIGVGV 230
Db 188 LR-----TLRAVRLRLPLKLVSGIPSLQVWLKIMKAMVPLLIQILGLLFFAILMFAIIGL 242
Qy 231 QMWAGLNRCLFENFSLPLSVDLERYQYOTENEDESFFICSPRENGMRCRSVPTLRG 290
Db 243 EFMGKFKHACF-----PNSTDAE-----PV---263
Qy 291 DGGGPGCGLDYEAYNSSNTTCVNNNOYTNCSAGEHNPFKGAIFNPDNIGYAMTAIFOV 350
Db 264 ---GDFFCKEAPARLCEGDTEC---REYWP-----GPNFGITNFDNIIIFAILTVFQC 310
Qy 351 ITLEGWVDIMYVMD-AHSFYNYFIYLLIIVGFFPMINCLVVIATOFSETKORES---406
Db 311 ITMEGTDLTYNTDAAGTWNWLYFIPLIIIGSFFMLNLVLGSLGFEFAKERVENRR 370
Qy 407 ---QLMREORVRLSNASTLASFPSEPGCYBELLYLYILKARLAQVSRAGVRVG 463
Db 371 AFLKLRQQQIE-----RELNGYLEWIFKABEVMLEAEDRNA-----407
Qy 464 LLSSPAPLGGQETOPSSSCSRSHRLSVHLLVHHHHHHHHVHLGNGTLRAPRASPEIOD 523
Db 408 -----BEKSPDLVKRAATKSRNDLIH-----AEEGED 436
Qy 524 RDANGSRRLMLPPPTPALSGAPPGABSVHSFYHADCHLBPVRCQAPPPRSPSEASGRT 583
Db 437 RFAD-----440
Qy 584 VSGKVPYTVTSPPTLKEKALVEVAASSGPPTLTSNTPPGPYSSMHKLETTQSTGA 643
Db 441 -----440
Qy 644 QSSCKISSPCLKADSGAGDPCPCYCARAGAGEVELADREMPDSDEAVYEFTQDAQHS 703
Db 441 ---LCVSGSPPARASLKGKTESYFR-----KENMFRF-----473
Qy 704 DLDRPHSRQRSLGPDABSPSVLAFWRLLICDTFRKIVDSKYFGRGIMTAIIVLNTSMGIE 763
Db 474 -----FIRMVKAQSFYMWVLCVVALNTLCVAMV 502
Qy 764 YHEQBEELTNALETISNIYFTSLPALEMLLKLIVGPGYIKNPNIFDGVIVISVWEIV 823
Db 503 HYNQPRRLTTLTYFAEFYFLGLFTFEMSLKMYGLGFRSYFRSSFCNCFDGVIVGSVFVW 562
Qy 824 GQ-----QGGGLSVLRTPLRLRVKLRFPLALQRLVLMKTMNDVATFCMLLMLEFIF 878
Db 563 WAAIKPGSSFGISVLRAURLRLRIFKVTYKWSRLNVVSLNLSMKSIISLLFLFLFIW 622

Qy 879 PSILGMHLFGCKFASERDGDTLPRKKNPDSLLWALIVTVFQILTQEDWNKVLNMGH-----933
Db 623 FALLGMQLFGQGFNFQDETPT-----TNFDTPPAAILTVFQILTGEDMNAVMYHGIESQGG 678
Qy 934 ASTSSWAALFYFIALMTFGNYVLFNLLVAILVEGF-OAEEISK-----REDASQ-----981
Db 679 VSKGMFSFPFIVLTVLFNGYTLNVLVIAVDNLANAQELTKDEEMEAANKALQAKA 738
Qy 982 -----LSCIQLPVDSSQGDANKSESEPFFSPSLDGDGRKKCLALVS-----1024
Db 739 KEVAEVSPMASANTISAAQOONSAKARSVMQORASQLRQLNLQNLASCEALYSEMDPEERLR 798
Qy 1025 -----LGEHPELRKSLPLIHTAATPMSLP-----KSTSTGLGELGAPASR-----1067
Db 799 FATTTHRRRPMKTHLDRPLVVELGDCGARGVPGKARPEAAEPEGVPPRRHHHRDKD 858
Qy 1068 RTSSSG-----SAEPGA-----AHEMKSPPSARS-----SPH-----1094
Db 859 KTPAGQODRAEAPKASGEGFCAEERPRPHRSHSKEAAGPEARSEGRGPGEGGRRH 918
Qy 1095 ----SPMSAASSWTSR-RSSRNSLGRAPSLKRRSPSGERRSLSGEGQESQDESSSE-1148
Db 919 HRRGSPESAEREPHRAHRH---QDPSKACAGKERRARHRRGPPRAGPREAESGSEP 975
Qy 1149 -----ERASP-----AGSDHHRGSLEREAKSSFDLPDTL 1178
Db 976 ARRHARHKAQPAHEAVEKETTEKEATEKEAEIVEADKEKELRNHQPREPHCDLSTGV 1035
Qy 1179 QVPGHLRTASGRSASBEHODCNGKSASGLRALARLPDDP-----PLGDDADD 1226
Db 1036 TVGPMHTLPSTCLOKVEQPEDADQNRNVTGMSQPPDPNTIVHVPVMTGLGEATVVP 1095
Qy 1227 EGNL-----SKGER-----VRWIRARLPACYLERDSWSAYIFPPQSRFRLCHRIIT 1274
Db 1096 SGNVLESQABGKEVEADDVMSRGPPIVPS-----SMFCLSPNTLLRRFCHYIVT 1148
Qy 1275 HKMPDHVVLVIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTVKVALGW 1334
Db 1149 MRYEVEVILVIALSSIALAEDP-VRTDPSRNALKYLDYIFTGVTFEVMIKMIDGL 1207
Qy 1335 CFQGOAVLRSSWNVLDGLLVLSVIDIIVSMV-SDSGTKILGMLRLRLRLTLRLRVS 1393
Db 1208 LLHPCAVFRDLWNILD-----PIVVGALVAFAGSGKGDINTIKSLAVLRLPKTIK 1263
Qy 1394 RAQGLKLVETLMSLKPIGNIVVICCAFFIIFGLVQLFKGKFFVQCGE-----DTR 1447
Db 1264 RLPKLVKAVFDCVNSLKNVLNLIIVYLMFMFIFAVIAVQLFKGFFYCTDESKELEDCR 1323
Qy 1448 N--ITNKSDDCAEASR-WVRHKYFNDFNLGQALMSLFLVLSKDGWVDIMYDGLDVGVDQO 1504
Db 1324 QOYLDYEKEVEAQPRQWKYDFHYDNVLMWALLTLFTVSTGEGWPMVLKHSVDATYEEQG 1383
Qy 1505 PIMNHNPMMLLYFISLLIIVAFVFLNMFVGVVVENFHKCRHQHEBEEARRREKRLRLE 1564
Db 1384 PSPGYRMELSIFYVYVYVFFVFFFFNFVFAUIITF-----QEGDKVME-----CSLE 1433
Qy 1565 KKREKA-----QCKPY--YSDYSR--FRLVHHLCTSHYLDLFTIGVGLNVVWMBHY 1615
Db 1434 KNERACIDFALSAPLTRYMPQNRQSFOYKWTWTFVSPFPFVFMAMIALNTVLMWKFY 1493
Qy 1616 QOQILDEALKICNYIFTVIFVLESVFKLVAFGFRFRFQDRWNQOLDLAILVLSINGITLE 1675
Db 1494 DAPYEYELMLKCLNIVETSMFSMBEVLKIIAFGLVNLNYFRDANNVPDFVTVLGSITDILT 1553
Qy 1676 BIEYNASLPINPTIIRIMRVLRIARVLKLVKQVMBRALLDTVMQALPQVGNLGLLMLL 1735
Db 1554 EIANNF---IN---LSFURLFRAARLIKLLRQGYTIRILLWTFFVQSFKALPVCLLIAML 1607
Qy 1736 PFIIPAALGVLEFGDLECDETHPCBGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMKDTLR 1795
Db 1608 PFIYALIGMOVFGNIALDDDD---TSINPHNNFRIFLQALMLLFRSATGEAMHEIMLSCLS 1664


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Db 2156 QEPGPHPGSGVNGSPLLSTSGASTGRCGRRLQPLTPPTPRPSITYTKTANSSPIHFAG 2215
Qy 2210 PRT--PP-SPQ-----ICLRRAPSSDKDPLASGPPDPSMAASPKKDVLSLSGL 2257
Db 2216 AQTSLPAPSPGRSLRGSLSEHNALLQDPLS---QFLAPG-----SRI 2254
Qy 2258 SSDP 2261
Db 2255 GSDP 2258

RESULT 15
US-08-223-305C-47
; Sequence 47, Application US/08223305C
; Patent No. 5851824
; GENERAL INFORMATION:
; APPLICANT: Harpold, Michael
; APPLICANT: Ellis, Steven
; APPLICANT: Williams, Mark
; APPLICANT: Feldman, Daniel
; APPLICANT: McCue, Ann
; APPLICANT: Bremer, Robert
; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
; TITLE OF INVENTION: METHODS
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Brown, Martin, Hallier & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/223,305C
; FILING DATE: April 4, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/868,354
; FILING DATE: April 10, 1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/745,206
; FILING DATE: 15-AUG-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/620,250
; FILING DATE: 30-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/482,384
; FILING DATE: 20-FEB-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/603,751
; FILING DATE: 04-APR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US89/01408
; FILING DATE: 04-APR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/176,899
; FILING DATE: 04-APR-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Seigman, Stephanie L.
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 52516 (P519739)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619)238-0999
; TELEFAX: (619)238-0062
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2339 amino acids
; TYPE: amino acid
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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-223-305C-47

Query Match 14.7%; Score 1748.5; DB 2; Length 2339;
Best Local Similarity 24.2%; Pred. No. 3.8e-133;
Matches 641; Conservative 359; Mismatches 825; Indels 819; Gaps 85;

Qy 27 GAGRPGGSAEKDPGSDADSEAGLPYPALAPVVF-----FYLQDSRP 70
Db 25 GAGGAGGPGGLQPGQORVLYKQSIARARTMALYNFPVKQNCFTVNRSLFSESDNVV 84
Qy 71 RSWCLRTVCNPFERISMLVILLNCVLTGMFRPCEDIACDSQRCRIQAQDD---FIFAF 127
Db 85 RYAKRITWPPFNMIATIIANCIVLAL---EQHLPDGDKTPMSERLDDIEFYIGI 140
Qy 128 FAVEMVVMVALG-IFGKKCYLGDWTNRLLDFVVIAGMLEYS---LDQNVFSAVTVR 183
Db 141 FCFEAGIKIIALGFFVHKGSYLRNGWVMDVVVVLTGILATAGTDFDLR-----TLRAVR 195
Qy 184 VLRLPRAINRVPSMRILVTLILLDTLPMIGNVLLCPFPFIFGIVGQVLWAGLLRNCFL 243
Db 196 VLRLPLKLVSGIPSLQVVLKSIKAMVPELLQIGLLLFPAILMFALIGLEFYNGKFKHACF- 254
Qy 244 PENFSLPLSVDLERYQYOTENEDESPPFCSPRENGMRSCRSVPTLRGDGGGPPCGLDYE 303
Db 255 -----PNSTDAE-----PV-----GDFPCGKEAP 273
Qy 304 AYNSSNTTCVNNQYNTCSAGEHNPFGKAINFDNIGYAMIAIFQVITLEGWVDIMYFV 363
Db 274 ARLCGEGDTEC---REYWP-----GNFGITNFDNILFAITVFOCITMEGWTDILYNT 323
Qy 364 MD-AHSFYNEIYPTLLIIVGSEFMNLCVAVIATOPSETKORES-----OLMREQVRVF 416
Db 324 NDAAGNTWNWLYFIPLIIIGSFFMLNLVLGVLSEFAKERERVENRRAFLKLRQQQIE- 382
Qy 417 LSNASTLASPFSPGSCVEELLKYLVILRKAARLAQVRAAGVRVGLLSSPAPLGQET 476
Db 383 -----RELNGYLEWIFKAEVWLAEDRNA-----EEK 410
Qy 477 QPSSSCSRSHRRLSVHHLVHHHHHHHHLGNTLRAPASPEIQORDANGSRRLMLPP 536
Db 411 SPLDLVKRAATKKSRLDIH-----ABEGEDRFAD----- 440
Qy 537 PSTPALSGAPPGGAESVHSFYHADCHLEPVRCQAPPSPSPSEASGRVSGSKVYPTVHTS 596
Db 441 ----- 440
Qy 597 PPETLKEKALVEVAASSGPPTLTSLNIPPGYSSMHKLLTSTGACQSSCKISSPCLK 656
Db 441 -----LCAVGSPPAR 450
Qy 657 ADGACGPDSCPYCARAGAEVELADREMPDSEAVYEFTQDAHQSDLDLDPHRRORS 716
Db 451 ASLKSCKTESSESYFR-----KEMFRF----- 473
Qy 717 GPDAEPSSVLAFWRLICDTERKIVDSKYFCGRGIMIALVNTLSMGIEVHEQPELTNALE 776
Db 474 -----FIRRMVKAQSFYVVLVCVVALNTLCVAMVHYNQPRLLTTLTY 515
Qy 777 ISNIVFTSLFALEMLLKLVLVYGPFGYIKNPNYIPDGVIIVISVWEIVGQ-----QGGLS 831
Db 516 FAEFVFLGLFLETMSLKMVGLGPRSYRSSFNCFDFGVIVGVSFEVVWAAIKPGSSFGIS 575
Qy 832 VLRTFRLMRVLKLVRFPLPALQORQLVLMKTDNVATFCMLMLFIPTFSLGMHLFGCKF 891
Db 576 VLRALRLLRIRFKVTKYWSLSRLNLVSLNSMKSIISLLFLFLFVIVFALLGMQLGQGF 635
Qy 892 ASERDGDGTLPRKNFOSLLWAIIVTFQILTQEDWNKVLVNGM-----ASTSSWAALYFIA 946
Db 636 NFQDETPT-----TNFDTFPAAILTVFQLLTGEDNNAVYHGISQGGVSKGMPSSFYIV 691
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QY 947 LMTFGNYVLNLLVAILVEGF-QABEISK-REDA SQ-----LSCIQ 986
Db 692 LTLFGNYLLNVLNLAIAVDNLANAQLTKDEEMEEAANQKALQKAKEVAEVSMSAAN 751
QY 987 LPVDSQGDANKSESEPDFFSPSLDGDGRKKCLALVSLGE-----HPELRK 1033
Db 752 ISIAARQONSAKARSVMQSRASQLRLQNLRASCEALYSEMPDEERLRFPATTHLRLPDMT 811
QY 1034 SLLPLLIHTAATPMSLP-----KSTSTGLGEALGPASR-----RTSSG----- 1073
Db 812 HLDRLPVVVLGELRGARGPVGGKARPEAAEAEPEDPPRRHRHRDKTTPAAGQDRAEA 871
QY 1074 ---SAEPGA-----AHMKSPSPARS-----SPH-----SPWSAASSW 1103
Db 872 PKAESGEGAREERPRHRSHSKEAAGPEARSEGRGPGEGGRHRRHRRSPAEAERE 931
QY 1104 TSR-RSSNSLGRAPSLKRRSPSGERRSLLSGEGESQDEESBEE-----ERASP- 1153
Db 932 PRHRAH--QPSKECAGKERRARRHGGPRAGPREAESGEEPARRHRAHKAQPA 988
QY 1154 -----AGSDHRRGLEREAKSFDLPDLQVPLGHLRTASGRG 1191
Db 989 HEAVEKETTEKEATEKEAEIADAEKEKELRNHQPREPHCDLETSGTIVTGPMTLPSTCL 1048
QY 1192 SASEHODCNKGSASRLARLPDDP-----PLGDDADDECNL-----SKGE 1234
Db 1049 QKVEEQPEDADNQRNVTRMGSPDPNTVHI PVMLTGPLGEATVVPNGVDLESQAEGK 1108
QY 1235 R-----VRAWIARLPACYLERSDSWAYIFPPQSRPRLCHRIITHKMFHDVVLVIF 1287
Db 1109 KEVEADVWRSGPRIPVYS-----SMFCLSPNLLRRFCHIVTWRYFEVVLVIA 1161
QY 1288 LNCITIAMERPKIDPHSAERIFPLNSYIFTAFLAENTVKVALGWCFCGQAYLRSSWN 1347
Db 1162 LSSIALAEDP-VRTDSPNNALKYDIFGTGVTFFEMVIMIDILGLLHPGAYFRDLWN 1220
QY 1348 VLDGLVLIIVIDLVSNV-SDSGTKILGMLRVLRLLRTLRPLRVISRAQGLKLVETLM 1406
Db 1221 ILD-----FIVVSGALVAFAGSGKGKINTIKSLRVLRVLRPLTKIRKLPKLVAFDCV 1276
QY 1407 SSLKPIGNIVVICAFFIIFGILGVOLPKGFFVCOGE-----DTRN--ITNKSDCAEA 1458
Db 1277 NSLKNVLNLIIVMLFWFIFAVIAVOLFKGFFYCTDESKELERDCRGQYLOYEKEVEEA 1336
QY 1459 SYR-WVRHKYNFDNLQALMSFLVLASKDQWVDIMYDGLDAVGVDQDQIMNHNPMWLLYF 1517
Db 1337 QRQWKYDFHYDNVLMALLTLFTVSTGEGWPMVLKHSVDATYEEQGPSGYRMELSIFY 1396
QY 1518 ISFLIIVAFVLMFVGVVVENFHKROHQBEEARREERLRLEKRRKA-----QC 1572
Db 1397 VVYFVWFFPFVNFVALLIITP-----QBQDKWSE-----CSLEKNERACIDFAISA 1446
QY 1573 KPY--YSDYSR--FRLVHLCTSHYLDLFTIGVLNVVTWAMEHYQQOILDEALKIC 1628
Db 1447 KPLTRYMPQNSQFYKWTWTVVSPPEYFIMAMIALNTVLMKFDYDAPYEIMLUKCL 1506
QY 1629 NYIFTVFLRESVKLVAFGRFRFQDRWNOLDLAILLSIMGITLBEI-EVNASLPINP 1687
Db 1507 NIVFTSMFESMCLKIIAFGLNVFRDANNVDFVTVLGSITDILVETIAETN-----NF 1561
QY 1688 TIIRIMRVLRARVLKLUKAVGRALLDVTWQALPQVGNIGLLFMLLFFIPALGVELP 1747
Db 1562 INLSPLRLFRARLILKLRQGYTIRILLTWTQSFKALPVYVCLLIAMFFIYIIGMQVF 1621
QY 1748 GDLECDETHPCGELGRHATFRNFGMAPLTLFRVSTGDNWNGIMKDTLRD--CDOE--STC 1803
Db 1622 GNIALDDD---TSINRHNNTFFLOALMLLFRSATGEAWHEIMLSJCSNQACDQANATE 1678
QY 1804 YNTVISPIYFVSFVLTAQFVLNVVIAVIM-----KHLEE----- 1838
Db 1679 CGSDPAYFYFVSFIFLCSFLMLNFVAVIMDNFEVLTEDSSILGPHHLDLFEIRVWAEYDP 1738

QY 1839 ----- 1838
Db 1739 AACGRISYNDMFEMLKMSPPGLGKCPARVAYKRLVRMMMPISNEDMTVHTSTLMAL 1798
QY 1839 -----SNKEAKEAELEAELEMKTLSPQSPHSLGSPFLWPGVEGPDSPSP 1886
Db 1799 IRTALEIKLAPAGTKQHQCDAELAKEISVVWANL-PQKTLDLLVE-----PHKPDEN 1849
QY 1887 KPGALHPA-----AHARSASHFSLEHPTM-----QHPTELPGPD 1921
Db 1850 TVGVYAAALMIFDYKONKTTTRDQMOPAGLSQMGVPSLFHPLKATLEOTQPAVLRGAR 1909
QY 1922 LLTVKGSVSTHSLPNDYSWCRHSTAEGLGHRGWLKPAQSGSVLSVHSQPADTSVI 1981
Db 1910 VFLQKSTSLN-----GGAIQNESGIKESV-----SWG 1940
QY 1982 LQLPKDAPHLIQP-----HSAPTWTGTPKLPPLPPGSRPLAQPLRRQAIR-----TDS 2029
Db 1941 TQRTQDAPHEARPLERGHSTEI-----PVGSRGALAVDVQVQOSITRRGPDGEPQG 1992
QY 2030 LDVQGLSREDLLAEVSGP-----SPPLARAYFWGQSSTQAQOHSRSHSKISKHMTTPAPC 2086
Db 1993 LESQGRAASMPRLAAETQPVTDASPMKRSI-----STLAQPRGTHLCST---TPDRPP 2043
QY 2087 PG-----PEPNWKGPPETRRSSLELDTLSWISGDLPPGGQEEPPSP 2129
Db 2044 PSQASSHHHHRCHRRDRKQRSLEKGP---SLSDMDGAPSSAVGPGLPFG---EGPTGC 2098
QY 2130 RDLKKCYSVEAQSCORR-PTSWLDEQRRHSIAVCLDSG-----SQPHLG 2173
Db 2099 RREERQERGRSQERQPSSSSEKQRF---YSCDRFGGREPKPKPSLSHSTPTAG 2155
QY 2174 TDP-----SNLGGQPL-----GGGSRPXXKULSP-PSITI-----DPPEQQ 2209
Db 2156 QEPGPHPGGSGVNGSPLLSTSGASTPGRGRRQLPQTLTPRPSITYKTANSPIHFAG 2215
QY 2210 PRT--PP-SPQ-----ICLRRAPSSDSKDLASGPPDSMAASPCKDVLISLGL 2257
Db 2216 AQTSLPAPSGRLSRGLSEHNALLQRPDLS---QLAPG-----SRI 2254
QY 2258 SSDP 2261
Db 2255 GSDP 2258

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Job time : 91 secs

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OM protein - protein search, using sw model

Run on: April 13, 2005, 16:39:37 ; Search time 213 Seconds
(without alignments)
3535.925 Million cell updates/sec

Title: US-09-611-257A-37

Perfect score: 11904

Sequence: 1 MDEEDGAGAEESQPSFM.....PKDVLSLGLSDPADLDP 2266

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1421835 seqs, 332370683 residues

Total number of hits satisfying chosen parameters: 1421835

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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1: /cgn2_6/ptodata/2/pubaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubaa/US07_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubaa/US07_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/2/pubaa/US11_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubaa/US11_PUBCOMB.pep.*
19: /cgn2_6/ptodata/2/pubaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/2/pubaa/US60_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	11815.5	99.3	2377	16	US-10-757-262-16
2	11758.5	98.8	2243	16	US-10-408-765A-625
3	11111	93.3	2374	10	US-09-383-894-2
4	11111	93.3	2425	10	US-09-383-894-4
5	6315.5	53.1	1207	17	US-10-930-301-52
6	6212	52.2	2353	16	US-10-408-765A-1128
7	5492.5	46.1	2175	9	US-09-935-541-2
8	5492.5	46.1	2175	14	US-10-425-800-2
9	5484	46.1	2188	9	US-09-935-541-4
10	5484	46.1	2188	14	US-10-425-800-4
11	5366	45.1	1835	9	US-09-935-541-5
12	5366	45.1	1835	14	US-10-425-800-5
13	3959.5	33.3	1853	9	US-09-030-482B-19

14	3564.5	29.9	1657	15	US-10-369-493-6836	Sequence 6936, Ap
15	1753	14.7	2264	15	US-10-627-370-2	Sequence 2, Appli
16	1750.5	14.7	2343	13	US-10-033-026-4	Sequence 4, Appli
17	1748.5	14.7	2339	15	US-10-375-253-12	Sequence 12, Appli
18	1746.5	14.7	2339	13	US-10-033-026-6	Sequence 6, Appli
19	1743	14.6	2237	15	US-10-375-253-14	Sequence 14, Appli
20	1741	14.6	2237	13	US-10-033-026-8	Sequence 8, Appli
21	1722	14.5	2336	13	US-10-033-026-10	Sequence 10, Appli
22	1673.5	14.1	1745	15	US-10-627-370-4	Sequence 4, Appli
23	1667	14.0	2313	16	US-10-322-696-178	Sequence 178, App
24	1665	14.0	2270	15	US-10-375-253-40	Sequence 40, Appli
25	1663.5	14.0	2251	15	US-10-375-253-38	Sequence 38, Appli
26	1659	13.9	2270	16	US-10-322-696-176	Sequence 176, App
27	1657.5	13.9	2251	16	US-10-322-696-84	Sequence 84, Appli
28	1632	13.7	1873	13	US-10-029-413A-22	Sequence 22, Appli
29	1625.5	13.7	1748	16	US-10-408-765A-1968	Sequence 1968, Ap
30	1619.5	13.6	1984	10	US-09-457-571-10	Sequence 10, Appli
31	1615.5	13.6	1989	10	US-09-457-571-12	Sequence 12, Appli
32	1602	13.5	2016	16	US-10-632-342-2	Sequence 2, Appli
33	1602	13.5	2510	15	US-10-375-253-34	Sequence 34, Appli
34	1598.5	13.4	2015	16	US-10-632-342-6	Sequence 6, Appli
35	1597.5	13.4	2157	16	US-10-467-491-2	Sequence 2, Appli
36	1596.5	13.4	2151	16	US-10-467-491-4	Sequence 4, Appli
37	1594	13.4	2016	16	US-10-632-342-4	Sequence 4, Appli
38	1591	13.4	1854	13	US-10-029-413A-2	Sequence 2, Appli
39	1590.5	13.4	2015	14	US-10-077-054-2	Sequence 2, Appli
40	1590.5	13.4	2015	16	US-10-632-342-8	Sequence 8, Appli
41	1587	13.3	2016	10	US-09-896-994-2	Sequence 2, Appli
42	1586	13.3	1969	10	US-09-457-571-16	Sequence 16, Appli
43	1586	13.3	2016	9	US-09-840-125-4	Sequence 4, Appli
44	1586	13.3	2016	15	US-10-333-191-2	Sequence 2, Appli
45	1586	13.3	2016	16	US-10-914-133-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1

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US-10-757-262-16
; Sequence 16, Application US/10757262
; Publication No. US20040197825A1
; GENERAL INFORMATION:
; APPLICANT: Karicheti, Venkateswarlu
; APPLICANT: Silos-Santiago, Inmaculada
; APPLICANT: Eliasof, Scott D.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: UROLOGICAL DISORDERS USING 44390, 54181, 211, 5687, 884,
; TITLE OF INVENTION: 1405, 636, 4421, 5410, 30905, 2045, 16405, 18560, 2047,
; TITLE OF INVENTION: 33751, 52872, 14063, 20739, 32544, 43239, 44373, 51164,
; TITLE OF INVENTION: 53010, 16852, 1587, 2207, 22245, 2387, 52908, 69112, 14990,
; TITLE OF INVENTION: 18547, 115, 579, 15985, 15625, 760, 18603, 2395, 23554, 8675,
; TITLE OF INVENTION: 32720, 4809, 14303, 16816, 17827, 32620, 577, 619, 1423,
; TITLE OF INVENTION: 2158, 8263, 15402, 16209, 16386, 21165, 30911, 41897, 1643,
; TITLE OF INVENTION: 2543, 9626, 13231, 32409, 84260, 2882, 8203, 32678 OR
; FILE REFERENCE: MF103-007P1RNMNMIM
; CURRENT APPLICATION NUMBER: US/10757,262
; CURRENT FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: US 60/440,318
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/444,783
; PRIOR FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: US 60/457,901
; PRIOR FILING DATE: 2003-03-27
; PRIOR APPLICATION NUMBER: US 60/468,775
; PRIOR FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: US 60/471,614
; PRIOR FILING DATE: 2003-05-19
; PRIOR APPLICATION NUMBER: US 60/478,742
; PRIOR FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: US 60/488,529
; PRIOR FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 60/491,156
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; PRIOR FILING DATE: 2003-07-30		841		VLKLVRFALQROLVLMKTMNDVATFCMLLMFLFIFISILGMHLFGCKFASERDGTLL	900
; PRIOR APPLICATION NUMBER: US 60/499,594		Db			
; PRIOR FILING DATE: 2003-09-02		841		VLKLVRFALQROLVLMKTMNDVATFCMLLMFLFIFISILGMHLFGCKFASERDGTLL	900
; PRIOR APPLICATION NUMBER: US 60/506,332		Qy			
; PRIOR FILING DATE: 2003-09-26		Db		PRKKNFDSLLWAVTVFOILTQEDWNKVLNGMASTSSWAALYFIALMTFNGVLFNLLV	960
; NUMBER OF SEQ ID NOS: 136		Qy			
; SOFTWARE: FastSeq for Windows Version 4.0		Db		PRKKNFDSLLWAVTVFOILTQEDWNKVLNGMASTSSWAALYFIALMTFNGVLFNLLV	960
; SEQ ID NO 16		Qy			
; LENGTH: 2377		Db		ATLVGFOAEETSKREDASGQLSCIQLPVDQGGDANKSESEPFSPSLDGDGRKCL	1020
; TYPE: PRT		Qy			
; ORGANISM: Homo sapiens		Db		ATLVGFOAEETSKREDASGQLSCIQLPVDQGGDANKSESEPFSPSLDGDGRKCL	1020
; US-10-757-262-16		Qy			
Query Match 99.3%; Score 11815.5; DB 16; Length 2377;		1021		ALVSLGEHPELRKSLPLPLIIHTAATPMSLPKSTSTGLGEALGPASRTSSGSAEPGAA	1080
Best Local Similarity 95.2%; Pred. No. 0;		Db			
Matches 2364; Conservative 1; Mismatches 1; Indels 111; Gaps 2;		1021		ALVSLGEHPELRKSLPLPLIIHTAATPMSLPKSTSTGLGEALGPASRTSSGSAEPGAA	1080
Qy 1 MDEEDGAGAESGQPRSFMLNDLSGAGRPGPSAEKDPGSADSEAGLPPALAPVV		Qy		1081	HEMKPPSARSSPHSPWNAASWTSSRRNSLGRAPSLKRRSPSGERRLLSGGQSSQ
Db 1 MDEEDGAGAESGQPRSFMLNDLSGAGRPGPSAEKDPGSADSEAGLPPALAPVV		Db		1081	HEMKPPSARSSPHSPWNAASWTSSRRNSLGRAPSLKRRSPSGERRLLSGGQSSQ
Qy 61 PFYLSQSRPSRWCILRTVCNPFERISMLVILLNCVTLGMRPCEDIACDSQRCLIQAF		Qy		1141	DEEESSEERASPGSDHHRGSLEREAKSSFDLTQVPGHLHTASGRGSASHQDCN
Db 61 PFYLSQSRPSRWCILRTVCNPFERISMLVILLNCVTLGMRPCEDIACDSQRCLIQAF		Db		1141	DEEESSEERASPGSDHHRGSLEREAKSSFDLTQVPGHLHTASGRGSASHQDCN
Qy 121 DDFIAPFAFVAVVQKVALGIFGKCYLGDFTWNRLDFFIVTAGMLEYSLDLQNVFSFAVR		Qy		1201	GKSASGRALARALRPDDPPLDGDADDEGNLSKGERVIRARLPACYLERSWYATFP
Db 121 DDFIAPFAFVAVVQKVALGIFGKCYLGDFTWNRLDFFIVTAGMLEYSLDLQNVFSFAVR		Db		1201	GKSASGRALARALRPDDPPLDGDADDEGNLSKGERVIRARLPACYLERSWYATFP
Qy 181 TVRVLRPLRAINRVPSMILVTLMLDTPMLGNVLLLCFFVFFIFGIVGVQLMAGLLNR		Qy		1261	PQSRPFLLCRRITTHQMFHVVIIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAV
Db 181 TVRVLRPLRAINRVPSMILVTLMLDTPMLGNVLLLCFFVFFIFGIVGVQLMAGLLNR		Db		1261	PQSRPFLLCRRITTHQMFHVVIIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAV
Qy 241 CFLPENFSLPLSDVLEYYQTEDESPFICSPQRENMRSCRSVPTLRGGGGPPCGL		Qy		1321	FLAEMTVKVVAGLWCFCGEQAYLRSSNVNLDGLLVLSIVDILVSVSDSGTKILGMLRVL
Db 241 CFLPENFSLPLSDVLEYYQTEDESPFICSPQRENMRSCRSVPTLRGGGGPPCGL		Db		1321	FLAEMTVKVVAGLWCFCGEQAYLRSSNVNLDGLLVLSIVDILVSVSDSGTKILGMLRVL
Qy 301 DYEAVNSSNTTCVANNQYITNCSEAGHNPFGKALNFQNIQYAVIAIFQVITLEGWVDM		Qy		1381	RLARTLRPLRVISRAOGLKLVVETLMSLPKIGNIIVICCAFFIIFGILGVQLFKGKFPV
Db 301 DYEAVNSSNTTCVANNQYITNCSEAGHNPFGKALNFQNIQYAVIAIFQVITLEGWVDM		Db		1381	RLARTLRPLRVISRAOGLKLVVETLMSLPKIGNIIVICCAFFIIFGILGVQLFKGKFPV
Qy 361 YFVMDAHSFYNYFIFILLIIVGSFWMINCLVVIATQSETQKRSQMLRQVRFLSNA		Qy		1441	COGEDTRNITNKSDCAEASVYRVVHRKHYNFNDLQALMSLFLVASKDGWVDIMYDGLDVG
Db 361 YFVMDAHSFYNYFIFILLIIVGSFWMINCLVVIATQSETQKRSQMLRQVRFLSNA		Db		1441	COGEDTRNITNKSDCAEASVYRVVHRKHYNFNDLQALMSLFLVASKDGWVDIMYDGLDVG
Qy 421 STLASFSEPGSCYEELKLVYLILKAARLAQVRAQVRYGLSSPAPLGQGTQPS		Qy		1501	VDQOPIMHNPNMMLLYFISPELLIVAFVLMNVGVVVENFHKCRHQHEEERREERKRL
Db 421 STLASFSEPGSCYEELKLVYLILKAARLAQVRAQVRYGLSSPAPLGQGTQPS		Db		1501	VDQOPIMHNPNMMLLYFISPELLIVAFVLMNVGVVVENFHKCRHQHEEERREERKRL
Qy 481 SCRSRRLSVHHLVHHHHHHHHYHLGNGTLRAPASPEIQDRDANGSRRLMLPPSTP		Qy		1561	RRLEKKRR-----KAQCKPYYSYSRPRLLVHHLCTSHYLDLFTGV
Db 481 SCRSRRLSVHHLVHHHHHHHHYHLGNGTLRAPASPEIQDRDANGSRRLMLPPSTP		Db		1561	RRLEKKRRMLDDVIASSGSSASAASEAQCKPYYSYSRPRLLVHHLCTSHYLDLFTGV
Qy 541 ALSGAPGGAESVHSFYHADCHLEPVRCQAPPSPSEASGRVSGKVPVTVHTSPPE		Qy		1603	IGLVNVTMAHEHYQOQPOILDEALKIKNYIFTVIFVLESFVLAFFGRFFQDRWNOLDL
Db 541 ALSGAPGGAESVHSFYHADCHLEPVRCQAPPSPSEASGRVSGKVPVTVHTSPPE		Db		1621	IGLVNVTMAHEHYQOQPOILDEALKIKNYIFTVIFVLESFVLAFFGRFFQDRWNOLDL
Qy 601 TLKEKALVEAASGPTLTSLNIPPGPYSSMHKLELTQSTGACQSSCKISSPCLKADSG		Qy		1722	AVLLSTMGITLIEBIEVNASLPINPTIIRIMRVLIARVLKLLKMAVGMALDVTVMQAL
Db 601 TLKEKALVEAASGPTLTSLNIPPGPYSSMHKLELTQSTGACQSSCKISSPCLKADSG		Db		1740	AVLLSTMGITLIEBIEVNASLPINPTIIRIMRVLIARVLKLLKMAVGMALDVTVMQAL
Qy 661 ACQPDSCPYCARAGAGEVELADREMPDSSEAVYETQDAQHSDLDPHRRQRSIGPDA		Qy		1782	POVGNGLGLLFFLFFIAALGVLELPGDLCEDETHPCBGLGRHATFRNFGMAFLTFRVST
Db 661 ACQPDSCPYCARAGAGEVELADREMPDSSEAVYETQDAQHSDLDPHRRQRSIGPDA		Db		1782	POVGNGLGLLFFLFFIAALGVLELPGDLCEDETHPCBGLGRHATFRNFGMAFLTFRVST
Qy 721 EPSSVLAFWRLICDTFRKI VDSKFGKIMIALVNTLSMGIEYHQPBELTNALEISNI		Qy		1800	POVGNGLGLLFFLFFIAALGVLELPGDLCEDETHPCBGLGRHATFRNFGMAFLTFRVST
Db 721 EPSSVLAFWRLICDTFRKI VDSKFGKIMIALVNTLSMGIEYHQPBELTNALEISNI		Db		1800	POVGNGLGLLFFLFFIAALGVLELPGDLCEDETHPCBGLGRHATFRNFGMAFLTFRVST
Qy 781 VFTSLFALEMLKLLVYGPFGYIKNPYNIFDGVNIVISVWEIVGQCGGLSVLRTFLMR		Qy		1842	GDWNGIMKDTLRCDDESTCTNTVISPFIYFVSFVLTQAVLVNVTAVLMLKHEESNKE
Db 781 VFTSLFALEMLKLLVYGPFGYIKNPYNIFDGVNIVISVWEIVGQCGGLSVLRTFLMR		Db		1842	GDWNGIMKDTLRCDDESTCTNTVISPFIYFVSFVLTQAVLVNVTAVLMLKHEESNKE
Qy 840		Qy		1902	AKKEAELEAELEEMKLTSLSPQHPGLSPFLWPVGEQSPDSPKPGALHPAAHARSASH
Db 840		Db		1902	AKKEAELEAELEEMKLTSLSPQHPGLSPFLWPVGEQSPDSPKPGALHPAAHARSASH
Qy 840		Qy		1909	PSLEHT-----
Db 840		Db		1909	PSLEHT-----

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Db 1921 FSLHPTDRQLFDITSLIIQSLWELKMDLGLAGGQGPAPSPAGLGGSDPQIPLAE 1980
Qy 1910 -----NQPHTELFPGDILLTVKSG 1929
Db 1981 MEALSLTSEIVSEPCSLALTDDSLDDMDHTLLLSALESNMQPHTELPFGDILLTVKSG 2040
Qy 1930 VSRHSLNDNYSYMRHSGTAGPLGHRGWGLPKAQSGSVLSVHSGPADTSYIQLPKDAP 1989
Db 2041 VSRHSLNDNYSYMRHSGTAGPLGHRGWGLPKAQSGSVLSVHSGPADTSYIQLPKDAP 2100
Qy 1990 HLLQPHSAPTWTTPKLPKPPGRSPLAQRPLRRQAAIRTDSDLDVGLGSRDILLAEVSGPS 2049
Db 2101 HLLQPHSAPTWTTPKLPKPPGRSPLAQRPLRRQAAIRTDSDLDVGLGSRDILLAEVSGPS 2160
Qy 2050 PPLARAYSFQGSSTQAQHSRSHSKISKHMTTPAPCPGPEPNMGKGPETRRSLELDT 2109
Db 2161 PPLARAYSFQGSSTQAQHSRSHSKISKHMTTPAPCPGPEPNMGKGPETRRSLELDT 2220
Qy 2110 LSWISGDLPPGQGEPPSPDLKKCYSEVAQSCORRPTSWLDBORRHSIAVCLDGSQ 2169
Db 2221 LSWISGDLPPGQGEPPSPDLKKCYSEVAQSCORRPTSWLDBORRHSIAVCLDGSQ 2280
Qy 2170 PHLTGDRSNLGGQPLGGPSRPPKXLSPPSITIDPPESQGPRTPPSGICLRRRAPSDS 2229
Db 2281 PHLTGDRSNLGGQPLGGPSRPPKXLSPPSITIDPPESQGPRTPPSGICLRRRAPSDS 2340
Qy 2230 KDPLASGPPDQMAASPSPKDVLISLGLSSDPADLDP 2266
Db 2341 KDPLASGPPDQMAASPSPKDVLISLGLSSDPADLDP 2377
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RESULT 2

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US-10-408-765A-625
; Sequence 625, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Watnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 625
; LENGTH: 2243
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-625
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Query Match 98.8%; Score 11758.5; DB 16; Length 2243;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 2242; Conservative 0; Mismatches 1; Indels 23; Gaps 1;

Qy 1 MDEEDGAGAESGQPRSFMRNLDSGAGRGPGSAEKDPGSDADSEAEGLPYPALAPV 60
Db 1 MDEEDGAGAESGQPRSFMRNLDSGAGRGPGSAEKDPGSDADSEAEGLPYPALAPV 60
Qy 61 FFYLSQDSRPSWCLRTVCNPFERISMLVILLNCVTLGMRPCEDTACDSQRCRILQAF 120
Db 61 FFYLSQDSRPSWCLRTVCNPFERISMLVILLNCVTLGMRPCEDTACDSQRCRILQAF 120
Qy 121 DDFIFAFVAVWVWVWALGIFGKKCYLGDWTNRLDFFIVTAGMLEYSLDQNVSFSAVR 180
Db 121 DDFIFAFVAVWVWVWALGIFGKKCYLGDWTNRLDFFIVTAGMLEYSLDQNVSFSAVR 180
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Qy 181 TVRVLRPLRAINRVPSMRILVTLILLDPLMGNVLLLCFFVFPIFGIVGVQVWAGLLNR 240
Db 181 TVRVLRPLRAINRVPSMRILVTLILLDPLMGNVLLLCFFVFPIFGIVGVQVWAGLLNR 240
Qy 241 CFLPENFSLPLSVDLERYOTENEDESPFFICSQPRENGMRSCRSVPTLRGGGGPPGCL 300
Db 241 CFLPENFSLPLSVDLERYOTENEDESPFFICSQPRENGMRSCRSVPTLRGGGGPPGCL 300
Qy 301 DYEAYNSSNTTVCNNQYNTCSAGBNHPKGAINDNICYAWIAI PQVITLLEGWVDM 360
Db 301 DYEAYNSSNTTVCNNQYNTCSAGBNHPKGAINDNICYAWIAI PQVITLLEGWVDM 360
Qy 361 YFVMDAHSFYNYFIYFIILLIIVGSFFMINCLVATOFSETKQRESQMRQRVRLSNA 420
Db 361 YFVMDAHSFYNYFIYFIILLIIVGSFFMINCLVATOFSETKQRESQMRQRVRLSNA 420
Qy 421 STLASFSEPGSCYEELKYLVIILKKAARRLAQVSRAGVRVGLLSSPAPLGGQSTQPS 480
Db 421 STLASFSEPGSCYEELKYLVIILKKAARRLAQVSRAGVRVGLLSSPAPLGGQSTQPS 480
Qy 481 SCSRSHRRLSVHLLVHHHHHHHHYHLNGTTLRAPRASPEIQDRDANGSRRLMLPPPSTP 540
Db 481 SCSRSHRRLSVHLLVHHHHHHHHYHLNGTTLRAPRASPEIQDRDANGSRRLMLPPPSTP 540
Qy 541 ALSGAPPGCAESVHSFYHADCHLEPVRCQAPPPRSPSEASGRTVSGSKVYTVHTSPPE 600
Db 541 ALSGAPPGCAESVHSFYHADCHLEPVRCQAPPPRSPSEASGRTVSGSKVYTVHTSPPE 600
Qy 601 TLKEKALVEVAASSGPPFTLSLNPFGPYSMHKLLETQSTGACQSSCKISSPCLKADSG 660
Db 601 TLKEKALVEVAASSGPPFTLSLNPFGPYSMHKLLETQSTGACQSSCKISSPCLKADSG 660
Qy 661 ACPGDCPYCARAGAGEVELADREMPDSSEAVYEFTQDAQHSDLRDPHRSRQSLGPA 720
Db 661 ACPGDCPYCARAGAGEVELADREMPDSSEAVYEFTQDAQHSDLRDPHRSRQSLGPA 720
Qy 721 EPSSVLAFWRLICDTFRKIYVDSKYFGRGIMAILVNTLSMGIYHEQPEELTNALEISNI 780
Db 721 EPSSVLAFWRLICDTFRKIYVDSKYFGRGIMAILVNTLSMGIYHEQPEELTNALEISNI 780
Qy 781 VFTSLFALEMLLKVLYGPGFYIKNPYNI PDGVIWISVWEI VGOQGGGLSVLRTFLMR 840
Db 781 VFTSLFALEMLLKVLYGPGFYIKNPYNI PDGVIWISVWEI VGOQGGGLSVLRTFLMR 840
Qy 841 VLKLVRELPAQLQOLVVLMTDMNVATFCMLLMLEFIFISILGMHLFGCKFASERDGT 900
Db 841 VLKLVRELPAQLQOLVVLMTDMNVATFCMLLMLEFIFISILGMHLFGCKFASERDGT 900
Qy 901 PDRKNFDSLLWAIYTVFQILTOEDMNKLYNGMASTSSWAALYFIALTMTFGNYVFNLLV 960
Db 901 PDRKNFDSLLWAIYTVFQILTOEDMNKLYNGMASTSSWAALYFIALTMTFGNYVFNLLV 960
Qy 961 AILVEGFQABEISKREDASQGLSCIQLPVDSDGDKANSSEPPFPSPSLDGDGRKKCL 1020
Db 961 AILVEGFQABEISKREDASQGLSCIQLPVDSDGDKANSSEPPFPSPSLDGDGRKKCL 997
Qy 1021 ALVSLGHEPHELRLKSLPLIHTAATPMSLPKSTSTGLGEALGPASRRTSSGSAEPGAA 1080
Db 998 ALVSLGHEPHELRLKSLPLIHTAATPMSLPKSTSTGLGEALGPASRRTSSGSAEPGAA 1057
Qy 1081 HEMKSPPSARSSPHSPWSAASSWTSRRSRNSLGRAPSLKRSPSGERRSLLSSEGQBSQ 1140
Db 1058 HEMKSPPSARSSPHSPWSAASSWTSRRSRNSLGRAPSLKRSPSGERRSLLSSEGQBSQ 1117
Qy 1141 DEESSSEERAS PAGSDHRRHGSLEERAKSFDLPTLOVPLHRTASGRCSASEHODCN 1200
Db 1118 DEESSSEERAS PAGSDHRRHGSLEERAKSFDLPTLOVPLHRTASGRCSASEHODCN 1177
Qy 1201 GKSASGLARALRPDDPPLDGDADDDEGNLSKGRVRAWIRARLPACLYERDSWSAYIFP 1260
Db 1178 GKSASGLARALRPDDPPLDGDADDDEGNLSKGRVRAWIRARLPACLYERDSWSAYIFP 1237
Qy 1261 PQSRFLLCHRIITHKMPDHVVLVIIIFLNCITIAMERPKDTPHSAERIFLTLNVIITAV 1320
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1238 POSRFLLCRIITKMFDFHVLVILFNCITTIAMERPKIDPHSAERIIFLTLSNYIFTAV 1297
1321 FLAEMTVKVALGHCFCGEAYLRSSWNVLGLVLISVIDILVSMYSDSGTKILGMLRVL 1380
1298 FLAEMTVKVALGHCFCGEAYLRSSWNVLGLVLISVIDILVSMYSDSGTKILGMLRVL 1357
1381 RLRLTLPLRVRISRAOGLKLVETLMSLKPIGNIVVICCAFFIIFGILGVQLFKGPFV 1440
1358 RLRLTLPLRVRISRAOGLKLVETLMSLKPIGNIVVICCAFFIIFGILGVQLFKGPFV 1417
1441 COGEDTRNITKSDCAEASRYWVTHKYNFNDLQALMSLFLVASKOGWVDIMYDGLDVG 1500
1418 COGEDTRNITKSDCAEASRYWVTHKYNFNDLQALMSLFLVASKOGWVDIMYDGLDVG 1477
1501 VDQOPIMHNPWMLLYPISFLIIVAFVFNMFVGVVVENFHKCRHQHEEAEARRREKRL 1560
1478 VDQOPIMHNPWMLLYPISFLIIVAFVFNMFVGVVVENFHKCRHQHEEAEARRREKRL 1537
1561 RRLEKRRKAQCKPYSDYSRFRLLVHHLCTSHYLDLFTITGVIGLVNVTWAMEHYQOPOI 1620
1538 RRLEKRRKAQCKPYSDYSRFRLLVHHLCTSHYLDLFTITGVIGLVNVTWAMEHYQOPOI 1597
1621 LDEALKICNYITFTVIFVLESFKLVAFCGRFRFFQDRWNQLDLAIVLLSIMGITILEEVEN 1680
1598 LDEALKICNYITFTVIFVLESFKLVAFCGRFRFFQDRWNQLDLAIVLLSIMGITILEEVEN 1657
1681 ASLPINPTIIRIMVLRIRARVLLKLMVAGMRALLDTVMQALPOVGNLGLLFLMLFFIPA 1740
1658 ASLPINPTIIRIMVLRIRARVLLKLMVAGMRALLDTVMQALPOVGNLGLLFLMLFFIPA 1717
1741 ALGVLELFGDLEDETHPCBEGGRHATFRNFGMAELTTLFRVSTGDNWNGIMKDTLRDCDOE 1800
1718 ALGVLELFGDLEDETHPCBEGGRHATFRNFGMAELTTLFRVSTGDNWNGIMKDTLRDCDOE 1777
1801 STCYNTVISPFIYFVSVFLTAQVFLVNVVIAVLMLKHEESNKEAEAELEAELEMKTL 1860
1778 STCYNTVISPFIYFVSVFLTAQVFLVNVVIAVLMLKHEESNKEAEAELEAELEMKTL 1837
1861 SPOPHSPLSGPLWPGVEGDPSPKPGALHPAAHARSASHFSLEHPTMOPHPTLPGP 1920
1838 SPOPHSPLSGPLWPGVEGDPSPKPGALHPAAHARSASHFSLEHPTMOPHPTLPGP 1897
1921 DILLTVRKSGVSRTHSLPNDSPYCRGSGTAEGPLHGRGWLKPAQSGSVLSVHSQPADTSY 1980
1898 DILLTVRKSGVSRTHSLPNDSPYCRGSGTAEGPLHGRGWLKPAQSGSVLSVHSQPADTSY 1957
1981 ILQLPKDAPHLLOPHSAPTWTGTPKLPPLPGRGLAQRPLRQAAIRTDSDLVQGLGSRD 2040
1958 ILQLPKDAPHLLOPHSAPTWTGTPKLPPLPGRGLAQRPLRQAAIRTDSDLVQGLGSRD 2017
2041 LLAEVSGSPPLARAYSFWQSGSTQAQHSRSHKISKHMTPPAPCPGPEPNWKGPPET 2100
2018 LLAEVSGSPPLARAYSFWQSGSTQAQHSRSHKISKHMTPPAPCPGPEPNWKGPPET 2077
2101 RSSLELDTLSWISGDLPLPGGEEPPSPDLKKCYSVSAQSCORRPTSWLDEQRHSTA 2160
2078 RSSLELDTLSWISGDLPLPGGEEPPSPDLKKCYSVSAQSCORRPTSWLDEQRHSTA 2137
2161 VSCLDGSGPHLGTDPNLGQPLGGSPKPKLSPSTTTDPPESQGPRTPPSPGICL 2220
2138 VSCLDGSGPHLGTDPNLGQPLGGSPKPKLSPSTTTDPPESQGPRTPPSPGICL 2197
2221 RRRAPSSDSKDPPLASGPPDSMAASPSPKKDVLSLSGLSSDPADLDP 2266
2198 RRRAPSSDSKDPPLASGPPDSMAASPSPKKDVLSLSGLSSDPADLDP 2243

RESULT 3
US-09-383-894-2
; Sequence 2, Application US/09383894
; Publication No. US20030125269A1
; GENERAL INFORMATION:

APPLICANT: Li, Ming
; TITLE OF INVENTION: T-Type Calcium Channel
; FILE REFERENCE: 004.00191
; CURRENT APPLICATION NUMBER: US/09/383,894
; EARLIER FILING DATE: 1999-08-26
; EARLIER APPLICATION NUMBER: US 60/098,004
; EARLIER FILING DATE: 1998-08-26
; EARLIER APPLICATION NUMBER: US 60/117,399
; EARLIER FILING DATE: 1999-01-27
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 2374
; TYPE: PRT
; ORGANISM: Rattus sp.
; US-09-383-894-2

Query Match 93.3%; Score 11111; DB 10; Length 2374;
Best Local Similarity 93.3%; Pred. No. 0;
Matches 2135; Conservative 35; Mismatches 95; Indels 24; Gaps 5;

QY 1 MDEEDGAGAESGGPRGPRFMRNLNLSGAGRPGPGSAEKDPGSADSEAGLPYPALAPV 60
DB 1 MDEEDGAGAESGGPRGPRFMRNLNLSGAGRPGPGSAEKDPGSADSEAGLPYPALAPV 60
QY 61 FFYLSQDSRPRSWCLRTVCNPFERISMLVILLNCVTLMFRPCEDIAACDSORCILQAF 120
DB 61 FFYLSQDSRPRSWCLRTVCNPFERISMLVILLNCVTLMFRPCEDIAACDSORCILQAF 120
QY 121 DDFIFAFVAVMVMVAVGIFGKCYLGDTWNRLLDFFIVIAAGMLEYSIDLQNVFSAVR 180
DB 121 DDFIFAFVAVMVMVAVGIFGKCYLGDTWNRLLDFFIVIAAGMLEYSIDLQNVFSAVR 180
QY 181 TVRLVRLPRAINRVPMSRILVTLLDTPMLGNVLLCFFVFFIFGIVGVQVWAGLLNR 240
DB 181 TVRLVRLPRAINRVPMSRILVTLLDTPMLGNVLLCFFVFFIFGIVGVQVWAGLLNR 240
QY 241 CFIPEFNSPLSDVLEERYQTEDESPFCISQPRENGMRSCSVPTLRGDCGGGPPCSL 300
DB 241 CFIPEFNSPLSDVLEERYQTEDESPFCISQPRENGMRSCSVPTLRGDCGGGPPCSL 300
QY 301 DYETNYSNNTTCVNNQYVYVNCNAGEHNPFGKAINFDNIGYAWIAI FQVITLEGWVDM 360
DB 301 DYETNYSNNTTCVNNQYVYVNCNAGEHNPFGKAINFDNIGYAWIAI FQVITLEGWVDM 360
QY 361 YFVMDAHSFYNYFIYFILLIIVGFFMINCLVVIATQFSETKORESQLMREQVRFLSNA 420
DB 361 YFVMDAHSFYNYFIYFILLIIVGFFMINCLVVIATQFSETKORESQLMREQVRFLSNA 420
QY 421 STLASFSEPGSCYEELIKYLVYILRKAARLAQVRAAGVVRVGLLSSPAPLGGQETQPS 480
DB 421 STLASFSEPGSCYEELIKYLVYILRKAARLAQVRAAGVVRVGLLSSPAPLGGQETQPS 480
QY 481 SCRSRRLSVHLLVHHHHHHHHHNGTLRAPRASPEIQDRDANGSRMLMPPSTP 540
DB 481 SCRSRRLSVHLLVHHHHHHHHHNGTLRAPRASPEIQDRDANGSRMLMPPSTP 540
QY 541 ALSGAPCGAESVHSFYHADCHLEPVRCQAPPPRSPSEASGRTVSGSKVPTVHTSPPE 600
DB 541 TPGSGPPRGAEVHSFYHADCHLEPVRCQAPPPRSPSEASGRTVSGSKVPTVHTSPPE 600
QY 601 TLKEKALVEVAASGSPPTLTSLNIPPGPYSMHKLLETQSTGACQSSCKISSPCLKADSG 660
DB 601 TLKEKALVEVAASGSPPTLTSLNIPPGPYSMHKLLETQSTGACQSSCKISSPCLKADSG 660
QY 661 ACPDSCPCYCARAGAVEVLAADREMPDSDSEAVYFTQDAQHSDLRDPHS -RRORSGLPD 719
DB 661 ACPDSCPCYCARAGAVEVLAADREMPDSDSEAVYFTQDAQHSDLRDPHS -RRORSGLPD 720
QY 720 AEPSSVLAFWRLICDTFRKIVDSKYFGRGIMAILVNTLSMGIYHQBELTNALEISN 779
DB 721 AEPSSVLAFWRLICDTFRKIVDSKYFGRGIMAILVNTLSMGIYHQBELTNALEISN 780

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QY 780 IVFTSLFALEMLKLLVYGPYIKNPYNI PDGVIWVLSVMEIVCOQGGGLSVLRTPLM 839
Db 781 IVFTSLFALEMLKLLVYGPYIKNPYNI PDGVIWVLSVMEIVCOQGGGLSVLRTPLM 840
QY 840 RVLKLVRLPALQRLVLMKTMNDVATFCMLLMLEFIIFSILGMLHFGCKFASERDGD 899
Db 841 RVLKLVRLPALQRLVLMKTMNDVATFCMLLMLEFIIFSILGMLHFGCKFASERDGD 900
QY 900 LPDRKNFOSLLWAI VTVFQILTOEDWNVKLVNGMASTSSWAALYFIALMTFGNYVLFNLL 959
Db 901 LPDRKNFOSLLWAI VTVFQILTOEDWNVKLVNGMASTSSWAALYFIALMTFGNYVLFNLL 960
QY 960 VAILVEGFOAEIEIKREDASGOLSCIQLPVNSOGGDANKSESEDFPSIDGDRKKC 1019
Db 961 VAILVEGFOAEIEIKREDASGOLSCIQLPVNSOGGDANKSESEDFPSIDGDRKKR 1020
QY 1020 LALVSLGHPHRLKSLPPLIHTAATPMSLPKSTSTGLGALGPASRRTSSSGSAEPGA 1079
Db 1021 LALVALGEHAELRKSLPPLIHTAATPMSLPKSSSTGVEALGSGSRTSSSGSAEPGA 1080
QY 1080 A-HEMKSPPSARSSPHSPWSAASWTSRRSRNSLGRAPSLKRRSPSGERSLLSGEQE 1138
Db 1081 AHHEMKSPPSARSSPHSPWSAASWTSRRSRNSLGRAPSLKRRSPSGERSLLSGEQE 1140
QY 1139 SODEEESSEERASPGSDHHRGSLEREAKSSFDLPTLQVPGHRTASGRSASEHOD 1198
Db 1141 SODEEESSEERASPGSDHHRGSLEREAKSSFDLPTLQVPGHRTASGRSASEHOD 1200
QY 1199 CNGKSASGLARALRPPDPLDGDADDDEGNLSKGERVRAWIRARLPACYLERSWSAYI 1258
Db 1201 CNGKSASGLARTLTDDPQLDGDNDDEGNLSKGERIQAWRSRLPACCRERSWSAYI 1260
QY 1259 FPPOSFRLCHRIITHQFMDHVLVLIIFLNCITIAMERPKIDPHASERIFLTLSNYIFT 1318
Db 1261 FPPOSFRLCHRIITHQFMDHVLVLIIFLNCITIAMERPKIDPHASERIFLTLSNYIFT 1320
QY 1319 AVFLAEMTVKVALGWCGEQAYLRSSWNVDLGLLVLSVIDILVMSVSDSGTKILGMLR 1378
Db 1321 AVFLAEMTVKVALGWCGEQAYLRSSWNVDLGLLVLSVIDILVMSVSDSGTKILGMLR 1380
QY 1379 VLRLRLRLRLVLSRAQGLKLVETLMSLKPIGNI VVICAFPIIFGILGVOLFKGKF 1438
Db 1381 VLRLRLRLRLVLSRAQGLKLVETLMSLKPIGNI VVICAFPIIFGILGVOLFKGKF 1440
QY 1439 FVCGQEDTRNITNKSDCABAYRWYRHKYNFDNLGQALMSLFLVLSKDGWVDIMYDGLDA 1498
Db 1441 FVCGQEDTRNITNKSDCABAYRWYRHKYNFDNLGQALMSLFLVLSKDGWVDIMYDGLDA 1500
QY 1499 VGVDOQPIIMNHPWMLLYFISFLIVAFVFLNMFGVVVNFPHKCRQHQEERAREEK 1558
Db 1501 VGVDOQPIIMNHPWMLLYFISFLIVAFVFLNMFGVVVNFPHKCRQHQEERAREEK 1560
QY 1559 RLRLLEKKRR-----KAQCKPYSDYSRFRLLVHHLCTSHYLDLFT 1600
Db 1561 RLRLLEKKRNLMDLDDVITASGSSAASEAQCKPYSDYSRFRLLVHHLCTSHYLDLFT 1620
QY 1601 QVIGLVNVTWAMEHYQQOILDEALKI CNYIFTVIFVLESFVFLGVAQFRFRFFQDRWNQL 1660
Db 1621 QVIGLVNVTWAMEHYQQOILDEALKI CNYIFTVIFVLESFVFLGVAQFRFRFFQDRWNQL 1680
QY 1661 DLAIIVLSIMGITILEEIEVNASLPINPTIIRIMRVLRARVLRKLVKMAVGRALLDTVMQ 1720
Db 1681 DLAIIVLSIMGITILEEIEVNASLPINPTIIRIMRVLRARVLRKLVKMAVGRALLDTVMQ 1740
QY 1721 ALPOVGNLGLLFLMLFFIIFALGVLELFGDLECDETHPCGEGRHATFRNFGMAFLTFRV 1780
Db 1741 ALPOVGNLGLLFLMLFFIIFALGVLELFGDLECDETHPCGEGRHATFRNFGMAFLTFRV 1800
QY 1781 STGDNWNGIMKMDTLRDCDQESTCYNTVISPFIYFVSFVLTAQFVLNVNVIIVLAKHLEESN 1840
Db 1801 STGDNWNGIMKMDTLRDCDQESTCYNTVISPFIYFVSFVLTAQFVLNVNVIIVLAKHLEESN 1860
QY 1841 KEAKEAELEAELEEMKTLSPQSPHSPLGSPFLPWPVGVEGSDSPSPKPGALHPAAHAKSA 1900
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Db 1861 KEAKEAELEAELEEMKTLSPQSPHSPLGSPFLPWPVGVEGSDSPSPKPGAPHTTAAHIGAA 1920
QY 1901 SHFSLEHPTMOPHPTLP---GPDLLTVRKSGVSRTHSLPNDSYNCRHGSTAEGPLGHRG 1957
Db 1921 SGFSLEHPTMYPHEEVPVPLGPDLLTVRKSGVSRTHSLPNDSYNCRNGSTAERSLGHG 1980
QY 1958 WGLPKAAGSVLSVHSQPADTSYIILQPKDAPHLLOPHASPTWGTIPKLPDPPGRSPLAQ 2017
Db 1981 WGLPKAAGSVLSVHSQPADTSYIILQPKDAPHLLOPHASPTWGTIPKLPDPPGRSPLAQ 2040
QY 2018 PLRQQAIRTDLSVQGLGSRREDLAEVSGSPPLARAYSFWGOSSTQAOQHSRSHSKTS 2077
Db 2041 PLRQQAIRTDLSVQGLGSRREDLAEVSGSPPLARAYSFWGOSSTQAOQHSRSHSKTS 2100
QY 2078 KHMTPAPCPGPEPNWKGPPETRSSLELDELTELSEWISGDLPLPGQEPEPPPRDLKKCYS 2137
Db 2101 KHIRLPAPCPGLEFSMAKDPETRSSLELDELTELSEWISGDLPLPGQEPEPPPRDLKKCYS 2159
QY 2138 VEAQSCORRPTSWLDEORRHSIAVCLDSGQPHLGTDPNSLGGQPLGGGSRPKKULSP 2197
Db 2160 VETQSCRRRPGSWLDEORRHSIAVCLDSGQPHLGTDPNSLGGQPLGGGSRPKKULSP 2219
QY 2198 PSITIDPESOGPRTPPSPRGICLRRRAPSSDSKDPPLASGPPDSMAASPSPKDVLISLGL 2257
Db 2220 PSITIDPESOGSRRPPCSPGVCLRRRAPASDSKDPVSSPLDSTAASPSPKDVLISLGL 2279
QY 2258 SSSDPAIDLDP 2266
Db 2280 SSSDPAIDLDP 2288

RESULT 4
US-09-383-894-4
; Sequence 4, Application US/09383894
; Publication No. US20030125269A1
; GENERAL INFORMATION:
; APPLICANT: Li, Ming
; TITLE OF INVENTION: T-Type Calcium Channel
; FILE REFERENCE: 004.00191
; CURRENT APPLICATION NUMBER: US/09/383.894
; CURRENT FILING DATE: 1999-08-26
; EARLIER APPLICATION NUMBER: US 60/098.004
; EARLIER FILING DATE: 1998-08-26
; EARLIER APPLICATION NUMBER: US 60/117.399
; EARLIER FILING DATE: 1999-01-27
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 4
; LENGTH: 2425
; TYPE: PRT
; ORGANISM: Rattus sp.
US-09-383-894-4
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Query Match 93.3%; Score 11111; DB 10; Length 2425;
Best Local Similarity 93.3%; Pred. No. 0;
Matches 2135; Conservative 35; Mismatches 95; Indels 24; Gaps 5;

QY 1 MDEEDGAGAEESQSPRSFVRLNDLSGAGGRPGSGAEKDPGSADSEAEGLPYPALAPV 60
Db 52 MDEEDGAGAEESQSPRSFVRLNDLSGAGGRPGSGAEKDPGSADSEAEGLPYPALAPV 111
QY 61 FFYLSQDSRPRSWCLRTVCNPFWRISMLVILLNCVLTGMFRPCEDIACDSQRCILQAF 120
Db 112 FFYLSQDSRPRSWCLRTVCNPFWRISMLVILLNCVLTGMFRPCEDIACDSQRCILQAF 171
QY 121 DDFTFAPFAVEMVVMVALGIFGKKCYLGDWTNRDLDFIIVIAHMLVSLDLQNVFSFAVR 180
Db 172 DDFTFAPFAVEMVVMVALGIFGKKCYLGDWTNRDLDFIIVIAHMLVSLDLQNVFSFAVR 231
QY 181 TVRVLRLPRLAIRNPVSRILVTLTLLDTPMLGNVLLLCFFVFFIFGIVGVQLWAGLLNR 240
Db 232 TVRVLRLPRLAIRNPVSRILVTLTLLDTPMLGNVLLLCFFVFFIFGIVGVQLWAGLLNR 291
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QY	1319	AVFLAEMTVKVALGWCFCGEQAYLRSSNVLDGLLLVLSVIDILVSVSDSGTKILGMLR	1378
DB	1372	AVFLAEMTVKVALGWCFCGEQAYLRSSNVLDGLLLVLSVIDILVSVSDSGTKILGMLR	1431
QY	1379	VLRLLRTLRPLRVISRAQGLKLVVETLMSSLPKIGNIWIWICCAFFIIFGILGVOLFPGKF	1438
DB	1432	VLRLLRTLRPLRVISRAQGLKLVVETLMSSLPKIGNIWIWICCAFFIIFGILGVOLFPGKF	1491
QY	1439	FVCOGEDTRNITNKSDCAEASYRVRHRYNFDNLGOALMSLVFLASKDQWVDIMYDGLDA	1498
DB	1492	FVCOGEDTRNITNKSDCAEASYRVRHRYNFDNLGOALMSLVFLASKDQWVDIMYDGLDA	1551
QY	1499	VGVDOOPIMNHNPMMLLYFISFLLIIVAFVLMFVGVVVENFHKROHOBEEARRREK	1558
DB	1552	VGVDOOPIMNHNPMMLLYFISFLLIIVAFVLMFVGVVVENFHKROHOBEEARRREK	1611
QY	1559	RURLEKKER-----KAOCKPYSDYSRFRLLVHHLCTSHYLDLFT	1600
DB	1612	RURLEKKERMLMDODVITAGSSASAAEAQCKPYSDYSRFRLLVHHLCTSHYLDLFT	1671
QY	1601	GVIGLNVVTMAEHYQQPQILDALKICNYITVTIVFVLESVFKLVAFQFRFPFQDRWNL	1660
DB	1672	GVIGLNVVTMAEHYQQPQILDALKICNYITVTIVFVLESVFKLVAFQFRFPFQDRWNL	1731
QY	1661	DLAIVLLSIMGITLBEIEVNASLPINPTIIRIMRVLRIRARVLKLMKMAVGRALLDVTMQ	1720
DB	1732	DLAIVLLSIMGITLBEIEVNASLPINPTIIRIMRVLRIRARVLKLMKMAVGRALLDVTMQ	1791
QY	1721	ALPOVGNLGLLFWLFFIFAALGVELFGDCEDETHPCBGLGRHATFRNFGMAFTLFRV	1780
DB	1792	ALPOVGNLGLLFWLFFIFAALGVELFGDCEDETHPCBGLGRHATFRNFGMAFTLFRV	1851
QY	1781	STGDNWNGIMKOTLRDCDOESTCYNTVISPITYFVSFVLTAQFVNVNVIJAVLMKHEESN	1840
DB	1852	STGDNWNGIMKOTLRDCDOESTCYNTVISPITYFVSFVLTAQFVNVNVIJAVLMKHEESN	1911
QY	1841	KEAKEAEAELELEMKLTPHPSPLGSPFLMPCVEGPDSPDPSPKPGALHPAAHARS	1900
DB	1912	KEAKEAEAELELEMKLTPHPSPLGSPFLMPCVEGPDSPDPSPKPGALHPAAHARS	1971
QY	1901	SHFSLEHPTMQPHTELP--GPDLLTVRKSGVSRTHSLPNDSYMCRHSGTAEGPLGHRG	1957
DB	1972	SGFSLEHPTMQPHTELP--GPDLLTVRKSGVSRTHSLPNDSYMCRHSGTAEGPLGHRG	2031
QY	1958	WGLPKAQSGLSVHSGPADTSLVLOLPKADPHLOPHSAPTWTGTIPKLPPLPGSRPLAQR	2017
DB	2032	WGLPKAQSGLSVHSGPADTSLVLOLPKADPHLOPHSAPTWTGTIPKLPPLPGSRPLAQR	2091
QY	2018	PLRQAAIRTDSDLDVQGLSREDLLAEVSGPSPPLARAYSFWQGSSTQAQOHRSHKIS	2077
DB	2092	PLRQAAIRTDSDLDVQGLSREDLLAEVSGPSPPLARAYSFWQGSSTQAQOHRSHKIS	2151
QY	2078	KHMTPPAPCPGPPBNWKGPPETRSLSLELDELTELISWISGDLPLPGGOEPPSPRDLKKYS	2137
DB	2152	KHMTPPAPCPGPPBNWKGPPETRSLSLELDELTELISWISGDLPLPGGOEPPSPRDLKKYS	2210
QY	2138	VEAQCORRPTSLWDEORRHISIAVSLDQSGQHLGTDPSNLGQGLPGGPGSRPKKLSP	2197
DB	2211	VETOSCRRRPGSLWDEORRHISIAVSLDQSGQHLGTDPSNLGQGLPGGPGSRPKKLSP	2270
QY	2198	PSITIDPPESQGRTPPSPGICLRRRAPSSDSKDPPLASGPPDWAASPPKDVLSLGL	2257
DB	2271	PSISIDPPESQGRTPPSPGICLRRRAPSSDSKDPPLASGPPDWAASPPKDVLSLGL	2330
QY	2258	SSDPAADLDP	2266
DB	2331	SSDPTDMDP	2339

RESULT 5
US-10-930-301-52
; Sequence 52, Application US/10930301
; Publication No. US20050026207A1

Db	145	APFAVEMVIOXVALGFGQCYLGDTWNRDFFIVVAGMEYSLDGHNVLSAIRTVRL	204	Db	1171	KGKSTDDDE--AEDGSAAPGPRATPLRRAESLDPRPLPAALPPTKCRDRDQVVALPSDF	1228
Qy	186	RPLRAINRVSRLVTLVLLDTPMLGNVLLLCFFVFFIFIGVQVWAGLNRCLPE	245	Qy	1185	--RTASGRGSASEHDCNGKSGASGRARALRDPDDPPLDGDADDDEGNLSKGERVAMTRA	1242
Db	205	RPLRAINRVSRLVTLVLLDTPMLGNVLLLCFFVFFIFIGVQVWAGLNRCLFDS	264	Db	1229	FLRIDSHREDRAELDDSDSCCLRLHKVLEPKP-----QWCRS	1268
Qy	246	NFSLPLSVD--LERYOTENDESPFICSQPRENGMRSRVP---TLRGDGGGPGCLD	301	Qy	1243	RLPACYLBRDSWSAYIFPPQSRFRLLCHRIITHKMFHDHVLVVIIFLNCITIAMERPKIDP	1302
Db	265	AFVRNNNLTRPYOTEEGEPFICSSRRDGMQKSHIPGRREL-----MPCITLG	318	Db	1269	-----REAWALYLFSPQNRFRVSCQVITHKMFHDHVLVFIPLNCVTIALERPDIDP	1320
Qy	302	YEAN-----SSNTTCVNNQYTNCSAGEHNPFGKAINFDNIGYAMIAIFQVITLE	354	Qy	1303	HSABRIFLTLNVIYITAVFLAEMTVKVALWCFCGEQAVLRSSWNVLDDLGLVLISVIDIL	1362
Db	319	WEAYTOQAEGVAGARNACINWQYTNVCSGDSNPENGAINFDNIGYAMIAIFQVITLE	378	Db	1321	GSTERVFLSVSNYIFTAIFVAMVMVKVALGLLSGEHAYLQSSWNVLDDLGLVLVSLDIV	1380
Qy	355	GWVDIMYVMDAHSFYNIYFILLIIVGSPFMNLCIUVIATOFSETKQRESOLMRQRV	414	Qy	1363	VSMVSDSGTKILGMLRVLRLRLTLRLRVRISRAOGLKLWETLMSLSPKIPGINVVICAF	1422
Db	379	GWVDIMYVMDAHSFYNIYFILLIIVGSPFMNLCIUVIATOFSETKQRESOLMRQRA	438	Db	1381	VAMASAGGAKILGVLRLRLTLRLRVLRAVISRAPGLKLVETLISLSPKIPGINVICAF	1440
Qy	415	RFLNASTLASFPSPGCEYELLKXVYLKKAARLQAQVSRAGVRVGLSSPAPLGGQ	474	Qy	1423	FIIFILGVLQPKGPFVCOGEDTRNITNKSDEASVYRVRHKYNFONLGOALMSLFLV	1482
Db	439	RHLSNDSTLASFPSPGCEYELLKXVGHIFKVRRLRLYARWQSRWKKVDPSPAVOQQ	498	Db	1441	FIIFILGVLQPKGPFVCOGEDTRNITNKSDEASVYRVRHKYNFONLGOALMSLFLV	1500
Qy	475	ETQSSSSCSRHR--LSVHLV--HHHHHHHHHHLGNGTLRAPRASPEIQORDANGSRL	532	Qy	1483	ASKDGWVDIMYDGLDAVGDQOPIMNHNPMWLLYFISFLIIVAFFVLNMFVVVENPHK	1542
Db	499	--GPHRRORAGRHTASVHVLVYHHHHHHHHHSHGSPRRPGPEPCACD-----TRLV	551	Db	1501	SKDGWVDIMYDGLDAVGDQOPVQNHNPWMLLYFISFLIIVSFFVLNMFVVVENPHK	1560
Qy	533	MLPPSTPALSGAPPGAESVHSFYHADCHLE--PVRQAPPSPSPSEASGR--TVSGKV	589	Qy	1543	CRHQHEEERREERREKRLRLEKGR-----KAQCKPYSDYSRFRLLVHHLCTSHYLD	1596
Db	552	RAGAPSPSPGCGPPDPAESVHSFYHADCHTEGQERARVAHAATAAASRLATGLGTM	611	Db	1561	CRHQHEEERREERREKRLRLEKGR-----KAQCKPYSDYSRFRLLVHHLCTSHYLD	1620
Qy	590	YPTV-----HTSP-----PPETLKEKALVEAASSGPPPTLTSINIPGPY	629	Qy	1597	LFTITGVLNVTMAHEHYQOQILDEALKICNYITFVIFLESVFKLVAQFRFRFQDR	1656
Db	612	NYPTLPGVSGKSGTSPGKWKAGPPGT-----GGHPLSLNS-----PDY	657	Db	1621	LFTITGVLNVTMAHEHYQOQILDEALKICNYITFVIFLESVFKLVAQFRFRFQDR	1680
Qy	630	SMHKLLETQSTGACQS-----SKTISPLCLKADSGACGDPSCPYCARA--GAGEVELA	681	Qy	1657	WNOLDLAILVLLSIMGITLLEEIEVNASLNPINTIIRIMRVLRIARVLLKLMVAVGRLALD	1716
Db	658	EKIPIHVGEHGLQAPGHLGSLVPCPLPSP--PAGTLTCLKSCPYCTRALEDPEGELS	715	Db	1681	WNOLDLAILVLLSIMGITLLEEIEVNASLNPINTIIRIMRVLRIARVLLKLMVAVGRLALD	1740
Qy	682	DREMPDSEAVYETQDAQSHDLRP-----HSSRORSGLPDAEPSSV	725	Qy	1717	TVNQALPQVGNLGLLFWLLFFIPALGVELFGDLECDTHPCBGLGRHATFRNFGMAFLT	1776
Db	716	GSESGDSGRGYEFTQDVRHGRDPTPRPATDTPGPGSGPQRRQAQAAAGEPGWM	775	Db	1741	TVNQALPQVGNLGLLFWLLFFIPALGVELFGDLECDTHPCBGLGRHATFRNFGMAFLT	1800
Qy	726	LAFWELICTDKIIVDSKYFGRGIMAILVNTLSMGIYHEHQPELTNALSINIVFTSL	785	Qy	1777	LFRVSTGDNWNGIMKOTLRDC---DOESTCYNTVISPFIYFVSFVLTAQFVLNVVIAVLM	1833
Db	776	GLRWTFSSKLARIIVDSKYFSGIMWAILVNTLSMGEVHEHQPELTNALSINIVFTSM	835	Db	1801	LFRVSTGDNWNGIMKOTLRDCSREDEKHLCLSYLPALSPVITFVLVAQFVLNVVIAVLM	1860
Qy	786	FALEMLLKLVTYGPYIKNPNIIPDGIIVISWEIVGQGGGLSVLRTFLMRVLKV	845	Qy	1834	KLHEESNKEAKEAEAELELEMLKTLSPQPHSPGLSPFLMPGVEGDSF--DSKPKGA	1890
Db	836	FALEMLLKLACGLYIRNPYNIIPDGIIVISWEIVGQADGGLSVLRTFLMRVLKV	895	Db	1861	KLHEESNKEAKEAEAELELEMLKTLSPQPHSPGLSPFLMPGVEGDSF--DSKPKGA	1899
Qy	846	RELPAOROLAVLMTMDNVATFCMLLFIIFISILGMHLPFGCKFASERD--GDTLPDRK	904	Qy	1891	LHPAAHARSASHFSLEHPTMQPHTELPG---PDLLTVRKSGVSRTHSLPNDSYMCRHG	1946
Db	896	RELPAOROLAVLMTMDNVATFCMLLFIIFISILGMHLPFGCKFASERD--GDTLPDRK	955	Db	1900	-----PLQESFGARDAPNLV--ARKVSVRMLSLPNDSYMCRPV	1937
Qy	905	NFDSLWLAIWTVFQILTQEDWNVNMGMASTSSWAALFYFIALMTFGNYVLENNLVAIV	964	Qy	1947	STABGP-----LGHGWLGLPKAOSGVSLSVHSQPADTSYIQLPKDAPHLLQPHSA	1997
Db	956	NFDSLWLAIWTVFQILTQEDWNVNMGMASTSSWAALFYFIALMTFGNYVLENNLVAIV	1015	Db	1938	VPASAPHRPLQEVEMETRYAGTP---LGSVASVHSPPAESCASLQIP-----LAVSSPA	1989
Qy	965	EGFOAEISKREDASQLSQILPVDSQCGDANKSESEDPFSPSLDGD-----GD	1015	Qy	1998	PTWGTIPLKPPG--RSLPAORPLRQAAARTDSDVQGLGSRREDLL--AEVSGSP--P	2051
Db	1016	EGFOAE-----GDANRSDTDDEKTSVHFEEDFKLRELQYTE	1052	Db	1990	RSGEPLHALSPRGTAARSPSLRLLCRQEAHVTDLSLEGK--IDSPRDTLDPAEPGEKTVRP	2048
Qy	1016	RKCLALVLSLGEHPELRKSLPLLIITHAATPMSLPKSTSTGLGEALGPASRRTSSGSA	1075	Qy	2052	LARAYFWG--QSTQAQOQHSRHSKISKMTTPAP--CPGPEPNWKGKPPETRSSLEDT	2108
Db	1053	LKMCSLAVTPNGHLEGRGSLSPPLINCTAATPMTPKSSPFLDAAAPSLPDSRRGSSSGD	1112	Db	2049	VTQGSLSQSPRSPRSPASVTRKHT--FGQHCVSRRPAAPGGE-----EAEASDPADE	2099
Qy	1076	EPGAAHEMKPPGARSPPHSPWGAASWTSSRSLGRASLKRSPSGRRSLTSGE	1135	Qy	2109	ELSWISGDLPL-----PGQEEPP-----SPDLKKCYSVEAQSCORRPTSLWLDQRHSI	2159
Db	1113	PP--LGDQKPPASLRSSPCAPWPGSGAWSRRSSSLGRASLKRSGCGRESLLSGE	1170	Db	2100	EVSHITSSACQWQPTABPHGPEASPVAGGERDLRLYSVDAQGLDKP--GRADSQWAPSA	2158
Qy	1136	GOESQDEESESSEERASPA--GSDHRRHSGLEAKSSFDLPDTL-----QVPGHL---	1184	Qy	2160	AVSCLDSSQHLGTDPSNLGQPLGGGSRPKKLLGPPSITIDPP--ESQPRTPPPSP--	2216
				Db	2159	ELGSGEGEAKAWGPE-----AEP--ALGARKKKMFPPCISVFPPEADEGSAARPSAEG	2211

Qy 2217 -GICLRRAPS-----SDSKDPL-----ASGPPDSMA---ASPPKDVLSLGLSDPA 2262
Db 2212 GSTTLRRTSPCEATPHRDSLEPTGSGAGDPAKGERWQASCRAEHLTVPSFAPEPL 2271
Qy 2263 DL-----DP 2266
Db 2272 DLGVPSGDP 2280

RESULT 7
US-09-935-541-2
; Sequence 2, Application US/09935541
; Patent No. US20020150911A1
; GENERAL INFORMATION:
; APPLICANT: Dietrich, Paul S.
; APPLICANT: McGivern, Joseph G.
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
; TITLE OF INVENTION: AND USES
; FILE REFERENCE: R0043B-REG sequence listing
; CURRENT APPLICATION NUMBER: US/09/935,541
; CURRENT FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: 09/404,650
; PRIOR FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 2
; LENGTH: 2175
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-935-541-2

Query Match 46.1%; Score 5492.5; DB 9; Length 2175;
Best Local Similarity 51.3%; Pred. NO. 0;
Matches 1233; Conservative 214; Mismatches 508; Indels 447; Gaps 55;

Qy 31 RPPGSAEKDPSADSEAG-----LPPALAPVFFYLSQDSRPSRSLRVTCHNPFERI 86
Db 25 QPGRSPSSPPGLEPDLGDADPHVPHDLPAPIAFFCLRQTSPRNWCIMVCPNPFECV 84
Qy 87 SMLVILLNCVTLGMFRPCEDIACDSQRCRILOAFDDFIAPFAVVMVVMVALGIFGKCC 146
Db 85 SMLVILLNCVTLGMVQPCDDMDCLSDCKILLOVDDFIAPFAVVMVVMVALGIFGKCC 144
Qy 147 YLGDTWNRDLFFVIAGLMVLSLQNVFSVAVTRVRLRLRINRVPMSRILLVTLLED 206
Db 145 YLGDTWNRDLFFVIAGLMVLSLQNVFSVAVTRVRLRLRINRVPMSRILLVTLLED 204
Qy 207 TPLMGNVLLLCFFVFRTFEGIVGVQLWAGLARNRCLFNPENSLPLSVDLERYQOTENEDE 266
Db 205 TPLMGNVLLLCFFVFRTFEGIVGVQLWAGLARNRCLFNPENSLPLSVDLERYQOTENEDE 264
Qy 267 SPFICSPQRENGMRSRVPTLRGDDGGGPPCGL-----DYEAYNSSNTT--CVNWNQ 318
Db 265 MPFICSLSGDNGMGCHIEIPKESQ---GRECCLSKDDVDFGAGRODLNAGLCVWNWR 321
Qy 319 YTTNCSAGEHNPFGAINFDNIGYAWIAFQVITLEGWVDIMYFVMDAHSYFNFIYFILL 378
Db 322 YNNVCRGTGANPHKGAINFDNIGYAWIIVFQVITLEGWVEIMYVMDAHSYFNFIYFILL 381
Qy 379 IIVGSFPMINCLVVIATQFSETQKORSQMRQORVFLSNASTLASFEPGSCYBELLK 438
Db 382 IIVGSFPMINCLVVIATQFSETQKORHRLMQRQYLS--SSTVASAEFGDCYEIFQ 440
Qy 439 YLVVTLKAAARLAQVSAAGVRYGCLLSSPAPLGQOETQPSSSCSRSHRRLSVHHLVHH 498
Db 441 YVCHILRAKR-----RAGLYQALQRRQALG----- 468
Qy 499 HHHHHHLYNGTLRAPRASPEIQDRDANGSRRLMLPPSTPALSGAPPGAESVHSFYH 558
Db 469 -----PEAPA--PAKPGP-----H 480
Qy 559 ADCHLEPVRQAPPPRSPSEASGRVTGSGKVPVTHVTSPPPETLKEKALVEVAASGPPT 618

Db 481 AK---EPRHYQLCQHSPFLDTPHTL-----VOPIPATL----- 511
Qy 619 LTSNLNPPGPYSSMHKLETTOSTGACOSSCKISSPCLKADSGACGPDSCPYCAR----- 672
Db 512 -----ASDPASCPCCOHEGDRRP 529
Qy 673 AGAGEVELADREMPDSDSEAVVEFTQDAQHSDLRDPHRRORSIGPDAPESVL----- 726
Db 530 SGLGSTD--SQEGSGSGSSAGGE--DEADGAGARSSSEDGASSELKEEBEEDGAGVWL 586
Qy 727 --AFWRLICDTFRKIVDSKYFGRGIMAILVNTLSMGIEYHEQBEELNALEISNIVFTS 784
Db 587 CGDVWRETRAKLRIGIVDSKYFNIRGIMAILVNTVSMGIEHHEQBEELNILEICNVFTS 646
Qy 785 LFALEMLLKLVYQPGFYIKNPYINFDGVIIVISWIEIVGQGGGLSVLRTRFLMRVLKL 844
Db 647 MFALEMLLKLAAGFLDYLRPNYINFDGVIIVISWIEIVGQGGGLSVLRTRFLMRVLKL 706
Qy 845 VRFLPALORQLVVLKMTMDNVATFCMLLMLEFIFISILGMHLFCCKPASERD--GDTLPDR 903
Db 707 VRFPALRRQLVVLKMTMDNVATFCMLLMLEFIFISILGMHLFCCKPASERD--GDTLPDR 766
Qy 904 KNFDSLAWIIVTFQIILTOEDNKNVLYNGMASTSSMAALYFIALMTFGNLYVFLNVLVAIL 963
Db 767 KNFDSLAWIIVTFQIILTOEDNKNVLYNGMASTSSMAALYFIALMTFGNLYVFLNVLVAIL 826
Qy 964 VEGFQABEISKREDASQGLSCIQLPVDSQGGDANKSESEPDFFSPPS-----LDGD 1013
Db 827 VEGFQAE-----GDANRSYDEDOSSSNIEEPDKLQSLDSS 863
Qy 1014 GDRKKCLALVSLGBHPELRKSLPLLIHTAATPMGLPKSTSTGLGEALGPASRRT----- 1069
Db 864 GDRKKCLPIPTPNH-----LDP-----SLPLGHLGPAGAAGAPAPRLSLOPD 906
Qy 1070 -----SSGSAEPGAAHEMKSPPSARSSPHSPMSAASWTSSRRSRSLGRAPSLK 1120
Db 907 PMLVALGSRKSSVMSLGRMSYDQKSLSSRSYYPGWRSAWASRRSSWN-----SLK 960
Qy 1121 RRSPPGRRRLSLSGE--QGESQDEESEE--ERASPAAGSDH-----RHRG 1162
Db 961 HKPSPAESHSLSAERGAGARVCEVAADGPPRAAPLHTPHAHIIHGHPLAHRHRHR 1020
Qy 1163 SLERAKSSPDLPTLQVPLHRTASGR--GSASEHQDCNKSASGRALARALRDPDPLD 1220
Db 1021 TSLDNRDSVDLAEVLPAVGAHRAAGAPAGPACHEDCNGRMPSIAKDVFTKMGDRGR 1080
Qy 1221 GDDADDGNGLSKGRVRVARIARLPACVLERDSNAVIFPPQSRFLLCHRIITHKMPDH 1280
Db 1081 GED--EEDIDYTLCPVRKMDVYKPDWCEVEDSVLFSPENRFRVLCQTIIAHLKFDY 1139
Qy 1281 VLVIIIFLNCITITAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTVKVALGWCFCGSA 1340
Db 1140 VVLAFLNCITITALEPQIEAGSTERIFLTVSNYIFTAIFVGMTLVKVSGLYFGSA 1199
Qy 1341 YLRSSNVLDGLVLISVIDILVMSVSDGTYKILGMLRVLRLLRTRPLRVISRAQGLK 1400
Db 1200 YLRSSNVLDGLVFSVSIIDIVVSLASAGGAKILGLVLRLLRTRPLRVISRAQGLK 1259
Qy 1401 VVETLMSLPIGNIVVICCAFFIIFGLGVOLFKGFFVCCGEDTRNITNKSCEAEASY 1460
Db 1260 VVETLMSLPIGNIVVICCAFFIIFGLGVOLFKGFFVCCGEDTRNITNKSCEAEASY 1319
Qy 1461 RWVRKHNFNQALMSLFLVASKDGMVDIMYDGLDAGVDQDQPMNHNPMWLLYFISF 1520
Db 1320 RWVRKHNFNQALMSLFLVASKDGMVIMYDGLDAGVDQDQPMNHNPMWLLYFISF 1379
Qy 1521 LLIVAFVLMVGVVVENFHCKHOHEEERREERREKRLRREKRRKACKPKYPSYS 1580
Db 1380 LLIVAFVLMVGVVVENFHCKHOHEEERREERREKRLRREKRRKACKPKYPSYS 1439
Qy 1581 RPELLVHLCTSHVLDLFIITGVIGLVNVVWAMEHVQQPQILDEALKICNYIFTVIFVLES 1640
Db 1581 RPELLVHLCTSHVLDLFIITGVIGLVNVVWAMEHVQQPQILDEALKICNYIFTVIFVLES 1640

1440 HTRLLHSMCTSHVDFITFIICLVNVTMSLEHYNQPTSLTALKYCNMFTTVFVLEA 1499
1641 VFKLAVFRFFQDRWNQDLAIVLSINGITLIEEIVNASLIPNPTIIRIMRVLRIAR 1700
1500 VLKLVAFGLRFFKDRWNQDLAIVLSVNGITLIEEIVNAALPINPTIIRIMRVLRIAR 1559
1701 VLKLLKMAVGNRALLDTVMQALPOVGNLGLLFFMLFFIFAALGVLEFGLDECDTHPCBG 1760
1560 VLKLLKMAVGNRALLDTVMQALPOVGNLGLLFFMLFFIFAALGVLEFGLKVCNDENPCBG 1619
1761 LGRHATFRNFGMAFLTLFRYSTGDNWNGIMKOTLRDC-DOESTCYNTV--ISPIYVSFV 1817
1620 MSRHATTENFGMAFLTLFOVSTGDNWNGIMKOTLRDC-DOESTCYNTV--ISPIYVSFV 1679
1818 LTAQVLNVNVIAMVHGLEESKEAEAELEAELEEM-KTSLPOHSPHPLSGPFWPC 1876
1680 LTAQVLNVNVIAMVHGLEESKEAEAELEAELEEM-KTSLPOHSPHPLSGPFWPC 1738
1877 VEGPDSPD-----SPKPGAL-----HPAAHA----- 1897
1739 -RGPGAGGGDTGGLCRRCYSPAQDSLEGELTIIDNLSGSIPIHHYSSPAGCKCHDK 1797
1898 -----RSAS-----HFSLEHPTWQP-----HPTLPDPLLTVRKSG-- 1929
1798 QEVQLAETEAFSLNDRSSILLGDLSDLEPTACPPGRKDSKGLDPPPPMRVGDLDGEC 1857
1930 ---VSRTHSLPN-DSYMCRRHGSTAEGPLHGRWGGLPKAQSGSVLSVHSQPADTSTIOLP 1985
1858 FPLASTAVSPDPENFLCEMEIEIPNPV--RSW--LKHDSSQAPSPSPDASSPLLPMP 1913
1986 KDAPH-----LQPHSAPWTGIIKLPPLPG-----RSLAQRLRQAAIRTSOLDVQG 2034
1914 ABEPHFAVSAQSGKEGTGTGLTKIALQGSWASLRSPVNCVTLRQATGSDTSLD--- 1970
2035 LGSREDDLLAEVSPSPPLARAYSFVQSGSTQAOQHSRSHKSIKHMTPPAPCPGEPNMG 2094
1971 -----ASPSSASGLQTTLEDLSLSDSPRA-----LGPPAPAGPFRAGLS 2012
2095 KGPETTRSSILELDELTSWISGLLPPGQOEPPSPRLKCYSAEQSCORRPTSWLDEQ 2154
2013 ---PAARRRLSL-----RGRGLFSLRGLRA-----HQ 2036
2155 RHUSIAVCLDSQSQHLGTDPSN---LGQPLGGPGSRPKKLSPPSIT---IDPPESQ 2208
2037 RSHSSGGS-TSPGCTHDSMDPDEBGRGAGGGAGSEHSETLSLSLTSLSFCPP--- 2092
2209 GPRTPPSPGICLRRRAPSDS-----KDPASGPPDSMAASPSPKDVLSSLGSDPADL 2264
2093 ---PPAPGLTPARKFSTSSLAAPGRPHAAALAHGLARSPSWAAD-----RSKDPGR 2143
2265 DP 2266
2144 AP 2145

RESULT 8
US-10-425-800-2
; Sequence 2, Application US/10425800
; Publication No. US20030180886A1
; GENERAL INFORMATION:
; APPLICANT: Dietrich, Paul S.
; APPLICANT: McGivern, Joseph G.
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
; TITLE OF INVENTION: AND USES
; FILE REFERENCE: R0043B-REG sequence listing
; CURRENT APPLICATION NUMBER: US/10/425,800
; PRIOR FILING DATE: 2003-04-29
; PRIOR APPLICATION NUMBER: US/09/404,650
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 2175

; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-425-800-2

Query Match 46.1%; Score 5492.5; DB 14; Length 2175;
Best Local Similarity 51.3%; Pred. No. 0;
Matches 1233; Conservative 214; Mismatches 508; Indels 447; Gaps 55;

31 RPGSGRAEKDGSADSEAG---LPPALAPVVFVYLSQDSRPSRWCILRTVCNPFERI 86
25 QGPRSPSPSPGLEEDGADPHVPHDLAPAFCLRTTSPRNWCIMKVCNPFECV 84
87 SMLVILLNCVTLGMFRPCEDIACDSQRILQAFDDFIAPFAVAVVVMKVALGIFGKCC 146
85 SMLVILLNCVTLGMYPQCDMDCLSDRCKILOVDFDDFIFIFAMVEMVLMKVALGIFGKCC 144
147 YIGDTWNLDFFIIVAGMLVSLDLQNVFSVAVTRVLRPLRINRVPMSRILVLLLD 206
145 YIGDTWNLDFFIIVAGMVEYSLDLQNLINLSAINTVLRPLRINRVPMSRILVLLLD 204
207 TLPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLPENFSLPLVDLERYQTENEDE 266
205 TLPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLPENFTIQGDVALPYQPEEDEDE 264
267 SPFICQSPRENGMRSRVPILRGDGGGPPCGL-----DYEAYNSSNTT--CVNWNQ 318
265 MPFICSLSGDNGIMGCHIEPPLKEQ---GRECCLSKDDVDFGAGRQDLNASGLCVNWR 321
319 YTNCSAGHNPFKGAINDNIGYAMIAIQVITLEGWVIMYFVMDAHSYNYFIYFILL 378
322 YNVCTGTSANPHKGAINDNIGYAMIVIFVITLEGWVEIMYVMDAHSYNYFIYFILL 381
379 IIVGSPFMNLCVIAIATQFSETKQRESQLREORVRLSNASTLASPEGSCVYEEELK 438
382 IIVGSPFMNLCVIAIATQFSETKQREHRLMUEQRIYLS--SSTVASAEFGDCVYEEIFQ 440
439 YLVYILKARRLAQVSRRAQVRVGLLSPALPGQETQPSSSCSRSHRRLSVHHLVHH 498
441 YVCHILRKAKR-----RALGLYQALOSRRQALG----- 468
499 HHHHHYHLNGTILRAPRASPEIQDRDANGSRRLMLPPSTPALSGAPGGAESVHSFVH 558
469 -----PEAPA--PAKEGP-----H 480
559 ADCHLEVRVCOAPPSPSEASGRTVSGKGYPTVHTSPPTLKEKALVEVAASSGPPT 618
481 AK--EPRHYQLCPQHSPLDAPHTL-----VQPIPATL----- 511
619 LTSLNIPPGPYSSMHKLLTQSTGACQSCCKISSPCLKADSGACGSDSCPFCAR----- 672
512 -----ASDPASCPCCQHEGRRP 529
673 AGAGEVELADREMPDSDSEAVYEFTODAQHSDLRDPHSRRQRSIGLSPDAEPSVL----- 726
530 SGLGSTD--SQEGSGSGSSAGGE--DEADGDSGASSEDGASSELGKEEEEQADGAVWL 586
727 --AFWRLLICDTFRKIVDSKYFGRGIMTIAILVNTLSMGIYEHQPEELTNALFISNIVFTS 784
587 GCDVWRETRAKLGIIVDSKYFNIRGIMAILVNTVSMGIEHHEQPEELTNILEICNVVFTS 646
785 LFALEMLKLLVYGPFGYIKNPYNIEDGVIVISVWIEVIGQGGGLSVLRTFRMLRVKL 844
647 MFALEMLKLLAAGFLDYLRNPYNIEDGVIVISVWIEVIGQGGGLSVLRTFRMLRVKL 706
845 VRFLPALORQLVLMKMTMDNVATFCMLMLFIFISILGMHLFCCKPASERD--GDTLPDR 903
707 VRFPALRRQLVLMKMTMDNVATFCMLMLFIFISILGMHLFCCKPASERD--GDTLPDR 766
904 KNFDSLLMAIVTVFOILLQEDWNKVLNGMASTSSWALYFIALMTFCNLYVFNLLVAIL 963
767 KNFDSLLMAIVTVFOILLQEDWNVVLNGMASTSPWASLYFVALMTFCNLYVFNLLVAIL 826
964 VEGFQAEIEISKREDASGQLSCLQLPVDVSGGDKANKSESEPFDFSPS-----LDGD 1013

319 YITNCSAGEHPPKGAIFDNIGYAMIAIQQVITLEGWDVIMYVMDAHSFYNYFIILL 378
322 YVNCRTGSANPHKGAIFDNIGYAMIVIFQVITLEGWEIYVYVMDAHSFYNYFIILL 381
379 IIVGSPFMINCLVVIATQSETKQREQLMRQRVFLSNASTLASFSEPCSCYEELAK 438
382 IIVGSPFMINCLVVIATQSETKQREQLMRQRVFLSNASTLASFSEPCSCYEELAK 440
439 YLVYILKABARLQAQVRAAGVRVGLLSSPAPLGQOETQPSSCSRSHRRLSVHHLVHHH 498
441 YVCHILAKAR-----RALGLYALQSRQALG----- 468
499 HHHHHHHLGNGTLRAPRASPEIQDRDANGSRRLMLPPPPTPALSGAPGAEVSHFVH 558
469 -----PEAPA--PAKPGP-----H 480
559 ADCHLEPVRQAPPPSPSEASGTVGSKVYPTVHTSPPELTKEKALVEVAASGPPT 618
481 AK---EPHYQLCPQHSPLDAPHTL-----VQIPATL----- 511
619 LTSLNIPPGPYSSNMHKLLETQSTGACOSCKISSPCCLKADSGAGCPDSCYCAR----- 672
512 -----ASDPASCPCCOHEDGRP 529
673 AGAGEVELADREMPDSDSEANVEFTQDAHSDLRDPHRRQRSIGPDAEPSSVL----- 726
530 SGLGSTD-SGORGSGSGSAGGE--DEADGGARSSDGGASSELGKEEEEEQADGAVWL 586
727 --AFWRLICDTRKIVDSKYFORGIMAILVNTLSMGIEYHEQPEELTNALEISNYFTS 784
587 CGDWRETRAKRGIVDSKYFNRGIMAILVNTVSMGIEHEQPEELTNALEISNYFTS 646
785 LFALEMLKLLVYGPFGYKPNYINFDGVIVVISWEIYVGOQGGSLVLRFLRMLVKL 844
647 MFALEMLKLAAGFLFDVLRNPNYINFDGVIVVISWEIYVGOQGGSLVLRFLRMLVKL 706
845 VRFPLALQOLVLMKMTDNVATFCMLLMFLIFISILGMLFGCKFASERD-GDTLPDR 903
707 VRFMPALRQLVLMKMTDNVATFCMLLMFLIFISILGMLFGCKFASERD-GDTLPDR 766
904 KNFDSLMAIVTVFQILTQEDWNKVLVYNGMASTSWAALYFTALMTFGYVLFNLLVAIL 963
767 KNFDSLMAIVTVFQILTQEDWNKVLVYNGMASTSWAALYFTALMTFGYVLFNLLVAIL 826
964 VEGFOABEISKEDASGQLSCQLPVDOSGGANKSESEDFSPS-----LDGD 1013
827 VEGFOAE-----GDANKSYDEDOSSNIEBFDKLOEGLDSS 863
1014 GDRKKCLALVSLGEHPRLAKSLPLLIHTAATPMSLPKSTSTGLGEALGPASRT----- 1069
864 GDPKLCFIPWTPNGH-----LDP-----SLPLGHLGPAGAAGAPAPRLSLQPD 906
1070 -----SSGSABFGAAHEMKSPSARSSPHSPWSAASWTSPRSRNSLGRAPSLK 1120
907 PMLVALGSRKSSVMSLGRMSYDQRLSSSRSSSYGPGWSAASWASRSSWN-----SLK 960
1121 RSPSGRRSILGSE-QOESQDEESSEE--ERASPAAGSDH-----RHRG 1162
961 HKPPSAHESLLEAERGCGARVCEVADEGPPAPLHTPHAHIIHGHPLAHRHRHR 1020
1163 SLERAKSFDLPRTLQVGLHTASGR--GSASEHODCNKGSASGELARALRPPDPLD 1220
1021 TSLDNRDSVDLAELVPAVGAHPRAAWRAAGAPAGHEDCNRMPSIAKVFTKMGDRGR 1080
1221 GDDADDEGNLSKGRVRAWRARLAPACYLERDSWSAYIFPPQSRFRLLCHRIITHOMFDH 1280
1081 GED-EEEDYTLCLFRVRKMDIVYKPCWCEVREDWSVYLFSPENRFRVLCQTLIAHLFDY 1139
1281 VVLVIIIFLNCITIAMERPKIDPHSAERIFLTSNYIFTAVFLAEMTKVVALGCEQA 1340
1140 VVLAFLIFLNCITIALERPOIEAGSTERIFLTSNYIFTAVFVGMETLKVVSGLYFGEQA 1199
1341 YLRSSWNVLDGLLVLIIVIDILVSMVSDSGTKILGMLRVLRLRLTLRPLRVISRAOGLKL 1400

1200 YLRSSWNVLDGLFVFSVSIIDVWSLAGAGAKILGVLRLRLTLRPLRVISRAOGLKL 1259
1401 VVETIMSLKPIGNIVIVICCAFFIIFGLGVQLFKGKFFVCOGEDTRNITNKSDCAEASY 1460
1260 VVETILSLKPIGNIVILICCAFFIIFGLGVQLFKGKFFVCOGEDTRNITNKSDCAEASY 1319
1461 RWRHKYNFNDLQALMSLFLVLSKDGWDMYDGLDAVGVDQOPIIMNHNPMMLLYFISF 1520
1320 RWRHKYNFNDLQALMSLFLVLSKDGWDMYDGLDAVGVDQOPIIMNHNPMMLLYFISF 1379
1521 LLIIVAFFVNNPMFVGVVENFHKCHQHEEAREERERERERERERERERERERERER 1580
1380 LLIIVAFFVNNPMFVGVVENFHKCHQHEEAREERERERERERERERERERERERER 1439
1581 RFLIAVHLCTSHYLDLFTIGVILNVVTVMAMHYQOPIIDLEALKICNYIFTVIFVLES 1640
1440 HFRLIHSMCTSHYLDLFTIGVILNVVTVMAMHYQOPIIDLEALKICNYIFTVIFVLES 1499
1641 VFKLVAFGFRFPFQDRWNQDLAIIVLSIMGITLIEEIVNASLIPNPTIIRIMVLRAR 1700
1500 VFKLVAFGFRFPFQDRWNQDLAIIVLSIMGITLIEEIVNASLIPNPTIIRIMVLRAR 1559
1701 VFKLVAFGFRFPFQDRWNQDLAIIVLSIMGITLIEEIVNASLIPNPTIIRIMVLRAR 1760
1560 VFKLVAFGFRFPFQDRWNQDLAIIVLSIMGITLIEEIVNASLIPNPTIIRIMVLRAR 1619
1761 LGRHATFRNFMGMAFLTLFRVSTGDNWNGIMKDTLRDC-DOESTCYNTV--ISPIYFVSFV 1817
1620 MSHATFRNFMGMAFLTLFRVSTGDNWNGIMKDTLRDC-DOESTCYNTV--ISPIYFVSFV 1679
1818 LTAQFVLNVVAVLWMLHLESNKEAEAELEAELEEM-KTLPSPHSPGLSGPFLWPG 1876
1680 LTAQFVLNVVAVLWMLHLESNKEAEAELEAELEEM-KTLPSPHSPGLSGPFLWPG 1738
1877 VEGPD-----SP-----DSPKGAH-- 1892
1739 -RPGAGGGGTEGGLCRCCYSPAENLWLDVSLIIKDSLEGELTIIDNLSGSIFFHY 1797
1893 --PAA-----HARSAS-----HFSLEHPTMQP-----HPTLP 1918
1798 SSPAGCKKHDKQVQLAEATEAFSLNSDRSSILGDDLSLEDDPTACPPGRKDSKGLD 1857
1919 GPDLLTVYKSG-----VSRTHSLPN--DSYMCRHGSTAEGPLGHRGWLPAQSGSVLSVH 1972
1858 PPBPMRVGDLGECFFPLSSTAVSPDENFLCEMEEIPENPV--RSW--LKHDSSQAPPSP 1913
1973 SQPADTSYIILQPKDAPH-----LIQPHSAPTWTGIIPKLPPG-----RSPLAQRLRR 2021
1914 FSPDASSPLLPMPAEFFHPAVSASQKPEKGTGTGTPLKIALQGSWASLRSPRVNCTLLR 1973
2022 QAAITRDSLDVQGLGSRDLEAEVSGSPPLARAYSGWQSSTQAQOHSRSHSKIKHMT 2081
1974 QATGSDTSLD-----ASPSAGSLQITLEDLSLTLSDSPPRA-----LG 2012
2082 PPAPCPGPENPMWKGPPETRSSILELDELTSWI SGDLLPPGQOEPPEPPROLKCYVSEAQ 2141
2013 PPAPAPGPRAGLS--PAARRRLSL-----RGRGLFSLRGLRA-- 2047
2142 SCORRPTSWLDEQRHSLIAVCLDSSGQPHLGTDPSPN---LGGQPLGCGSRPKKLSPP 2198
2048 -----HORSHSGGS--TSPGCTHDDSDMPSDEERGAGGAGGAGSEHSETLSSL 2095
2199 SIT---IDPPESQGRPRTPSPGICLRRRAPSSDS---KOPLAGSPDPSMAASPSKDV 2251
2096 SLTSLFCPPP-----PPAPGLTPARKFSSTSLAAPGRPHAAALAHGLARSFSAAD- 2148
2252 LSLGLSSDPADLDP 2266
2149 -----RSKDPGPRAP 2158

RESULT 10

Db 1620 MSRAHTEFNGMAFLTLFQVSTGDNWNGIMKOTLRDCTHDSRSLSSLOFVSPLYFVSFV 1679
Qy 1818 LTAQFVLNVVIAVLMKHEESKEAEAEAELEEM-KTLSPOHSPGLSGSPPLWPG 1876
Db 1680 LTAQFVLNVVIAVLMKHLDSNKEAQEDAEMDAELEMAHGLGPGKPLPTGSGQA-EG 1738
Qy 1877 VEGPD-----SP-----DSPKPGALH-- 1892
Db 1739 -RPGGAGGGDTEGGLCRRCYSPAQENLWDSVLSLIKDSLSELTIIDNLSGSIFHY 1797
Qy 1893 --PAA-----HARSAS-----HFSLEHTWOP-----HTELP 1918
Db 1798 SSPAGCKKHDKQEVQAEAFSLNSDRSSILLGDDLSLEDPTACPPGRKXDSGELD 1857
Qy 1919 GPDLLTVRKSG-----VSRTHSLPN-DSYMRHSGSTAEGPLGHRGWLKPAQSGSVLSVH 1972
Db 1858 PPEPMRVGDLGECFFPLSSTAVSPDENFLCEMEEIFPNV--RSW--LKHDSQAPPSP 1913
Qy 1973 SOPADTSYIOLPKDAPH-----LLOPHSAPTWTGTTIKLPPPG-----RSLAQRPLR 2021
Db 1914 RSPDASSPLLPMAEAEFFHPAVASQKPEKGTGTGLPKIALQGSWASLSPRVNCTLLR 1973
Qy 2022 QAAIRTSLSVOGLSREDLLAEVSGSPPLARAYFWGQSSTOAOQHSHRSKISHMT 2081
Db 1974 QATGSDTSLD-----ASPSSAGSIQTTLEDLSLSDSPRA-----IG 2012
Qy 2082 PPAPCGPEPNWKGPPETRSLSLELDTLSWISGDLPLPPGQOEPPSPRDLKKCYVDAQ 2141
Db 2013 PPAPAGPPAGLS-----PAARRLSL-----RGRGLFSLRGLRA- 2047
Qy 2142 SCQRAPTSWLDQRHSTAVSCLDGSGOPHLGTDPSN-----LGGQPLGPGSRPKKLSP 2198
Db 2048 -----HQRSHSGGS-TSPGCTHDSMDPDEEGRGAGGGAGGSEHSETLSL 2095
Qy 2199 SIT--IDPESQGRTPSPGICLRRRAPSSDS-----KDPPLASGPPDSMAASPSKDV 2251
Db 2096 SLTSLFCPPP-----PPAPGLTPARKFSSSTSSLAAPCRPHAAALHGLARSFSPAAD- 2148
Qy 2252 LSLGSLSDPADLDP 2266
Db 2149 -----RSKOPPPGRAP 2158

RESULT 11
US-09-935-541-5
; Sequence 5, Application US/09935541
; Patent No. US20020150911A1
; GENERAL INFORMATION:
; APPLICANT: Dietrich, Paul S.
; APPLICANT: McGivern, Joseph G.
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
; TITLE OF INVENTION: AND USES
; FILE REFERENCE: R00438-REG sequence listing
; CURRENT APPLICATION NUMBER: US/09/935,541
; CURRENT FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: 09/404,650
; PRIOR FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 5
; LENGTH: 1835
; TYPE: PRT
; ORGANISM: Rattus sp.
US-09-935-541-5

Query Match 45.1%; Score 5366; DB 9; Length 1835;
Best Local Similarity 56.8%; Pred. No. 0;
Matches 1138; Conservative 183; Mismatches 346; Indels 336; Gaps 38;
Qy 27 GAGGPPGSAEKOPGSAADSEABG-----LPYALAPVVVFFYLSQDSRPSWCLRTVCNWP 82
Db 19 GITEQGRSPSPPPGEELEFLEGTINPDVPHDLAPVAFFCLRTQTTSPRNWCIMKVCNWP 78

Qy 83 PERISMLVILNCVTLMGMPCEBDIACDSORCRILQAFDDFIEAFFAVEMVVRQVALGIF 142
Db 79 FECVSMVILNCVTLMGNYQFCDMECLDRCKILQVDFDDFIFFAFAMVLRQVALGIF 138
Qy 143 GKCYLGDWTNRDLFFIAGMLEYSLDLQNVFSFSAVRTVRLPLRPLNRPVSMRLVLT 202
Db 139 GKCYLGDWTNRDLFFIAGMVEYSLDLQNVINLSAIRTVRVLRPLKAINRPVSMRLV 198
Qy 203 LLLDTLPMGNVLLCFVFFIIGVQLWAGLRNRCFLPENFSLPLSVDLERYQTE 262
Db 199 LLLDTLPMGNVLLCFVFFIIGVQLWAGLRNRCFLPENFTIQGDVALPPYQPE 258
Qy 263 NEDSPFICSPRENMRSCRSVPTLRGCGGGPPCGL-----DYFAYNSSNTT--CV 314
Db 259 EDEMPFICSLTGDNGINGCHEIPLKEQ-----GRECCLSKDDVYDFGAGRQDLNASGLCV 315
Qy 315 NNNQYVYVNCSEHNPFGAIFNFDNIQYAWTAIQVITLEGWVDIMVFMVMDAHFYNFIY 374
Db 316 NNNRYVYVNCRTGNANPHKGAIFNFDNIQYAGVIFQVITLEGWVEIMVYVMDAHFYNFIY 375
Qy 375 FILLIIVGSFFMINCLVVIATQFSETKQRESQLMREQVRFLSNASTLASFSFGSCYE 434
Db 376 FILLIIVGSFFMINCLVVIATQFSETKQREHRLMLEQRYLS-SSTVASYABPGDCE 434
Qy 435 ELLKYLVLTKRAARLQAQVSAAQVRLGSSPAPLGGQETQPSSSCSRSHRSLVHHL 494
Db 435 EIFOYVCHLRKAKERRALGLYQALQR-----RQMG-----PGTFA--PAKPGP- 461
Qy 495 VHHHHHHHHHHLNGTLRAPASPEIQDRDANGSRRLMLPPPSTPALSGAPPGAESVH 554
Db 462 -----RQMG-----PGTFA--PAKPGP- 477
Qy 555 SFYHADCHLEPVRCQAPPSPSEASGRVTGSGKVPYVTHSPPTETLKERALVEVAASS 614
Db 478 ---HAK---EPHCKLCPRHSPLD-----PTPHTLVQP----- 504
Qy 615 GPPTLTSLNIPPGPYSSMHKLLTQSTGACQSSCKISSPCLKADGACGPDSCPYCAR-- 672
Db 505 -----ISAILASD-----PSSCPHQHEA 523
Qy 673 ---AGAGEVELADREMPDSDSEAVYFTQDAQHSDLRDPHRRORSLSGPDAPSPVLA- 727
Db 524 GRPSPGLGSTD-SGQSGSGSGSAAEANGDG-----LQSSDGVSSDLKKEEEDQEDGAAR 578
Qy 728 ---FWRLICDTPRKIVDSKYFCRGIMIALVNTLSMGIEYHEQPEELTNALEISNIVFT 783
Db 579 LCGDVWRETRKRLGIVDSKYFNRGIMMALVNTVSMGIEHHEQPEELTNALEICNVFT 638
Qy 784 SLFALEMLLKLAVVGPFGYIKNPYNIFDGVIVVISVWEIVGQGGGLSVLTPRLMRVLK 843
Db 639 SMPALEMLKLAAFGLEFDYLRNPNYIFDSIIVISWEIVGQADGGLSVLTPRLMRVLK 698
Qy 844 LVRELPALQRLVLMKTMNDVATFCMLMLFIFISILGMHLFGCKFASERD-GDTLPD 902
Db 699 LVREMPALRQLVLMKTMNDVATFCMLMLFIFISILGMHLFGCKFASERTGTDTVPD 758
Qy 903 RKNFDSLLMAIVTVFOILTQEDWNKVLNGMASTSSWAALYFIALMTFGNYVLNLLVAI 962
Db 759 RKNFDSLLMAIVTVFOILTQEDWNVLYNGMASTTPWASLYFVALMTFGNYVLNLLVAI 818
Qy 963 LVEGFQAEIISKREDASGQLSCIQLPVDOSQGDANKSESEPPDFSPS-----LDG 1012
Db 819 LVEGFQAE-----GDANRSCDEQSSNLEEFDKLPEGLDN 855
Qy 1013 GDRKKCLALVSLGHEHPELRKSLPLLIHTAATPMSLPKSTSTGLGEALGPA-SRRTSS 1071
Db 856 SRDLKCLCIPMTPNGH-----LDP-----SLP-----LGAHLGPACTMGATP 892
Qy 1072 SGASAPG-----AAHEMKSPPSARSSPHSPWSAASSWTSRSSRNSL 1113
Db 893 RLSLQDPDVLVALDSKSSVMGLGRMSYDQRLSSRSRSTYYGPMGRSGTWAASSRSMN-- 950

Qy	1114	GRAPSLXRSPSGRRSILLSEGGQESQDEE--ESSEEE---RASPAGSDH-----11558
Db	951	----SLKHPPSABHESILLSEGGGSCVRACEGAREEAPRTATPLHAPHAHGHPHLA1006
Qy	1159	---RHRGSLEREAKSFDDLPTDLQVPLHRTAS--CRGSASHEQDCNGKSASGRLARAL1212
Db	1007	HRHRHRTLSLDRDSVDLGEPLFVVCASRAAWRGAGQAPHGDCNGRMPNIAKDVF1066
Qy	1213	RPDDPLDGDADDGEGNLSKGERVRAIRARLPACYLERDSWSGAYIFPPQSRFRLLC1272
Db	1067	KMDRRDRGED-EEEDYTLFCFRVRKMDVYKPDWCVEVDWSVYLFSPENKFRILCQT1125
Qy	1273	ITHQMPDHVVLVIIFLNCITIAMRPPKIDPHSAERIFLITSNYIFTAVFLAEMTVKVAL1332
Db	1126	IAHKLFDYVVLAFILFLNCITIALRPPQIEAGSTERIFLTVSNYIFTAIFVGEMTLKVVS1185
Qy	1333	GWCFGEQAYLRSSNNVLDGLLVLSVIDILVSMVSDSGTKILGMRLVRLRLTLPLRVI1392
Db	1186	GLYFGEQAYLRSSNNVLDGLLVFSVIDIIVVSVASAGGAKILGVRLVRLRLTLPLRVI1245
Qy	1393	SRAOGLXVLVETLMSLLKPIGNIVICAPFIIFGILGVOLFVKGPVPCOGEDTRNITNK1452
Db	1246	SRAPLKXVLVETLISLLKPIGNIVLICAPFIIFGILGVOLFVKGFVHGLGVDTNTR1305
Qy	1453	SDCAEASRYRWYRHKYFNFDNLGOALMSJFVLASKDQWVDIMYDGLDAVGDVQDQPMHNPW1512
Db	1306	SDCVAANYRWYHKKYFNFDNLGOALMSJFVLASKDQWVIMYNGLDVAVADVQDQVTHNPPW1365
Qy	1513	MLLYFISFLLIIVAFPLVMFVGVVFNPHKCRQHOEBEABRREKRLRLEKKRKAQC1572
Db	1366	MLLYFISFLLIIVSFVLMFVGVVFNPHKCRQHOEAEABRREKRLRLEKKRKAQR1425
Qy	1573	KPYYSYSRFRLLVHRLCTSHYLDLFTTGVIGLVNVTMAMEHYQOQIOLDEALKICNYIF1632
Db	1426	LPYVATYCPTRLLSHCTSHYLDIFITFICLVNVTMSLEHNQPTSLTAKYICNYMF1485
Qy	1633	TVIFVLESFVKLVAFGRFRFQDRWNQDLAIIVLLSIMGITLBEIEVNASLPINPTIIRI1692
Db	1486	TTVFVLEAVLKLVAFLGLRRFFKORWNQDLAIIVLLSWGITLBEIEINAALPINPTIIRI1545
Qy	1693	MRVLRIARVLKLLQAVGMRAALLDTVNOALPQVGNLGLLPMLLFFPTPAALGVBLFGDLEC1752
Db	1546	MRVLRIARVLKLLQAVTGMRAALLDTVVOALPQVGNLGLLPMLLFFIYAALGVBLFGKLVC1605
Qy	1753	DETHPCBGLGRHATFRPNFGMAFLTLFRVSTGDNWNGIMKDTLRDC-DOESTCYNTV--TS1809
Db	1606	NDENPCBGMGRHATFENFGMAFLTLFQVSTGDNWNGIMKDTLRDCTHDETCILSSQFVS1665
Qy	1810	PIYFVSFVLTAQFVLVNVVIAVLMLKHLBESNKAEABEAELELEM-KTLSPQPHSPL1868
Db	1666	PLIFVVSFVLTAQFVLVNVVIAVLMLKHLDDSNKAEQDAEMDAIELEMAHGLGFCP----1721
Qy	1869	GSPFLMFWVEGPDSPDKPCALHPAAHARSASHFSLEHPTMQPHFTELPFGPDLLTV---1925
Db	1722	-----GPCPG-----FCPCPCPCACGPRLLPTSSPG1747
Qy	1926	---RKSGVSRTHSLPNDSYMCRH1945
Db	1748	APRGSGGAGAGG-DTESHLCRH1769

RESULT 12

RE3001.12
 US-10-425-800-5
 ; Sequence 5, Application US/10425800
 ; Publication No. US20030180886A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Dietrich, Paul S.
 ; APPLICANT: McGivern, Joseph G.
 ; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
 ; TITLE OF INVENTION: AND USES
 ; FILE REFERENCE: R0043B-REG sequence listing
 ; CURRENT APPLICATION NUMBER: US/10/425,800
 ; CURRENT FILING DATE: 2003-04-29

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; PRIOR APPLICATION NUMBER: US/09/404,650
; PRIOR FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 5
; LENGTH: 1835
; TYPE: PRT
; ORGANISM: Rattus sp.
US-10-425-800-5

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Query Match	45.1%	Score 5366;	DB 14;	Length 10355;
Best Local Similarity	56.8%;	Pred. No. 0;		
Matches 1138;	Conservative, 183;	Mismatches 346;	Indels 336;	Gaps 38;
Qy	27	GAGRRPGGSAEKDPGSADSEAG----	LVYPALAPVVPFYLSQDSRPSWCLRTVCNPW	82
Db	19	GITEQGPGRPPSPGCLBEPGLGTNPDPVHPDLAPVAFCLQQTTSFRNWCIMWVCNPW	78	
Qy	83	FERISMLVILLNCVTLGLMFRPCEDIACDSORCILQAFDDFIFAFFAVENVVKKVALGIF	142	
Db	79	PECVSMVILLNCVTLGLMYQPCDDMECLSDRCKILQVDFDFIIFPAMENVVKKVALGIF	138	
Qy	143	GKCYLGDTWNRLLDFFVIAGMLSEYSLDLQNVGSFSAVTVRVLRPRAINRVPSMRILVT	202	
Db	139	GKCYLGDTWNRLLDFFVIAGMWVEYSLDLQNVLSAIRTVRVLRPLKAINRVPSMRILVN	198	
Qy	203	LLDITLPMLGNVLLLCFFVFFIIGIVGVQLWAGLLNRRCFLPENFSLPLSVDLERYVQTE	262	
Db	199	LLDITLPMLGNVLLLCFFVFFIIGIVGVQLWAGLLNRRCFLEENFTIQGVVALPPYVQPE	258	
Qy	263	NEDESPPICQPRENGMRSCRSVPTLRDGGGGPPCGL-----	DYEAYNSSNTT--CV	314
Db	259	EDDEMPPICSLTDGNGIMGCHEIPLPKBQ--GRECLSKDDVYDFGAGRQDLNAGSLCV	315	
Qy	315	NWQNYTNCAGEHNPFGKAINFDNIGYAMIAIPOVITLEGWDIMFYFMDAISFYNFYIY	374	
Db	316	NWRYYNVCTGNANPHKGAINFDNIGYAGIVIFQVITLEGWVEIMYVYMDAISFYNFYIY	375	
Qy	375	FILLIIVGSEFMNLCLVLTATQSETKQESOLMREORVRFISNASTLASFESEPGSCYE	434	
Db	376	FILLIIVGSEFMNLCLVLTATQSETKQEHRLMLEQORYIUS--SSTVASYAEPGGDCYE	434	
Qy	435	ELLKYLVIYILRKAARLQAQVRAAGVRVGLLSSPAPLGGQETQPSSCSRSHRRLSVHHL	494	
Db	435	EIQVYCHILRKAARLGLYQALQNR-----	461	
Qy	495	VHHHHHHHHYHNGTGLRAPRASPIQRDRANGSRRLMLPPSTPALSGAPPGGAESVH	554	
Db	462	-----RQAMG-----	PCTPA--PAKPGP----	477
Qy	555	SFYHADCHLEPVRCAQPPSPSEASGRTVGSGKVYPTVHTSPPETLKEKALVEVAASS	614	
Db	478	---HAK---EPSHCKLCPRHSPLD-----	PTPHLVQP-----	504
Qy	615	GPPTLTSLNPPGPYSMMHKLLETQSTGACQSCCKISSPCLKADSGACGPDSCPYPAR--	672	
Db	505	-----ISAILASD-----	PSSCPHCOHEA	523
Qy	673	---AGAGEVELADREWPQSDSEAVYEFQDAQHSDLRDPHSRRQRSLGDPDAPSSVLA-	727	
Db	524	GRRPSGLGSTD-SQEGSGSGGSAEAEANGD-----	LQSSDEGVSSDLGKEEEDCAAR	578
Qy	728	----FWRLICDTRFKIVDSKYFCRGMIALVNTLSNGTGYEHQEPBELTNVAISINIVFT	763	
Db	579	LCGDVRETRKKLRGIVDSKYFNRGIMMALVNTVSVNGIEHHPQEBELTNILBICNVVFT	638	
Qy	784	SLFALEMLLKLIVYGPFGYIKNPYINFDGVIIVISVWEIVGQCGGLSVLRTFLMRVLK	843	
Db	639	SMFALEMLLKLAAFGFLDYLRNPNYINFDISIIVISWEIVGQDGLSVLRTFLMRVLK	698	
Qy	844	LVFLPALQRQLVVLKMTMDNVATFCMLMLFTIFSLGMHLFGCKFASERD-GDTLPD	902	
Db	699	LVFMPALRQLVVLKMTMDNVATFCMLMLFTIFSLGMHLFGCKFSLRTDGTGTPD	758	

QY 903 RKNFDSLLWAVTVFOILTOEDWNKVLNGMASTSSWAALYFIATMTFGNYVFLNLLVAI 962
Db 759 RKNFDSLLWAVTVFOILTOEDWNKVLNGMASTSSWAALYFIATMTFGNYVFLNLLVAI 818
QY 963 LVEGFOAEEISKREDASGQSCITQLPVDSSGGDANKSESEPPDFSPS-----LDG 1012
Db 819 LVEGFOAE-----GDANRSCDEQSSNLEBEFKLPGLD 855
QY 1013 DGDRKKCLAVSLGEHPRLKSLPLLIHTAATPMSLPKSTSTGTGLGEALGPA-SRRTSS 1071
Db 856 SRDLKLPFIPMTNGH-----LDP-----SLP-----LGALHGPAGTGTAP 892
QY 1072 SGSAEPG-----AAHEMKPSPARSPPHSPWSAASWTSRSPNSL 1113
Db 893 RLSLQDPVLVALDSKSSVMGLRMSYDQRLSSLSRSSSYGPGWGRSGTWSARRSSWN-- 950
QY 1114 GRAPSLKRSPSGERSLLSGEQSDEE-ESSEEB---RASPAGSDH----- 1158
Db 951 ----SLKHKPPSAEHESLLSGEGGSCVRACEGAREEAPTAPLHAPHAAHAGHPLA 1006
QY 1159 ----RHRGSLEREAKSSFDLTTLQVPLHRTAS--GRGSASEHODCNKGSASGRALAR 1212
Db 1007 HHRHRRHTLSLDTEDSDVLGELVPVVGAAHRAWRGAGQAPGHEDCNGRMPNIAKDVT 1066
QY 1213 RPDDPPLDGDADDENGLSKGERVAVIRARLPACYLERDSWSAYIFPPQSRPRLCHRI 1272
Db 1067 KMDDRRDRGED-EEBIDYTLCFVRVKRMDVYKPDWCEVREDWSVLSPEKNFILLQTI 1125
QY 1273 ITHKMFHDVVLVIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTVKVV 1332
Db 1126 IAHKLFYVVLVAFIFLNCITIALERPOIAGSTERIFLTVSNYIFTAIFVCEMTLKVVSL 1185
QY 1333 GWCFGQAYLRSSWNVLDGLLVLSVIDILVSMVSDSGTKILGMLRLRLRLRLRLRVI 1392
Db 1186 GLYFGQAYLRSSWNVLDGLVFSVSIIDVSVASAGGAKILGVLRLRLRLRLRLRVI 1245
QY 1393 SRAQGLKLVETLMSLKPIGNIVVICCAFFIIFGLIGVQLFKGFFVCOGEDTRNITNK 1452
Db 1246 SRAQGLKLVETLMSLKPIGNIVVICCAFFIIFGLIGVQLFKGFFVCOGEDTRNITNR 1305
QY 1453 SDCAEASVRWVRKYNFNDLQALMSLFLVASKOGWVIDIMYDGLDAGVDQOPIMNHPW 1512
Db 1306 SDCAEASVRWVRKYNFNDLQALMSLFLVASKOGWVIDIMYDGLDAGVDQOPIMNHPW 1365
QY 1513 MLLYFISFLIIVAFVFLNMFVGVVVENFHKRQHEEBAERREKRLRLLEKRRKQAC 1572
Db 1366 MLLYFISFLIIVAFVFLNMFVGVVVENFHKRQHEEBAERREKRLRLLEKRRKQAC 1425
QY 1573 KPYSDYSRRLVHLCTSHYLDLFTIGVIGLVNVTMAMEHYQQOPIIDALKICNYIF 1632
Db 1426 LPYATYCPTRLLIHSNCTSHYLDLFTIGVIGLVNVTMAMEHYQQOPIIDALKICNYIF 1485
QY 1633 TVIPVLESVKLVAFGRPRFRQWQOLDIAVLVLSIMGTILEEIEVNASLNPINPIRI 1692
Db 1486 TVIPVLESVKLVAFGRPRFRQWQOLDIAVLVLSIMGTILEEIEVNASLNPINPIRI 1545
QY 1693 MRVLIARVLKLVAGVGMALLDTVMQALPQVGNLGLLPMLLFFIIPALGVLFGLDEC 1752
Db 1546 MRVLIARVLKLVAGVGMALLDTVMQALPQVGNLGLLPMLLFFIIPALGVLFGLDEC 1605
QY 1753 DETHPCGLGRHATFRNFGMAFLTLFRVSTGDWNGIMKDTLRDC-DOESTCVNTV--IS 1809
Db 1606 NDENPCGMSRHATFENFGMAFLTLFRVSTGDWNGIMKDTLRDC-DOESTCVNTV--IS 1665
QY 1810 PIYFVSFVLTAQFVLNVAIVLMLKLEESNKEAEAELEAELEEM-KTSLSPQSPHSL 1868
Db 1666 PIYFVSFVLTAQFVLNVAIVLMLKLEESNKEAEAELEAELEEM-KTSLSPQSPHSL 1721
QY 1869 GSPFLWPGVEGDPSPDKPALHAPAAHARSASHFSLEHTMQPHPTLPCPDLTV--- 1925
Db 1722 -----GPCPG-----PCPCPCPCPCPRLFTSSPG 1747

QY 1926 ---RKSGVSRTHSLPNDSYMCRH 1945
Db 1748 APGRSGGAGAGG-DTSHLCRH 1769
RESULT 13
US-09-030-482B-19
; Sequence 19, Application US/09030482B
; Patent No. US20020009772A1
; GENERAL INFORMATION:
; APPLICANT: Smutch, Terry
; APPLICANT: Neuromed Technologies, Inc.
; TITLE OF INVENTION: NOVEL HUMAN CALCIUM CHANNELS AND RELATED
; TITLE OF INVENTION: PROBES, CELL LINES AND METHODS
; FILE REFERENCE: 38109-20007.00
; CURRENT APPLICATION NUMBER: US/09/030.482B
; CURRENT FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: US 60/039,204
; PRIOR FILING DATE: 1997-02-28
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 1853
; TYPE: PRT
; ORGANISM: Human
; US-09-030-482B-19
Query Match 33.3%; Score 3959.5; DB 9; Length 1853;
Best Local Similarity 46.8%; Pred. No. 4e-241;
Matches 908; Conservative 158; Mismatches 361; Indels 515; Gaps 42;
QY 27 GAGGRG-----PGSAEKDPGSDSBAEGLPYPALAPVVFYLSQDSRPSMCLRTVC 79
Db 76 GTGMHTGTFOGABPSSOHPEAQATYTAGTPTAGTPTCCFVLD-----LVC 124
QY 80 NPWERISMLVILLNCVTILGMPCEDIACDSQRCRILQAFDDPIFAFVEMVVMVAL 139
Db 125 T-WFECVSMVILLNCVTILGMPCEDIACDSQRCRILQAFDDPIFAFVEMVVMVAL 183
QY 140 GIFGKCYLGDWNRLLDFFIVTAGMLEYSLDLQNVFSFSAVRTVRLRLRLRLRLR 199
Db 184 GIFGKCYLGDWNRLLDFFIVTAGMLEYSLDLQNVFSFSAVRTVRLRLRLRLRLR 234
QY 200 LVTLILLDTLPMGNVLLLCFFVFFIFIGVIGVQLWAGLNRCLPNSFLPLSVLERY 259
Db 235 LVNLLDTLPMGNVLLLCFFVFFIFIGVIGVQLWAGLNRCLPNSFLPLSVLERY 294
QY 260 QTEDESPFICSPQRENMRSCRSVPTLGDGGGPPCGL-----DYEAVNSSNTT- 312
Db 295 QTEDESPFICSPQRENMRSCRSVPTLGDGGGPPCGL-----DYEAVNSSNTT- 351
QY 313 -CVNNNOYTNCSAGHNPKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYN 371
Db 352 LCVNNNOYTNCSAGHNPKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYN 411
QY 372 FIYFILLI----- 380
Db 412 FIYFILLI----- 471
QY 381 ----- 380
Db 472 ENLAGTSKGBESYLLRLAGSQVHQAQMLGRGLGPESLETGBEPHSWSPRATRRDPQ 531
QY 381 -----VGSFFMINCLVVIATQPSFETQRESQLMREORVFLSNASTLAS 425
Db 532 COPQGPLPHFMQAVGVSFFMINCLVVIATQPSFETQRESQLMREORVFLSNASTLAS 590
QY 426 FSEPGSCVBEELLKYLVIYILKAAARLQVSRAGVVRVGLLSSPAPLQGOETQPSSCSRS 485
Db 591 YAEPCDCEYEFQVYCHILIRAKR-----RALGLYQALQSRQALGPEAPAKP--- 640
QY 486 HRRLSVHLVHHHHHHHHHHHGLNGTLRAPRASFEIQRDRANGSRRLMLPPSTPALSGA 545

Db 641 -----GPHAKEPRHYPLTWESILGRQAEECTLRAA-----AHPSSGAS 679
Qy 546 PPG-GAESVHSFYHADCHLEBVRQAPPPRSPERASGRTVSGKYVPVHTSPPETLKE 604
Db 680 HPGVGSSEA-----PELC---PQHSPLDAPHTL-----VQPIPATL-- 713
Qy 605 KALVEAASSGPPTLTSLNIPPGVPYSSMHKLETSQSTGACOSSCKISSPCLKADSGACGP 664
Db 714 -----ASDP 717
Qy 665 DSCPYCAR-----AGAGEVELADREMPDSDSEAVYEFTOAQHSDLRDPHSRRQSLGP 718
Db 718 ASCPCCOHEGRRPSGLSTD-SQEGSGSGSSAGGE--DEADGDGARSSEDGASSELGK 774
Qy 719 DAEPSVL-----AFWRLICDTRFKIVDSKFGRGIMTAILVNTLSMGIEVHEQPE- 769
Db 775 EEEEEQADGAVMLCGDWMRETRAKLGIIVDSKYFNRGIMMAILVNTVSMGIEHQAASA 834
Qy 770 -----ELTNAL-----ISNIV----- 781
Db 835 AOPGRACRGONPDCLMTLKAAPCLCHNVPSGQGVLSHPVTPHTAPWRMETGKQHGCE 894
Qy 782 -----FTSLFALEMLKLLVYGPFGYIKPNYINFDGVIVVISWEIVGQGGGLSVLRT 835
Db 895 EGPGRSSDMFALEMILKLAAGFLDYLRNPNYINFDISIIVISWEIVGQADGGLSVLRT 954
Qy 836 FRLMRVLKVRFLPALQOLVVLKMTDNVATFCMLMLFIPISILGMHLFGCKFASER 895
Db 955 FRLRLVLKVRFPALRQOLVVLKMTDNVATFCMLMLFIPISILGMHLFGCKFASER 1014
Qy 896 D-GDTLPDRKNPDSLLWAIVTFOLLTOEDANKVLYNGMASTSSWAALYFTALMTGNYV 954
Db 1015 DTGDTVPDRKNPDSLLWAIVTFOLLTOEDANKVLYNGMASTSSWAALYFTALMTGNYV 1074
Qy 955 LFNLLVAILVEGFOAE-EISKREDA-----SGQLSCQLP 988
Db 1075 LFNLLVAILVEGFOAEVTVLAEAPPQGLRGTGRGGLDGGGLQFLLAGNL-SLKEG 1133
Qy 989 VDSGGDANKSEBPPFPSPS-----LDGGRKKCLALVSGEHPELAKSLPP 1038
Db 1134 VADEVDANRYSDEDOSSNIEBDFKLQGLDSSGDPKLCPIPTPNHG-----LDP 1186
Qy 1039 LIHTAATPMSLPKSTSGLEALGPA-----SRTS----- 1070
Db 1187 -----SLPGGHLPAGAGAPAPRLSLQDPDMLVALGSRKSSVMSLGRMSYDQRS 1236
Qy 1071 -----SGSAEPGAAMKSP-----PSARSSPHSPMSAASWTSRRSS 1109
Db 1237 LVGGLRATAGVQAAGFLVPPQWVCLMGADPNNGNSFQSSRSYYGPGWRSAAWASRSS 1296
Qy 1110 RNSLGRAPSLKRRSPSGRRSLLSGE-QGESQDEEESER--ERASPAAGSDH----- 1158
Db 1297 WN-----SLKHKPPSAEHESLLSAERGGGARVEVADEGPPRAAPLHTPHAHVHRGP 1350
Qy 1159 -----RHRGSLREAKSSFDLPDLOVPGHRTASGR--GSASEHODCNKASGELA 1209
Db 1351 HLAHRRHRRHTLSLDRNDSVDLAELVPAVGAHPRAAWAAGAPAGHEDCNRMPSIAKD 1410
Qy 1210 RALRPDPPDGLDGDADD-----EGNLKSGRVRWIRARLPACVLERDSSAYTFP 1260
Db 1411 VFTKMGDRGDEDEEEDYVGGGAEGDLTLCFVRKMDIVYEDCEVEDSDSVLPS 1470
Qy 1261 POSRFR-----LJC-----HRIITHKMFHDVHLVIIFLNCITIAE 1296
Db 1471 PENLRDLGWSLECOGQGVGLVWVYVQRRQRQTIIAHKLFDYVLAFLIPLNCITIALE 1530
Qy 1297 RPKIDPASAERIPLTSLNYSITAVFLAEMTKVVALGHCFOEQAYLRSSWNLGLLVL 1356
Db 1531 RPOEAGSTERIFLTVSNYSITAVFLAEMTKVVALGHCFOEQAYLRSSWNLGLLVL 1590
Qy 1357 SVIDILVMSVSDGKILGMLRVLRLRLTLPLRVLISRAOGLKLVETFLMSSLPIGNIV 1416
Db 1591 SIIDIVSLASAGAKILGVLRVLRLLTLPLRVLISRAOGLKLVETFLMSSLPIGNIV 1650

Qy 1417 VICCAFFIIFGILGQVLFKGFYVCOGEDTRNITNKSDCAEASVYRWVHKNFNDNLGOAL 1476
Db 1651 LICCAFFIIFGILGQVLFKGFYVCOGEDTRNITNRSDCAEASVYRWVHKNFNDNLGOAL 1710
Qy 1477 MSLFVLASKDQWVDIMYDGLDVAVGDOQPINMHNPMMLLYFISFLLIYVAFVFLNMFVGV 1536
Db 1711 MSLFVLASKDQWVNIMYDGLDVAVGDOQPINMHNPMMLLYFISFLLIYVAFVFLNMFVGV 1770
Qy 1537 VENPHKCRQHOEAEARRREKRLRLEKKRKAQCKPKYYSYDSYRFRLLVHHLCTSHYLD 1596
Db 1771 VENPHKCRQHOEAEARRREKRLRLEKKRKAQCKPKYYSYDSYRFRLLVHHLCTSHYLD 1830
Qy 1597 LFIITGVIGLVNVTWAMEHYQOP 1618
Db 1831 IFITFIICLVNVTWMSLEHYNQP 1852
RESULT 14
US-10-369-493-6836
; Sequence 6836, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; PRIOR FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 6836
; LENGTH: 1657
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-6836

Query Match 29.9%; Score 3564.5; DB 15; Length 1657;
Best Local Similarity 42.2%; Pred. No. 3.3e-216;
Matches 822; Conservative 231; Mismatches 430; Indels 465; Gaps 50;

Qy 15 QPRSFMRNLDSGAGRPG-----PGSAEKDPG-----SADSEA 48
Db 56 QSQSTRREDVEALGSIEGSKETQLQSEHGLASSSEASPSRWEGROIENGNEQIEES 115
Qy 49 EGLPYALAPVVPFYLQDSRPSWCLRTVCNPFERISMLVILNCVTLMFRPCED-I 107
Db 116 E-LPYGFAAPALRCFYQARPPRKWALQWVMSPFDRITMAVIMINCVTLMGYPCEGP 174
Qy 108 ACDSQRCILQAFDDFIFAFVAVEMVQWALGFGKKCYLGDFTWNLDFIVTAGMLEY 167
Db 175 DCDTYRCQILDIDICDIFVYFAFVAKIMALGFGYPAAYMSDTWNLDFIVTAGIAEF 234
Qy 168 SLDLQ---NVSFSAVRVRLRPLRINRVPMSRILVTLTLDLPLMLGNVLLLCFFVFFI 224
Db 235 VLHEYLGNNILTAIRVRLRPLRINRVPMSRILVTLTLDLPLMLGNVLLLCFFVFFI 294
Qy 225 FGIYGVQWLAGLNRNCF--LPENFS-----LPISVLERYYQTEENEDSPFICSPREN 277
Db 295 FGIYGVQWLAGLNRNCF--LPENFS-----LPISVLERYYQTEENEDSPFICSPREN 353
Qy 278 GMRCSRVPILRGDGGGPGCLDYEAAYNSSTNTCTNNQYTNCSAG----- 326
Db 354 GLHTCSNLPPYVD---GVKCNLTLDYDKVTNDSNCINNNIYNECQVNIYPSLMTIAIS 410
Qy 327 -----EHNPKGAINFDNIGYAMIAIIFOVITLLEGGWVDIMYFVMDAHSFYNFIFILLI 380
Db 411 CFIKWQRNPFQSGVSDNIGFAVFLVLSLGGWTDIMYVQDAHSFYNFIFILLI 470

QY 1439 FVCGEDTRNITNKSDCAEASR--WVRHKYFNDFNLQALMSLFLVLASDQWVDIMYDGL 1496
 Db 1206 YHICGPEGVNTYKADICIE--DYENKVNHRYNFDNLQALMSLFLVLSSKDGWVSIYQGI 1264
 QY 1497 DAVGVDQOPIINNNPMLLYFISFLIVAFFLNMVGVVVENFHKCRQHOEBEERRE 1556
 Db 1265 DAVGVDQOPIENNEWEMIIYFISFLLVGFVLMNMFVVVENFHKCRQHOEBEERRE 1324
 QY 1557 EKRLRLLEK-----KRRKAQC-----KPYYSYSRFRLLVHHL 1590
 Db 1325 EKRLRLLEK-----KRRKAQC-----KPYYSYSRFRLLVHHL 1384
 QY 1591 TSHYLDLFTITGICLVNVTWAMEHYQOPIIDLEAKICNYFTFVFLVLESVEKLVAFGR 1650
 Db 1385 TSKYFOLAIAVINGINISMAFYMFMGLKYVLKALNYFFTAFTLEAMKLIAGFK 1444
 QY 1651 RPFQDRNOLDIAVLVLSIMGITLLEEVNASLPINPTIIRIMVLRIRARVLRKLVAVG 1710
 Db 1445 RPFTEKWRNLDLFIIVLSIAGIIFEEFEA--LELPINPTIIRVVRVLRIRARVLRKLVAVG 1503
 QY 1711 MRALDITVQALPOVGNLGLLFLMLFFIFAAALGVLELFGDLCEDETHCEGLGRHATNRF 1770
 Db 1504 IRSLLDTVGEALPOVGNLGLLFLMLFFIFAAALGVLELFGDLCEDETHCEGLGRHATNRF 1563
 QY 1771 GMAFLTLFRVSTGDNWNGIMKDTLR--DCD-----QESTCYNTVISPIYFVSVLTAQFVL 1824
 Db 1564 GMAFLTLFRVSTGDNWNGIMKDTLR--DCD-----QESTCYNTVISPIYFVSVLTAQFVL 1623
 QY 1825 VNVVAVLMLKLEESNKEAKEAELEAE 1852
 Db 1624 VNVVAVLMLKLEESN--KRDAEGPAE 1648
 RESULT 15
 US-10-627-370-2
 ; Sequence 2, Application US/10627370
 ; Publication No. US20040081988A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Johnson, Jason M.
 ; APPLICANT: Castle, John C.
 ; APPLICANT: Armour, Christopher D.
 ; TITLE OF INVENTION: SPLICE VARIANT ISOFORMS OF HUMAN CALCIUM CHANNEL CACNA1B
 ; FILE REFERENCE: RS0202Y
 ; CURRENT APPLICATION NUMBER: US/10/627,370
 ; CURRENT FILING DATE: 2003-07-25
 ; NUMBER OF SEQ ID NOS: 13
 ; SOFTWARE: Patent in version 3.2
 ; SEQ ID NO 2
 ; LENGTH: 2264
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-627-370-2
 Query Match 14.7%; Score 1753; DB 15; Length 2264;
 Best Local Similarity 24.8%; Pred. No. 2.1e-101;
 Matches 637; Conservative 358; Mismatches 830; Indels 744; Gaps 85;
 QY 27 GAGGPGGSAEKDPGSDSEAGLPYPALAPVVF-----FVLSQDSRP 70
 Db 25 GAGGAGGPGGLOPQGGVLYKQSIARARTMALYNIPVKONGCTVNRSLFVSEDNV 84
 QY 71 RSWCLRTVCNPFWRISMLVLLNCVILGMPCEPCDIACDSORCIRLOAFDD---FIFAF 127
 Db 85 RYAKRITWPPFPFEMILATIANCIVLAL-----EQHLPGDKTPMSERLDDTEPYFIGI 140
 QY 128 FAVENVVVMVAG--IFGKCKYLGDTNRLDFFIVIAAGMEYS---LQNVSVSAFTVR 183
 Db 141 FCFEAGIKIILGPFVFKSGYLRNGWVMDPVVLTGILATAGTDFDLR-----TLRAVR 195
 QY 184 VLRLPRAINRVSMRILVLLDITLMLCNVLLLCFFVFFGVGVQVLMAGLNRNCF 243
 Db 196 VLRLPLKLVGSPISQVLSKINAMVPLQLGLLFFAILMFAILGIEFYMGKFKACF-- 254

QY 381 VGSFMINCLVVIATOFSETKOBESQLEORVRFLSNASTLASPERG-----S 431
 Db 471 IGAFPMINCLVVIATOFSETKOBESQLEORVRFLSNASTLASPERG-----S 530
 QY 432 CYBELLKVLVILKAAARRLAQVSRAGVRVGLSSPAPLGGQETOPSSCSRRRLSV 491
 Db 531 VYAFVRFIHTFR--TKBAKKKYTAYMEE----- 560
 QY 492 HHLVHHHHHHHHVHLNGTLRAPASPEIQDRDANGSRMLPPTPALSGAPPGAE 551
 Db 561 -----RAERKSSERQOR-----RKSLLDDWAT--LS----- 584
 QY 552 SVHSFYHADCHLEPVRQAPPSPSEASGRVUGSKVYPTVHTSPPTLKEKALVEVA 611
 Db 585 -----RIEBAEDE-- 593
 QY 612 ASSGPPTLTSNIPGPYSSMHKLEFQSTGACOSSCKI--SSPCLKADSGACGPDSCPYC 670
 Db 594 --EDETTITREN-----GDDQTEQNGDGVRIKRVKIBEEPKIKGN--GNSNGPHY 640
 QY 671 ARAGAGEVELADREMPDSDSEAVVEFTQDAQHSDLRDPHSRRQSLGPDAPSSVLAFWR 730
 Db 641 KHSSDE-----ESDEGEDQVYDGEAAKKS-----TPSKL--W- 675
 QY 731 LICDTRFKIVDSKYFGRGIMIALVNTLSMGIEYHQPELTNALETSNIVFTSLFALEM 790
 Db 676 -FREKIQKFVICDHFTRGILVAILVNTLSMGVEYHQPELTNALETSNIVFTSLFALEM 734
 QY 791 LKLLVYGPFGIKPYNIFDGVIVISVWEIVGQGGGLSVLRFRMLRVKLVRFLPA 850
 Db 735 LKIIIASGLFGYLDAGNFDGIVALSLELEFQEGKGLSVLRFRLLRLILKLVRFMPA 794
 QY 851 LQRLVLMKTDNVAFCWMLMLFIFPSILGMHLFGCKFASERD-----GTLP--DRKN 905
 Db 795 LRVQLVLMKTDNVAFCWMLMLFIFPSILGMHLFGCKFASERD-----GTLP--DRKN 854
 QY 906 FDSLLWAVTVFOILTOEDWKNVLYNGMASTSSWALYFIALMTFGNYLVFLNLAIVLE 965
 Db 855 FDTLLWAVTVFOILTOEDWKNVLYNGMASTSSWALYFIALMTFGNYLVFLNLAIVLE 914
 QY 966 GFQAEIESKREDASGOLSCIQLPVDSQGGDANKSESEPFPSLDGDRKCLALVSL 1025
 Db 915 GFQE--SKEE-----KQLEEDARKQAVEEEDERKRELEI-- 949
 QY 1026 GEHPELKSLLPPLIHTAATPMSLPKSTGTGLGEALGPASRRTSSGSAEPGAAHEMKS 1085
 Db 950 -----IAKTSFAPNNGVAF-----ECTQRPSSPEEPS 980
 QY 1086 PPSARSSPHSPWSAASSWTSRSLGRAPSLKRSPSG-----ERRSLSGEQESQ 1140
 Db 981 PRLLSANVH-----PSPERKHSANLDAIIDKRLV----- 1010
 QY 1141 DEEESSEERASAPAGSHRHGSLERAKSFDLPDTLOVGLHRTASGRGSAEHQDCN 1200
 Db 1011 --RNSAPDR--SPV--SEGRDSDRLNRHA--SLVLPVANGVP-----YRQRVH 1052
 QY 1201 GKSAGRLARALRPDDPLDGDADDGGLNLSKGE--RVRAWIRARL--PACYLERDSWAXI 1258
 Db 1053 SWKASQELKQAL-----ABEE-----KNEAKQNTFVRKLLKKTCLHNRTEFSLFL 1098
 QY 1259 FPPQSRFRLLCHRIITHOMFHVVLVIFLNCITIAMERPKIDPHSAERIFLTSNVIFT 1318
 Db 1099 MGPKNPLAIKLCLOTTQKKWFDYTVLFFIGINCITLAWERPSPDPSEFOTLHISGYIFT 1158
 QY 1319 AVFLAMTVKVALGWCFCGEQAYLRSSWNVLDDLVLISVIDILVMSVSDGKILGMLR 1378
 Db 1159 VIFTGEMMK----- 1168
 QY 1379 VLRLRLTLRLRVI SRAQGLKLVETLMSLKPIGNIVVICAPFIIFGLVQLPKGKF 1438
 Db 1169 -----VSHRIPTLKPIGNIVLICCTFTFIIFGLVQLPKGMM 1205

QY 244 PENFSLPLSVLDLRYVOTENEDSPFICSPQRENGMRSCRSVPTLRGDGGGPPCGLDYE 303
DB 255 -----PNSTDAE-----PV-----GDFPCGKEAP 273
QY 304 AYNSSNTTCVNMNOYTYNCSAGEHNPFGKAINFDNIGNYAMIAIPQVITLEGVDIMYFV 363
DB 274 ARLCEGDTEC---REYWP-----GPNFGITNPDNIFAILTVFQCITMEGWTDLINT 323
QY 364 MD-AHSFNFYFILLIIVGSPFMNLCIVVATOFSETKORES-----QIMRQRVRF 416
DB 324 NDAAGTWNWLYFIPLIIGSFPMNLVLVLSGEFAKERVENRRAFLKLRQOQIE- 382
QY 417 LSNASTLASFSEPGSCYBELLYVYLKKAARLQAQVRAAGVRVGLLSSPAPLGGQET 476
DB 393 -----RELNGYLEWIFKAEEVMLAEEDRNA-----BEK 410
QY 477 QPSSCSRSRHRRLSVHVLVHHHHHHHHHHLGNGTLRAPRASPEIQDRDANGSRRLMLPP 536
DB 411 SPLDVLKRAATCKSRNDLIH-----AEEGEDRFAD----- 440
QY 537 PSTALSCAPPGGAGSVHSFYHADCHLEPVRQCAPPPRSPSEASORTVSGKVYPTVHTS 596
DB 441 ----- 440
QY 597 PPTETLKEKALVEAASSGPPTLTSLNTPPGPYSSMHKLETFQSGACQSSCKLSSPCLK 656
DB 441 -----LCVSGSPFAR 450
QY 657 ADSGACGPDSCPYCARAGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHRRQRS 716
DB 451 ASLKGKTESSYPR-----KEKMERF----- 473
QY 717 GPDAPSSVLAFWRLICDTFKIVDSKYFGRGIMTALIVNLSMGIEVHEOPELITNALE 776
DB 474 -----FIRMVKAQSFYVWVLCVVALNTLCVAMVHYNQPRRLTTLTY 515
QY 777 ISNIVFTSLFALEMLKLLVVGPGYIKNPYINPDGVIVVSVMEIVGQ-----QGGGLS 831
DB 516 FAEFVGLGLFTEMLSKYIGLOPRSYFRSSNCFDGVIVGSFVFWAAIKPGSSFGIS 575
QY 832 VLRTFRLMRVLKVRFLPALORQLVLMKTMNDVATFCWLLMLFIFISILGMHLFGCKF 891
DB 576 VLRALRLRIRFKVTKYSSSLNVLVSLNLSMKSIIISLFLFLFVIVFALLGMQLFGQF 635
QY 892 ASERDGLTPRKPDLSLMAIVTVFQILTQEDWNKVLYNGM-----ASTSSWAALYFIA 946
DB 636 NFQDETPT---TNFDTFPAAILTVFQILTGEDMNAVHYGIESQGVSKGMFSFYFIV 691
QY 947 LMTFGNYVFLNLLVAILVEGF-QAEEISK---REDASQO-----LSCIQ 986
DB 692 LTLFGNYTLNVLVLAIVDNLANAQELTKDEEEMEAANQKALQAKEVAEVSFMSAAN 751
QY 987 LPVDSQGGDANKSESEPDFSPSLDGDGDRKKCLALVSLGE-----HPELRK 1033
DB 752 ISIAARQONSAKARSVWEQASQLRLQNLRASCEALYSEMPPEERLRFATTHLRPDMKT 811
QY 1034 SLLPLLIHTAATPMSLP-----KSTSTGLGEALGPASR-----RTSSG----- 1073
DB 812 HLDRLPVVELGRDARGVGGKARPEAAEPEGVDPPIRRHHRDKDKTPAAGQDRAEA 871
QY 1074 ---SAEPGA-----AHEMKSPSPARS-----SPH-----SPWSAASSW 1103
DB 872 PKASGEGEREPRRPHRSKGAAGPEARSEGRGFGGEGRRHRRGSPBEAARE 931
QY 1104 TSR-RSSNSLGRAPSLKRRSPSERRSLLSGEGQESQDEESGEE-----ERASP- 1153
DB 932 PRHRAHRH---QDPSKECAGAKERRARHGGPRAGPREAESGEEPARHRAHKAQPA 988
QY 1154 -----ASDHRHRSGLSREAKSSFDLPTLVQVGLHRTASGRG 1191
DB 989 HEAVEKETTEKEATEKEAIEVEADKEKELRNHQPREPHCDLETSGTIVTVPMTLPSLCL 1048
QY 1192 SASEHQDCNGKASGRLARALRPDDP-----PLGDDADDGGLN-----SKGE 1234

DB 1049 QKVEEQPEDAQNQRNVRMGSQPPDPNTIVHIPVMLTGPGLGEATVVPNGVDSQAEK 1108
QY 1235 R-----VRWIRARLPACYLERDSWAGYIFPPQSRFLLCHRITTHMFOHVVVLVIF 1287
DB 1109 KEVEADDVMSGRPRIVPYS-----SMFCLSPTNLLRRFCHYIVTMYRFEVVLVIA 1161
QY 1288 LNCITIANERPKIDPHSAERIFLTLNYSNIFATVFLAEMTVKVALGWCEGBOAYLRSSWN 1347
DB 1162 LSSIALAAEDP-VRTDSPRNALKYLDIFYTGVTFFEMVIKMDLGLLHPGAYFRDLWN 1220
QY 1348 VLDGLLVLSVIDILVSMV-SDSGTKILGMLRLVRLRLTLRLRPLRVISRAQGLKLVVETLM 1406
DB 1221 ILD-----FIVVSGALVAFAFSGSKGKINTIKSLRVLRLPLKTIKRLPKUKAVDCVV 1276
QY 1407 SSLKPIGNIVVICCAFFIIFGILGVQLFKGFVFCQGE-----DTRN---ITNKSDCABA 1458
DB 1277 NSLKNVLNIVYMLFMFIFAVIAVOLFKGFYCTDESKELEDCRQYLDYEKEVEA 1336
QY 1459 SYR-WVRHKYNFDNLGOALMSLFLVLASKDQWVDIMYDGLDVGVDQOQIMMHNPMWLLYP 1517
DB 1337 QPRQKKYDPRHYDNVLWALLTLFTVSTGEGPMLVKHSDATYEEQSPSGYRMBLSIF 1396
QY 1518 ISFLIIVAFVFLNMFVGVVVENEHKCRQHOQEEEARREERLRLRLEKRRKA-----QC 1572
DB 1397 VVYFVPPFFVFNIFVALIITF-----QSGDKVMS-----CSLEKNERACIDFALSA 1446
QY 1573 KPY---YSDYSR---FRLLVHLCSTHYLDLFTITGVIGLVNVTMAMEHYQOQIILDBALKIC 1628
DB 1447 KPLTRYMPQNRQSFQYKTTWTFVSPPPPEYFIMAMIALNTVLMKMFYDAPYELMLKCL 1506
QY 1629 NYITVIVLESVKLVAFGRFRFQDRWNQDLALIVLLSIMGITLBEI-EVNASLPINP 1687
DB 1507 NIVFTSMFMECVLKIIAFGLVNTYFRDANWVDFVTVLGSITDILVTIAETN-----NF 1561
QY 1688 TIIRIMVLRITARVLKLLKMAVGRALLDTVMQALPOVGNLGLLPMLLFFIFPAALGVLEL 1747
DB 1562 INLSFLRLFRARLILKLRQYTIIRLLWTFVQSFKALPYVCLLIAMLLFFIYIITGMQVF 1621
QY 1748 GDLECDETHCEGLGRHATFRNFGMAFILTFRVSTGDNWNGIMKDTLRD---CDQES---STC 1803
DB 1622 GNIALDDD---TSINRHNFRFTLQALMLLFRSATGEAWHEIMLSCLSNQACDEANATE 1678
QY 1804 YNTVISPIYFVSFVLTAQFV-----LVNVVIAVMKHLE-----ENK 1841
DB 1679 CGSDFAFYFYFVSFPLCSFLRLVRMNPISNEDMTVHTFTIMALTIRTALEIKLAPAGTK 1738
QY 1842 EAKEAELEAELEEMKTLSPQHPSLGSPFLWPGVEGDPSPSPKCALHPA----- 1894
DB 1739 QHQCDAELRKEISVWVANL-PQKTLDDLVP-----PHKPDENVKGVYAALMIFDFY 1789
QY 1895 -----AHARSASHFSLEHPTM---QPHPTELPGDPLLTVRKSQSVRTHSL 1936
DB 1790 KONKTTDRMQOAPGGLSQMGVPSLFLPHELKATLEQTQPAVLARGARVFLRQKSTSLN-- 1847
QY 1937 PNDSYMCHGSTATGPIGRWGLPKAQSGSVLSVHSOPADTSYILQIPKADPHLLQ-- 1994
DB 1948 -----GGAIQNQESGJKESV-----SMGTQRTQADPHEARPP 1880
QY 1995 ---HSAPTWGTIPKLPPGRSPLAQRLRRQAIR-----TDSLVDQGLGSRDDELLAE 2044
DB 1881 ERGHSTEI-----PVGRSGALAVDQMOQITRRGDPGPGQGLSGRAASMPRLAA 1932
QY 2045 VSGP---SPPLARAYSFWQSQSTQAQHSRSHSKISKHTMTTAPPCFG----- 2088
DB 1933 ETQPVTDASPMKRSI-----STLAQRPRGTHLCST---TPDRPPPSQASSHHHHHRCHR 1983
QY 2089 ---PENWKGKPPETRSSLELDTLWISGDLPLPGQOEBPPSPRDLKCKYSVBAQSQ 2144
DB 1984 RRDQRKORSEKGP---SLSADMDGAPSAVGPGLPPG---EGPTGCRERRERQRERQSOE 2038
QY 2145 RR-PTSMWLDORRHSIAVCLDSG-----SOPHLGTDP-----SNLGG 2181

us-09-611-257a-37.rapb

Mon Apr 18 12:41:44 2005

Db 2039 RROPSSSSSEKQRF---YSCDRFGREPPKPKPSLSHPTSTAGQEPGHPQGGSVNG 2095
Qy 2182 QPL-----GGFGRPKKLS-PSITI-----DPESQGPRT--PP-SPG----- 2217
Db 2096 SPLSTSGASTPGRGRRQLPQTPLTPRPSITYKTANSPIHEAGACTSLPAFSPGRLSR 2155
Qy 2218 -----ICLRRRAPSSDSKDPLASGPPDSMAASPXKXVLSLGLSDP 2261
Db 2156 GLSEHNALLQDPLS---QPLAPG-----SRIGSDP 2183

Search completed: April 13, 2005, 16:55:25
Job time : 242 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 13, 2005, 16:23:47 ; Search time 41 Seconds
(without alignments)
5317.736 Million cell updates/sec

Title: US-09-611-257a-37

Perfect score: 11904

Sequence: 1 MDEEDGAGAEESGQPRSF.....PKDVLSLGLSDPADLDP 2266

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	10945	91.9	2254	2 T09053	low voltage-activa
2	3564.5	29.9	1657	2 T15838	hypothetical prote
3	1746.5	14.7	2339	2 A42566	omega-conotoxin-se
4	1741	14.6	2237	2 T45115	N-type calcium cha
5	1711	14.4	2336	2 A45386	omega-conotoxin-se
6	1706	14.3	2288	2 S41080	calcium channel al
7	1697	14.3	2259	2 S29236	calcium channel pr
8	1689	14.2	1810	2 T31092	probable voltage-g
9	1681	14.1	2178	2 S29237	calcium channel pr
10	1681	14.1	2272	2 C54972	voltage-dependent
11	1665	14.0	2270	2 A54972	voltage-dependent
12	1664.5	14.0	1891	2 T43262	calcium channel al
13	1663.5	14.0	2251	2 B54972	voltage-dependent
14	1656	13.9	2223	2 A47447	calcium channel pr
15	1651.5	13.9	2222	2 A37490	voltage-dependent
16	1633	13.7	1911	2 T43048	calcium channel al
17	1632	13.7	1873	2 A30063	dihydropyridine re
18	1626	13.7	1993	2 T30902	calcium channel sca
19	1625.5	13.7	1852	2 A37860	calcium channel pr
20	1612	13.5	2143	2 JH0457	voltage-dependent
21	1602.5	13.5	2139	2 A4467	voltage-dependent
22	1597.5	13.4	1559	2 T30535	calcium channel al
23	1596.5	13.4	2166	2 S11339	calcium channel pr
24	1591	13.4	2019	2 A33996	sodium channel pro
25	1590	13.4	1783	2 T37258	probable voltage-d
26	1586	13.3	2016	2 A38195	sodium channel pro
27	1583.5	13.3	1873	2 A55645	calcium channel, v
28	1583	13.3	1977	2 S54771	sodium channel alp
29	1581.5	13.3	2171	2 S05094	calcium channel al

protein C48A7.1 [i
sodium channel pro
calcium channel pr
calcium channel al
voltage-dependent
sodium channel pro
calcium channel al
calcium channel pr
voltage-dependent
calcium channel al
calcium channel pr
calcium channel al
sodium channel alp
sodium channel pro
voltage-dependent

30 1578 13.3 1917 2 C88728
31 1573.5 13.2 1983 2 A60054
32 1572.5 13.2 2212 2 A41098
33 1568.5 13.2 1687 2 S41742
34 1566.5 13.2 2203 2 T42742
35 1565.5 13.2 1951 2 S00320
36 1564.5 13.1 2181 2 A38198
37 1561 13.1 2326 2 B47447
38 1560.5 13.1 1610 2 A46227
39 1557.5 13.1 2161 2 JH0564
40 1555 13.1 2220 2 A45290
41 1554 13.1 2262 2 T30890
42 1553.5 13.1 2005 2 A46269
43 1550 13.0 1957 2 S68453
44 1549.5 13.0 2009 2 A25019
45 1549 13.0 1646 2 JH0422

ALIGNMENTS

RESULT 1
T09053
low voltage-activated, T-type calcium channel alpha chain - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C:Accession: T09053
R:Perez-Reyes, E.; Cribbs, L.L.; Daud, A.; Lacerda, A.; Barclay, J.; Williamson, M.; Fox
Nature 391, 896, 1998
A:Title: Molecular characterization of a neuronal low voltage-activated, T-type, calcium
A:Reference number: Z16538; MUID:98154730; PMID:9495342
A:Accession: T09053
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-2254 <PER>
A:Cross-references: UNIPROT:O54898; EMBL:AF027984; NID:g3786350; PIDN:AAC67372.1; PID:g3
A:Experimental source: strain Sprague-Dawley; brain
C:Genetics:
A:Map position: 17
A:Note: CACNA1G
C:Superfamily: voltage-dependent calcium channel protein alpha-1 chain
C:Keywords: calcium channel, voltage-gated ion channel

Query Match 91.9%; Score 10945; DB 2; Length 2254;
Best Local Similarity 92.5%; Pred. No. 0;
Matches 2107; Conservative 34; Mismatches 101; Indels 36; Gaps 6;

Qy 1 MDEEDGAGAEESGQPRSFVRLNDLSGAGRGPGSGAEKDPGSDSSEAGLPYPALAPVV 60
Db 1 MDEEDGAGAEESGQPRSFVRLNDLSGAGRGPGSGAEKDPGSDSSEAGLPYPALAPVV 60
Qy 61 FFYLSQDSRRPRSCNVRTVCNPFERISMLVILLNCVTILGMFRPCEDIACDSQRCRILQAF 120
Db 61 FFYLSQDSRRPRSCNVRTVCNPFERISMLVILLNCVTILGMFRPCEDIACDSQRCRILQAF 120
Qy 121 DDIFAPFAVEMVVMVVALGIFGKKCYLGTWNLDPFIVTAGMVEYSLDLQNVSFSAVR 180
Db 121 DDIFAPFAVEMVVMVVALGIFGKKCYLGTWNLDPFIVTAGMVEYSLDLQNVSFSAVR 180
Qy 181 TVRVLRPLRAINRVPVSMRIIVTLTLLDTPMLGNVLLLCFFVFFIFGIVGVQWAGLLNR 240
Db 181 TVRVLRPLRAINRVPVSMRIIVTLTLLDTPMLGNVLLLCFFVFFIFGIVGVQWAGLLNR 240
Qy 241 CFLPENSLPLSDLEPYQTENEDESFFICSQPRENGMRSCRSVPTLRGGGGPPCGL 300
Db 241 CFLPENSLPLSDLEPYQTENEDESFFICSQPRENGMRSCRSVPTLRGGGGPPCGL 300
Qy 301 DYBAYNSSNTTCVNNQYTNCSAGHNPFKGAINFNDNIGYAWIAIPQVITLGGVDIM 360
Db 301 DYETYNSSNTTCVNNQYTNCSAGHNPFKGAINFNDNIGYAWIAIPQVITLGGVDIM 360
Qy 361 YFVMDAHSFYNYFILLIIVGSPFMINLCIVATOPSETKQESOLMRBQRYRELSNA 420
Db 361 YFVMDAHSFYNYFILLIIVGSPFMINLCIVATOPSETKQESOLMRBQRYRELSNA 420

Db 361 YFVMDAHSFYNYFIYILLIIVGFFYMINCLVVIATQFSETKQRESQLMREORVFLSNA 420
Qy 421 STLASFEPGSCVEELLKYLIVYILRKAARLAQVSRAGVYRGLSSPAPLGGQETQPS 480
Db 421 STLASFEPGSCVEELLKYLIVYILRKAARLAQVSRAGVYRGLSSPAPLGGQETQPS 480
Qy 481 SCRSRRLSVHLLVHHHHHHHHYHNGTLLRAPRASPEIQORDANGSRRLMLPPSP 540
Db 481 SCTRSRRLSVHLLVHHHHHHHHYHNGTLLRAPRASPEIQORDANGSRRLMLPPSP 540
Qy 541 ALSGAPGGAESVHSFVHADCHLEPVRCQAPPRSPSEASGRIVGSGKYVTVHTSPPE 600
Db 541 TPGGPPRGAEVHSFVHADCHLEPVRCQAPPRSPSEASGRIVGSGKYVTVHTSPPE 600
Qy 601 TLKELAVEAASGPPTLSNLIPPGYPMHKLLETOGTGACQSSCKISSPCLKADSG 660
Db 601 ILKDKALVEVAPSGPPTLSNLIPPGYPMHKLLETOGTGACQSSCKISSPCLKADSG 660
Qy 661 ACPDSCPYCARAGAEVADREMPDSDSEAVYFTQDAQHSDLDRPHS-RRQRSIGPD 719
Db 661 ACPDSCPYCARAGAEVADREMPDSDSEAVYFTQDAQHSDLDRPHS-RRQRSIGPD 720
Qy 720 AEPSSVLAFLWLI CDTRFKIVDSKYFGRGIMIALVNTLSMGIEYHQPBEELTNALEISN 779
Db 720 AEPSSVLAFLWLI CDTRFKIVDSKYFGRGIMIALVNTLSMGIEYHQPBEELTNALEISN 780
Qy 780 IVFTSLFALEMLKLLVYTPGPGYIKNPYNIPDGVIIVISVWEIVGQGGGLSVLRTFLM 839
Db 780 IVFTSLFALEMLKLLVYTPGPGYIKNPYNIPDGVIIVISVWEIVGQGGGLSVLRTFLM 840
Qy 840 RVKLAVRLPALORQLVLMKTMNDVATFCLMLLFIPIFISILGMHLFGCKFASERDGT 899
Db 840 RVKLAVRLPALORQLVLMKTMNDVATFCLMLLFIPIFISILGMHLFGCKFASERDGT 900
Qy 900 LPDRKNFDSLWAIYVTFQILTOEDWKNVLYNGMASTSSWAAALFIALMTFGNVLNLL 959
Db 900 LPDRKNFDSLWAIYVTFQILTOEDWKNVLYNGMASTSSWAAALFIALMTFGNVLNLL 960
Qy 960 VAILVEGFOAEISKREDAAGQLSCIQLPVDSQGDANKSESEPFPSLDGDRKCC 1019
Db 960 VAILVEGFOAEISKREDAAGQLSCIQLPVDSQGDANKSESEPFPSLDGDRKCC 1019
Qy 961 VAILVEGFOAEISKREDAAGQLSCIQLPVDSQGDANKSESEPFPSLDGDRKCC 997
Db 961 VAILVEGFOAEISKREDAAGQLSCIQLPVDSQGDANKSESEPFPSLDGDRKCC 997
Qy 1020 LALVSLGEHPELRKLLPLLIHTAATPMSPKSTGTGLGALGPASRRTSSGSAEPGA 1079
Db 998 LALVSLGEHPELRKLLPLLIHTAATPMSPKSTGTGLGALGPASRRTSSGSAEPGA 1057
Qy 1080 A-HEMKSPSARSSPHSPSAASSWTSRRSNSI GRAPSLKRRSPGERSLLSGEQE 1138
Db 1058 AHHEMKCPSPSARSSPHSPSAASSWTSRRSNSI GRAPSLKRRSPGERSLLSGEQE 1117
Qy 1139 SQDEESSSEERASPAAGSDHRRHSGSLEREAKSFDLPDTLQVPGHRTASGRGSAEHQD 1198
Db 1118 SQDEESSSEERASPAAGSDHRRHSGSLEREAKSFDLPDTLQVPGHRTASGRGSAEHQD 1177
Qy 1199 CNKGSASGRALRALRPPDPLDGDADDGNSLKGEPVAMIRARLPACYLERSDSWYI 1258
Db 1178 CNKGSASGRALRALRPPDPLDGDADDGNSLKGEPVAMIRARLPACYLERSDSWYI 1237
Qy 1259 FPQSRRLCHRIITHKDFHVLVLIIFLNCITTIAMERPKIDPHSAERIFLTLSNYIFT 1318
Db 1238 FPQSRRLCHRIITHKDFHVLVLIIFLNCITTIAMERPKIDPHSAERIFLTLSNYIFT 1297
Qy 1319 AVFLAEMTVKVALGWCFCGQAYLRSSWNVLDGLLVLISVIDILVSWSDSGTKILGMLR 1378
Db 1298 AVFLAEMTVKVALGWCFCGQAYLRSSWNVLDGLLVLISVIDILVSWSDSGTKILGMLR 1357
Qy 1379 VLRLRLRLRLRVISRAQGLKLVVETLMSLKPIGNIVVICCAFFIIFGILGVQLFKGKF 1438
Db 1358 VLRLRLRLRLRVISRAQGLKLVVETLMSLKPIGNIVVICCAFFIIFGILGVQLFKGKF 1417
Qy 1439 FVCGEDTRNITNKSDCAEASYRWRHRYNFNDLGOALMSLFLVLSKDGWDMYDGLDA 1498
Db 1418 FVCGEDTRNITNKSDCAEASYRWRHRYNFNDLGOALMSLFLVLSKDGWDMYDGLDA 1477

Qy 1499 VGVDQQPIIMHNPMWLLYFISFLLIIVAFVLMFVGVVVENFHKCRQHOOEERREK 1558
Db 1478 VGVDQQPIIMHNPMWLLYFISFLLIIVAFVLMFVGVVVENFHKCRQHOOEERREK 1537
Qy 1559 RLRLREKRR-----KAOCKPYSDYSRFRLLVHLLCTSHYLDLFTIGVIGLVVVTMA 1611
Db 1538 RLRLREKRRSKEQMAEACKPYSDYSRFRLLVHLLCTSHYLDLFTIGVIGLVVVTMA 1597
Qy 1612 MEHYQOQIILDEALKICNYIFTVIFVLESVFKLVAFGFRFFQDRWNQDLAIVLJSLMG 1671
Db 1598 MEHYQOQIILDEALKICNYIFTVIFVLESVFKLVAFGFRFFQDRWNQDLAIVLJSLMG 1657
Qy 1672 ITLBEIEVNASLPINPTIIRIMRVLRIARVLKLLKMAVGRALLDTVMQALPOVGNLGL 1731
Db 1658 ITLBEIEVNASLPINPTIIRIMRVLRIARVLKLLKMAVGRALLDTVMQALPOVGNLGL 1717
Qy 1732 FMLFFFAALGVELFGDCEDETHPCGELGRHATFRNFGMAFLTLFRVSTGDNWNGIMK 1791
Db 1718 FMLFFFAALGVELFGDCEDETHPCGELGRHATFRNFGMAFLTLFRVSTGDNWNGIMK 1777
Qy 1792 DTLRDCDOESTCYNTVISPIYFVSFVLTAQFVLNVNVIAMKHLSESNKEAKEAELEA 1851
Db 1778 DTLRDCDOESTCYNTVISPIYFVSFVLTAQFVLNVNVIAMKHLSESNKEAKEAELEA 1837
Qy 1852 ELELEMKTLSPQHPSPGLSPFLMPCGVEGSDSPDKPCALHPAAHARSASHFSLHPTMQ 1911
Db 1838 ELELEMKTLSPQHPSPGLSPFLMPCGVEGSDSPDKPCALHPAAHARSASHFSLHPTMQ 1897
Qy 1912 PHPTLPL--GPDLLTVRKSGVSRTHSLPNDSYNCRHGSTAEGPLHGRWGSLPQAQSGSV 1968
Db 1898 PHPEEVPVLGPDLLTVRKSGVSRTHSLPNDSYNCRHGSTAEGPLHGRWGSLPQAQSGSV 1957
Qy 1969 LSVHSPQADTSVILQPKADPHLQPHSAPTWTGIPKLPGRGSLAQORPLRRQAIRTD 2028
Db 1958 LSVHSPQADTSVILQPKADPHLQPHSAPTWTGIPKLPGRGSLAQORPLRRQAIRTD 2017
Qy 2029 SLDVQGLGSRDLLEAVSGSPPLARAYFWGQSTQAQHSRSHSKISKHMTTPAPCPG 2088
Db 2018 SLDVQGLGSRDLLEAVSGSPPLARAYFWGQSTQAQHSRSHSKISKHMTTPAPCPG 2077
Qy 2089 PEPNKGKPPETRSSLELDELTELDELTELDELTELDELTELDELTELDELTELDELTEL 2148
Db 2078 LEPNKGKPPETRSSLELDELTELDELTELDELTELDELTELDELTELDELTELDELTEL 2136
Qy 2149 SWLDEQRHRSIAVCLDSCSQHGLTDPNSIGQPLGPGSPKPKLAPPSITIDPPESQ 2208
Db 2137 FWLDEQRHRSIAVCLDSCSQHGLTDPNSIGQPLGPGSPKPKLAPPSITIDPPESQ 2196
Qy 2209 GPRTPSPGICLRRRAPSSDSKDPPLASGPPDMSAASPSPKKDVLSGLSSDPADLDP 2266
Db 2197 GSRPPCPGVCLRRRAPSSDSKDPPLASGPPDMSAASPSPKKDVLSGLSSDPADLDP 2254

RESULT 2

Ti5838
hypothetical protein C54D2.5 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 17-Mar-2000
R:Minx, P.
submitted to the EMBL Data Library, October 1995
A:Description: The sequence of C. elegans cosmid C54D2.
A:Reference number: Z18415
A:Accession: T15838
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-1657 <MIN>
A:Cross-references: EMBL:U37548; NID:g1017804; PID:g1017809; PIDN:AAA79201.1; CESP:C54D2
C:Genetics:
A:Gene: CESP:C54D2.5
A:Introns: 40/2; 67/3; 86/3; 121/2; 199/3; 230/2; 308/2; 334/2; 439/3; 470/3; 513/3
C:Superfamily: sodium channel protein

Query Match	29.9%	Score 3564.5	DB 2	Length 1657
Best Local Similarity	42.2%	Pred. No. 6.5e-210		
Matches	822	Conservative 231	Mismatches 430	Indels 465
Gaps	50			
Qy	15	QPRSFMRNLDSGAGGRPG-----PGSAEKDPG-----SADSEA	48	
Db	56	QSQSTRRHEDVEALGSIEGSKETQLSHGRLASSEASPSRWGRQIEWGNEEQIBES	115	
Qy	49	EGLPYPALAPVVFYFLSQDSRPSRWCLRTVCNPPFERISMLVILNCVTLGMFRCEP-I	107	
Db	116	E-LPYGFAEPALRCFYQARPPRKWALQWMSWPFDRITMAVIMINCVTLGMRECEQDP	174	
Qy	108	ACDSQRCRILLOAFDDFIPAFPAFVEMVVKVVALGIFGKKCYLGDTWNRLLDFFIVIA	167	
Db	175	DCDYRCQILDIIDNCIFVYFAFEMVIKIMALGFYGPAAVMSDTWNRLLDFFIVMAGIA	234	
Qy	168	SLDLQ---NVSFSAVRTVRLPLRAINRVPMSRILVTLTLLDITLPMIGNVILLCFEVP	224	
Db	235	VLHEYLGGINLTAIRTVRLPRAVNRIPMSRILVNLLLDITLPMIGNVILLCFEVPFI	294	
Qy	225	FGIVGVOLWAGLLNRCP--LPENFS-----LPLSVDLERYVOTENEDBSPICSQP	277	
Db	295	FGIVGVOLWAGLLNRCPVNIPLKTIENQSALFNNVKLTRFYIPE-DTSLVYICSPDAN	353	
Qy	278	GMRSCRSVPTLRGDDGGPPCGLDYEAYNSSNTTCVNMNQYTYNCASG-----	326	
Db	354	GLHTCSNLPPTVD--GVKCNLTLDYDKVTNDSINNVIYNECQVNIYPSLMTIAIS	410	
Qy	327	-----EHPKPGAINFENIGYAMIAIPQVITLEGWDMITFVMDAHGFYFIYILLI	380	
Db	411	CFIKVMQRNPPQGSVFNIGFAWVAIEPLVLSLEGWTDIMTVYQDAHFMMWIVFVLL	470	
Qy	381	VGSFPMNLCLAVLATQFSETKORESOLMRQRVFLSNASTLAFSPG-----S	431	
Db	471	IGAEMNLCLUVIATQPAETKRRETERMLQRKMLNRDSISCTGSGIGASSKEEGDT	530	
Qy	432	CYBELLYVYLKKAARLQAQVRAAGRVYGLLSSPAPLGGQETQPSSCSRSHRLSV	491	
Db	531	VYAAVFRFIGHTFR--TKRAAKKYTYAWE--	560	
Qy	492	HHLVHHHHHHHHVHLNGTTLRAPASPEIQORDANGSRRLMLPPSTPALSGAPPGAE	551	
Db	561	-----RAERKSSERQOR-----RKSKLDOMAT--LS-----	584	
Qy	552	SVHSFYHADCHLEPVRQAPPPRSPSEASGRTVSGKYYPTVHTSPPTLKEKALVEVA	611	
Db	585	-----RIEKADE-----	593	
Qy	612	ASSGPPTLTSLNIPPGYPSSMHKLELTQSTGACQSSCKI--SSPCLKADSGAGCPD	670	
Db	594	--EDETITREN-----GDDQIEQNGDGVRIKRVKIEEPKIKGN--GNSNGHY	640	
Qy	671	ARAGAGEVELADREMPDSDSEAVYFTQDAHSDLRDPHSRRQRGLGPDAPSSVLAF	730	
Db	641	KHSSSDE-----ESDEGDEQVYDGEAAKKGS-----TPSKL--NW-	675	
Qy	731	LI CDTPRKIVDSKYFGRGIMAILVNTLSMGIEYHEQPELTNALEISNIYFTSLFA	790	
Db	676	-FREKI QKFVTCDFHTRGILVAILNTLSMGVEYHQQPEILTVILEYSNLFTPALF	734	
Qy	791	LLKLLVGPFGVYKPNPYNIPDGVIVISVWEIVGQGGGLSVLRTFLMRVLKLVRLPA	850	
Db	735	LLKIIASGLFGYLDGFMFLPDGIVALSULEFQEGKGGLSVLRTFLRLIKLVRFMPA	794	
Qy	851	LQRQLVLMKTMNDNVATFCMLLMFIFIFISILGMHLFGCKFASERD--GDTLP--	905	
Db	795	LRYQLVLMRLTMDNVTVFGLLVLFIFIFISILGMNLFGCKFCVKEKFLGGLAKKER	854	
Qy	906	FDLSLLWALVTVQILITQBDWKKVLVNGMASTSSWAALYFIALMTGNVFLNLLVA	965	
Db	855	FDTLWALITVFQILITQBDWMMVLFNGMAQTNPAALYFVALMTGNVYLFNLLVA	914	

RESULT 3

A42566

omega-conotoxin-sensitive N-type calcium channel alpha 1B-1 subunit (alternatively spliced)

C,Species: homo sapiens (man)
C,Date: 04-Mar-1993 #sequence revision 18-Nov-1994 #text change 13-Sep-1998

C: Accession: A42566

C; Accession: A1350
R; Williams, M.E.; Brust, P.F.; Feldman, D.H.; Patthi, S.; Simeron, S.; Maroufi, A.; McC
Science 257, 389-395, 1992

A;Title: Structure and functional expression of an omega-conotoxin-sensitive human N-type
A;Reference number: A42566; MUID:92335886; PMID:1321501
A;Accession: A42566
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid
A;Residues: 1-2339 <MIL>
A;Experimental source: IMR32, hippocampus
A;Note: sequence extracted from NCBI backbone (NCBIP:109168)
C;Superfamily: voltage-dependent calcium channel protein alpha-1 chain

Query Match 14.7%; Score 1746.5; DB 2; Length 2339;
Best Local Similarity 24.2%; Pred. No. 2.2e-38;
Matches 641; Conservative 361; Mismatches 823; Indels 819; Gaps 86;

QY 27 GAGRPGGSAEKPDSADSEAGLPALAPVVF-----FYLQDSRP 70
DB 25 GAGAGGPGGLOGQGVLYKQIAQRATMALNPIPVKQCNFTNRSFLVSESDNVV 84
QY 71 RSWCLRTVCNPFWRISMLVILLNCVTILGMFRPCEDACSQRILQAFDD---FIFAF 127
DB 85 RYAKRITWPPFETMILATIANCIVAL-----EQHLPDGDKTPMSERLDDTEPIGI 140
QY 128 FAVEMVQWVALG-IFGKKCYLGDWNRDPIVIAGMLEYs---LDLQNVFSAVRTVR 183
DB 141 FCFEAGIKIILGFFHKGSLRGNWMDVVLVTGLATAGTDFDLR-----TLRAVR 195
QY 184 VLRLPRAINRVPSMRILVTLLDTPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRNCFL 243
DB 196 VLRLPLKVGIPSLQVLKSIKAMVPLQIGLLFFAILMFAIGLEFYMGFKHACF- 254
QY 244 PENFSLPLVDLERYQYOTENEDESPFCQSPRENGMRSCRVPILRGDGGGPGGLDYE 303
DB 255 -----PNSDTAE-----PV-----GDFPCQKEAP 273
QY 304 AYNSSTNTCVNWNQYVNCSSAGEHNPFGKAINFNIGYAMIAIPQVITLGGWDIMYFV 363
DB 274 ARLCBGDTEC---REYWP-----GNFGITNFDNILFAITVQCITMEGWDILYNT 323
QY 364 MD-AHSFNFIPIILLIIVGSPFMNLCLVVIATOFSTKORES-----OLMREQVRVF 416
DB 324 NDAAGNTWNLVPIPIIIGSPFMNLNLVGLVUSGEFAKERERENRAFLKLRQOQIE- 382
QY 417 LSNASTLASFSEPGCYEBELLYVYLKKAARLQVSRAGVRVGLLSSPAPLGGQET 476
DB 383 -----RELNGYLEWIFKAAEEMLAEDRNA-----BEK 410
QY 477 QPSSSCSRSHRRLSVHHLVHHHHHHHNGTLRAPRASPEIQDRDANGSRRLMLPP 536
DB 411 SPLDVLKRAATKKSRNDLTH-----AEEGEDRAD----- 440
QY 537 PSTPALSGAPPGGAESVHSFYHADCHLEPVRQAPPPSPSPSEASGRTVGSGKVPYTVHTS 596
DB 441 ----- 440
QY 597 PPPETLKEALVEAASSGPPTLTSLNIPPGPYSSMHKLETTQSTGACOSSCKISSPCLK 656
DB 441 -----LCAGSGPPAR 450
QY 657 ADSGACGPDSCPYCARAGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHSRQSL 716
DB 451 ASLKSQGTESSTSPRR-----KKNFRF----- 473
QY 717 GPDAEPSVLAFWRILICDTRFKIVDSKYFGRGIMAILNLTSLNGLEYHEQPELTNALE 776
DB 474 -----FIRRMVKAQSFYMWVLCVVALNTLCVAMVYNQPRRLTTLTY 515
QY 777 ISNIVFTSLFALEMLKLVVGGPYLKNPYNIPFDGVIVVISVMEIVG---OQGG--GLS 831
DB 516 FAEFVFLGLFTELSLKMVGLGPRSYFRSFCNCFDGVIVGSEFVVAIAIKPGSGFIS 575
QY 832 VLRLPRLMVLKLVFLPALQQLVLMKTMNDNVATFCMLIMLFIPIFSLIGHMLFGCKF 891
DB 576 VLRLALRLILRFKVTKYWSSLRNLVNLVSLNSMKSIISLLFLFLFVIVFALLQMLFGGQF 635

QY 892 ASERDGDTPDRKNFDSLLWAIWTVFQILTOEDMNKVLNGM-----ASTSSWAAIFYTA 946
DB 636 NFQDETFP-----TNFDTFFPAALITVQILTGEDWNAVYHGIESQGVSKGMFSSFYFV 691
QY 947 LMTFGNYVLFNLVAILVEGF-QAEISK-----REDASGQ-----LSCIQ 986
DB 692 LTLFGNYVTLNLVLAIVADNLANAQELTKDEEEMEEAANOKALQAKAEVAEVSFSAAN 751
QY 987 LPVDSQGDANKSESEPDFFPSIDGDRKKCLALVSLGE-----HPELRK 1033
DB 752 ISIAAROONSAKASVWEQASQLRLQNLRASCEALYSEMDPEERLRFATTRLRDMKT 811
QY 1034 SLLPLLIHTAATPMSLP-----KSTSTGLGEALGPASR-----RTSSSG----- 1073
DB 812 HLDRLVVELGRDARGVGKARPEAAEAPGVDPPIRRHHRDKDKTPAAGDQDRAEA 871
QY 1074 -----SABPGA-----AHMKSPPSARS-----SPH-----SPWSAASSW 1103
DB 872 PKAESGEFGAREERPRPHRSHSKEAAGPPARSRGRGPGEGRRHRRHRSPEEAAERE 931
QY 1104 TSR-RSSNSLGRAPSLKRRSPGERRSLLSGEGQESQDEEESER-----ERASP- 1153
DB 932 PRHRAHRI---QDPSKECAGKERRARHRRGPRAGPREAESGEEPARHRAHKAOPA 989
QY 1154 -----AGSDHHRGSLEREAKSFDLPDTPQLVGLHRTASGRG 1191
DB 989 HEAVEKETTEKEATEKEAEIVEADKEKELRNQHPREHCDLETSGTIVTVPMTLPSTCL 1048
QY 1192 SASEHQDCNGKSASGLARALRPDDP-----PLDGDADDDEGNI---SKGER- 1235
DB 1049 QKVEQPEDADNQRNVNRMGSPDPDPTIVHPVMTLGLGEATVPSGNVDLSQAEQK 1108
QY 1236 -----VRAMIRARLPACYLERSWSAYIFPPQSRFELLCHRIITHKMFHDVVLVIIF 1287
DB 1109 KEVEADDNRSGRPPIVPS-----SMFCLSPNLLRRFCHYIVTVRYEVLVIVIA 1161
QY 1288 LNCITITAMERPKI DPHSAERI FLTSLNYITFAVFLAEMTVKVALGWCFCGQAYLRSSWN 1347
DB 1162 LSLIALAADP-VRTDSPRNALKYLDYIFTGVTFFEMVIMKIDLGLLHFGAVFRDLWN 1220
QY 1348 VLDGLVLVLSVIDILVSMV-SDSGTKILGMLRVLLRTLRPLRVISRAQGLKLVETLM 1406
DB 1221 ILD-----FIVVSGALVAFAPSGSGKGDINTIKSLRVLRVLRPLKTIKRLPKLKA VDCV 1276
QY 1407 SSLKPIGNIWICCAFIIFGILGVQFKGFVQGE-----DTRN--INKSDCABA 1458
DB 1277 NSLKNVLNIIIVYMLFMFIPAVIAVOLFKGKFFCTDESKELERDCRGGLDYEEKEVEA 1336
QY 1459 SYR-WVRHKTNFDNLQALMSFLVASKDGVDDIMYDGLDVGVDQOPIMNHNPMWLLYF 1517
DB 1337 QPRQWKYDHYDNVLWALLTLFTVSTGEGWPMVLKHSVDATYEEQSPSGYRMELSIYF 1396
QY 1518 ISPLLIVAFVFLNMFVGVVVENFHKCRQHEEAREERREKRLRLEKERRKA-----QC 1572
DB 1397 VYFVFWPPFFNIFVALIIITF-----QEQDKWSE-----CSLEKNERACIDFAISA 1446
QY 1573 KPY--YSDYSR--FRLIVHHLCTSHYLDLFIITGVIGLVNVTWAMEHYQOQILDEALKIC 1628
DB 1447 KPLTRYMPQNRQSFQYKTYTWFVSPPEYFIMAMIALNTVLMKFDYAPYEYELMLKCL 1506
QY 1629 NYITFTVFLVESVKLVAFGRFRFPQDRWNQDLAIVLLSIMGITILEEI-EVNASLPINP 1687
DB 1507 NIVFTSMFSMECVLIIAFGLVNYFRDAMNVFVTVLGSITDILVETIAETN-----NF 1561
QY 1688 TIIRIMRVLRARVLKLLKMAVGRALLDTVMQALPOVGNLGLLMLLFFIFALGVELF 1747
DB 1562 INLSFLRLFRARLILKLRQGYTIRILLWTFSQKALPYVCLLIAMLFFIYAIIGQVF 1621
QY 1748 GDLCEDETHPCEGGRHATFRNFGMAFLTIFRVSTGDNWNGIMKDTLRD--CDOE--STC 1803
DB 1622 GNIALDDD---TSINRHNFTFLOALMLLFRSATGEAWHEIMLSCLSNQACDEQANATE 1678

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QY 1804 YNTVISPIYFVSFLTAQFVLNVVIAVLN-----KHEE----- 1838
Db 1579 CGSDFAIFYVFSFLCSFLNLFVAVIMDNFYLTRDSSILGPHHLDPIRWAEYDP 1738
QY 1839 ----- 1838
Db 1739 AACGRISYDNWFEMLKHSPLGLGKPCPARVAYKLVLRNMNMPISNEDMTVHFTSLMAL 1798
QY 1839 -----SKEAKEBAEAELEMKLTUSPOPHPLGSPFLWPVGEGDSDSP 1886
Db 1799 IRTALEIKLPAQTKQCHQDAELKEISVWVANI-PQKTLDDLVP-----PHKPEDEM 1849
QY 1887 KPGALHPA-----AHARSASHFSLHPTM-----OPHPTLPQPD 1921
Db 1850 TVGKYAALMIFDYKONKTRTDMQOAPGCLSQMGVSLFHPKATLEQTQPAVLRGAR 1909
QY 1922 LLTVRKSGVSRTHSLPNDSYNCRHGSTAEGPLGRHGMGLPKAQSGSVLSVHSQPADTSYI 1981
Db 1910 VFLRQKSSLSLN-----GGAIQNOESGIKESV-----SMQ 1940
QY 1982 LQPKDAPHLLQPHSAPTWTGTPKLPPGRSPLAQRPLRQAAIRTSLSLVQGLSRE-- 2039
Db 1941 TORTQDAPHEAR-----PPLERGHSTEIFVGRSGALAVD-VOMQSITRRQPD 1986
QY 2040 -----DLAEVSGSPPLARAYSFWGOSSTQAOQHSHSHKISK-----HM---TPAPC 2086
Db 1987 QEPQGLSQQRAASMPRLAAET---QPVTASPMKRSISTLAQRGTHLCSTTPDRPP 2043
QY 2087 PG-----PEPNWKGPPETTRSSLELDTLSWTSGLDPLPGGQEEPPSP 2129
Db 2044 PSQASSHHHRRCHRRDRKORSLEKGP---SLSDMDGAPSSAVGFLPG--EQPTQC 2098
QY 2130 RDLKKCVSAQSCQRR-PTSWLDQRHSHIAVCLDSG-----SQPHLG 2173
Db 2099 RRERRERQGRSGRQERQSSSEKQRF---YSCDRFGREGPPKPKPSLSHPTAG 2155
QY 2174 TDP-----SNLGGQPL-----CGPGR---PKKLS-PSITIDPES-----Q 2208
Db 2156 QEPGPHPGSGSVNGSPLLSTSGASTFGRRQORLPQTPTPRSITYKTANSPIHFAQ 2215
QY 2209 GPRTPP---SPG-----ICLRRAPSSDSKPLASGPPDSMAASPSKKOVLSSLGL 2257
Db 2216 AQTSLPAPSGRLSRLSEHNALLQRPDS---QPLAPG-----SRI 2254
QY 2258 SSDP 2261
Db 2255 GSDP 2258

RESULT 4
T45115
N-type calcium channel alpha-1 chain, omega-conotoxin-sensitive [imported] - human
C;Species: Homo sapiens (man)
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
C;Accession: T45115
R;Williams, M.E.; Brust, P.F.; Feldman, D.H.; Patthi, S.; Simerson, S.; Maroufi, A.; McC
Science 257, 389-395, 1992
A;Title: Structure and functional expression of an omega-conotoxin-sensitive human N-type
A;Reference number: A42566; MUID:92335886; PMID:1321501
A;Accession: T45115
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-2237 <MIL>
A;Cross-references: UNIPROT:Q00975; EMBL:M94173; NID:g179759; PIDN:AAA51898.1; PID:g1797
A;Experimental source: cell line IMR32; neuroblastoma
C;Genetics:
A;Note: CCHL1A2
C;Function:
A;Description: calcium influx
C;Superfamily: voltage-dependent calcium channel protein alpha-1 chain

Query Match 14.6%; Score 1741; DB 2; Length 2237;
Best Local Similarity 24.1%; Pred. No. 4.6e-96;
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Matches 629; Conservative 361; Mismatches 836; Indels 780; Gaps 80;
QY 27 GAGRPGPGSAEKDPGSADSEAEGLPYDALAPVVF-----FYLSQDSRP 70
Db 25 GAGGAGPGPGGLQPGQGVLYKQSIQAQARTMALNPIPVKQNCFTVNRSLFVSFSDNV 84
QY 71 RSWCLRTVCNWPWERISMLVILLNCVTLGMRPCEDIACQRCRILQAFD---FIFAF 127
Db 85 RKAKRITETPPPEYMTLATIANCIVAL---EQHLPGDKTTPMSERLDDTTPYFTGI 140
QY 128 FAVEMVVMKVALG-IFGKCKVLDGTWNRLDFFIVIAGMLEYS---LDLQNVSFSAVRTVR 183
Db 141 PCFEAGIKIATGALGFVFKHGLRVNWMDFVVLVLTGILATAGTDFDLR-----TLRAVR 195
QY 184 VLRLPRAINRVPNRILVLTLLDTPMLGNVLLCFFVFFIFGVQVQLWAGLRNRCFL 243
Db 196 VLRLPLKLVSGIPSLQVVKLSIMKAMVPLQLGILLFPAILMFAIIGLEFYMGKFKACF- 254
QY 244 PENFSLPLSVDLERYQTENEDESFFICSQPRENGMESCVRPTLRGDGGGPPCGLDYE 303
Db 255 -----PNSTDAB-----PV-----GDFPCGKEAP 273
QY 304 AYNSSTTTCVNNQYVTCNSAGEHNPFGKAINFDNICYAWIAIFQVITLEGWVDIMYFV 363
Db 274 ARLCGEGTEC---REYWP-----GNFGITNFDNILFALLTVFQCITWEGWTDILYNT 323
QY 364 MD-AHSFNYFIYFILLIIVGSPFMINCLVVIATQSETKQRES-----OLMREQVRVF 416
Db 324 NDAAGNTWNLYPIPLIIIGSFMLNLVLGSLGEFAKERERVENRRRAFLKLRQQQIE- 382
QY 417 LSNASTLASSEPGSCVEELLKVLVYLTKAARLAQVSRAGVVRVGLLSPAPLGGQET 476
Db 383 -----RELNGYLEWIFKAEVVMLEEDRNA-----EEK 410
QY 477 QPSSSCSRSHRRLSVHHLVHHHHHHHHHGLNGTLRAPRASPIQRDANGSRRLMLPP 536
Db 411 SPLDVLKRAATKSRNDLIH-----AEGERDPAD----- 440
QY 537 PSTALSGAPPGGAESVHSFYHADCHLEPVRCQAPPRSPSEASGRTVGSKVYPTVHTS 596
Db 441 ----- 440
QY 597 PPETLKEKALVEVAASSGPPTLTSLNIPGPYSSMHKLELTQSTGACQSCSKISSCLK 656
Db 441 -----LCVGSFPAR 450
QY 657 ADSGACGPDSCPYCARAGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRPHRRQRS 716
Db 451 ASLKSGETESSYFRR-----KEMFRP----- 473
QY 717 GPDAEPSSVLAFWRLICDTPRKIVDSKYFGRGIMAILVNTLSMGIEYHQEELTNALE 776
Db 474 -----FIRRMVKAQSFYVWVLCVVALNLTCLVAMVHYNQPRELTTLY 515
QY 777 ISNIVFTSLFALEMLKLLVYGPYIKNPYNIFDGVIVVLSWEIVGQ-----QGGLS 831
Db 516 FAFBFVLGLFTEKSLKMYGLGRSFRSFCDFGVIVGSEFVWMAIKPGSSFGIS 575
QY 832 VLRTFRLMRVLKVRFLAPQROLVLMKTMNDVNATFCMLLMPLFIFFISILGMHLFGCKF 891
Db 576 VLRAALRLRLRFKTKYWSLSRLNVLSNMSKSIISLLFLLFVIVFALLGMQLFGQGF 635
QY 892 ASERDGTLPDRKNFSLMLWAVTVFOILTQEDWNKVLNYGM-----ASTSSMAALFYIA 946
Db 636 NFQDETPT---TNFDTFPAALITVFOILTGEDWNVAMVHGIESQGVSKGMFSSFYFIV 691
QY 947 LMTFGNYVLNLLVALIVEGF-QAEEISK-----REDASGQ-----LSCIQ 986
Db 692 LTLFGNYTLNVLNVLATAVDNLANAQELTKDEEEMEAANKLQAKAEVAEVSFMSAAN 751
QY 987 LPVDSOGGDANKSESEPDFFPSPLDGDGDRKCKLALVLSGE-----HPSLRK 1033
Db 752 ISTAARQONSAKARSVWEQARSQRLQLNLRASCEALYSEMDPEERLRFATRHLPDPKT 811
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[illegible]

D	b	1032	TGVGSLHMLPSTCLQKVDEQP----	EADNQNVTRMGSQSPDSTTHVVPVLUTLPPGSA	1089
Q	y	1236	-----VRAMIRARLPACYLERDSWSAYI---	FPPQSFRLL	1268
D	b	1089	TVVPSANTDLEGQAEGKKEAADVLRGRPRIVP-	YSSMFCGLSFTNLLRRF	1140
Q	y	1269	CHRIITHMPDHVVULVIIFUNCITIAMERPKIDPHSAERIPLTSLNWIFTAVFLAEMTVK	1328	
D	b	1141	CHVTVMRYEWMILVVIALSSIALAAED-VRTDSFRNALXMYDIETGTVEPTFMVK	1199	
Q	y	1329	VVALGWCGFGQAVLRSSNNVLDCGLLVLSVIDI-LYSMVSDSCTKLGLMWRLRLARTLR	1387	
D	b	1200	MIDLGLLLHPGAFRDUNWLDFTIVSGVALFAFASFSGGSKGDINTIKSLURVLURLVLR	1259	
Q	y	1388	PLRVISRAOGLKLVETLMSSLKPIGNIVVICAPFIIFCIGLVOLFPGKFVCQGE---	1444	
D	b	1260	PLTKIKELPKLKAVFDCVNLSKNVLNILVYMLFMFIEFAVIAVOLFKGFFVCTDESKE	1319	
Q	y	1445	---DTRN--ITNKSDCAEASR-VWRHKYNFDNLGOALMSLFVLASKOGWDIMYDGLDA	1498	
D	b	1320	LERCRCQYLDEYEKEEVAEQPRQKKKYDFHYDNVLWALLTLFTVSTGEGPMWLKHSVDA	1379	
Q	y	1499	VGVDOQIPNMHNPMULLFYFSILLIAVFAFLVMFVGUVVENPHKCKHQHOESEEARREEK	1558	
D	b	1380	TYEGSQSGPFMRMELSIFYVYVFVFPFFFVNIFVALIIITF-----OEQDKWNSE--	1431	
Q	y	1559	RLRLEKKRKKA-----OCKPY--YSDYSR-FRLLVHHLCISHYLDLFTITGVIGLVNVT	1609	
D	b	1432	--CSLEKNEACIDPAISAKPLTRYMPQNKSQFYKTWTFFVSPPEYFIMAMIALNTVV	1489	
Q	y	1610	MAMEHYOOQOILDEALKICNYIFTVIIFVLESVKFLVAFGRFRFPQDRMNOLDLAIVLLSI	1669	
D	b	1490	LMMKFYPADYEYELMKLCLNI VFTSMFSELCILKIITAFGLVNYFRDANWVDFPVTVLGSI	1549	
Q	y	1670	MGITLEIEVNASLPINPITIIRMVLRITARVLKLLKMAVGMBALLDTVMQALPOVGNLG	1729	
D	b	1550	TDILVTEIANF---IN---LSFLIRFRAARLIKCRQGYTIRILLWTFVQSFKALPYVC	1603	
Q	y	1730	LLFMLLFFIPAALGVDELGCDETHPCBCEGLGRHATFRNFGMAFUFLTFRVSTGDNWNGI	1789	
D	b	1604	LLTAMLEFFIYAIIGMQVFGNIALDDG---TSINHNNFRTFLQALMLLFRSATGEAWHEI	1660	
Q	y	1790	MKOTL---RDCD---QBSTCVNTVISFIYFVSFVLTAQFVLNVNVIIVLM-	1833	
D	b	1661	MLSCLGNRACOPHANASEC-GSDFAYFYFVSFTFLCSFLMLNLFAVINMDNFYLTRDSS	1719	
Q	y	1934	----KHLEE-----	1838	
D	b	1720	ILGPHHLDEFIRVWAEDYPAAACGRISYNDMFEMLKMSPPGLGKCKCARVAYKRLVRWN	1779	
Q	y	1839	---SNKE-----AKEBAELEAELEMKTL---SPQHSPL	1868	
D	b	1780	MPTSNDMTVHTFTSLMALIRTALEIKLAPAGTKQHQCDAELREKELSSWANLPKQLDL	1839	
Q	y	1869	GSPFLMFGVBGPDPSPKPGALHPA-----AHARSASH-----FSLBH	1907	
D	b	1840	LVP-----PHKPDENVKGYYAALMIWFDFYKQNKTTDRDTHQAPGGLSQMGPSVSLFH	1891	
Q	y	1908	PTM-----QPHPTELPGDDLTVKSGSVSRTHSLPNDSYMCRGSTAEGPLHRHGWLCPKA	1963	
D	b	1892	PLKATLEQTQPAVLARGARVELROKSAT-----SLSNGGAIQTQESGIKESL---SWGTQRT	1944	
Q	y	1964	QSGSVLSVHSQPADTSYLLQPKDAAPHLLQ-----PHSAPTWG-----TI	2003	
D	b	1945	Q--DVLYEARAPLERGHSAEIPVQGQCALADVQMOMTLRGPDGFQPGLESQGBRAAM	2002	
Q	y	2004	PKL-----PPPGRSP-----LAORPLRQAAIRTDSDLVOGLGSRBDLLAEVSGPSP	2051	
D	b	2003	PRLAAETQAPAPNASPMKRISITLAPRHGTQ-----LCNTVLDLRPPP	2044	
Q	y	2052	LARAYFWGOSSTQAOQHSHRSKISKHMTPPACPFGPENWKGKBPETRSSLJLDE---	2109	
D	b	2045	-----SQVSHHHHRRRRUK-----KQRSLEKGP-----SLSDVTEGA	2079	

2110 LSWISGDLPPGQOEPPRDLKKCYSEVAQCORRPTSMLEORRHSAIVSCLDGSG- 2168
2080 PSTAAGSGLPHG--EGSTGCRERKQGRGSOB-RKQPSSSSEKQRP---YSCDRFGSR 2133
2169 ----QPHLCTDP-----SNLGGQPL-----GGPSRPPKKLS 2196
2134 EPPQKESLSHSPISPTAALEPGHPQGSGSYNGSLMSTGASTPGRGRRQLPQTPLT 2193
2197 P-PSITIDPPES-----QGRTPP--SPG-----ICLERRAPSSDSKDPLASGPP 2238
2194 PRPSITYKTANSFVHFAEGSGGLPAFSPGRLSRGLSEHNALLQKEPLS---QPLASGR 2250
2239 ----DSMAASPSPKKVLSL-----SGLSS 2259
2251 IGSDFYLGQRLDSEASAHNLPEDTLTPEEAVATNSGRSS 2289

RESULT 6
S41080
calcium channel alpha-1 chain - mouse
C:Species: Mus musculus (house mouse)
C:Date: 07-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 17-Mar-1999
C:Accession: S41080
R:Coppola, T.; Waldmann, R.; Borsotto, M.; Heurteaux, C.; Romey, G.; Mattei, M.G.; Lazdu
RBS Lett. 338, 1-5, 1994
A:Title: Molecular cloning of a murine N-type calcium channel alpha-1 subunit. Evidence
A:Reference number: S41080; MUID:94139884; PMID:8307146
A:Accession: S41080
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-2288 <COP>
C:Superfamily: voltage-dependent calcium channel protein alpha-1 chain

Query Match 14.3%; Score 1706; DB 2; Length 2288;
Best Local Similarity 24.5%; Pred. No. 6.6e-96;
Matches 646; Conservative 363; Mismatches 802; Indels 828; Gaps 98;

27 GAGRGPGSAEKDPSGADSEAGLPYPALAPVVF-----FYLSDQSRP 70
25 GAGGAGGPGGGLPPGQRLYKQSTAQARATWALNPVVKONCTVRSFLVSEDNV 84
71 RSWCLTVNCPWPERISMLVILLNVTGLMFRPCEDACDSQRCRILQAFDD---FTAF 127
85 RKVAKRTEPPEYMIATIANCVIAL-----EQHLPDQKTPMSERLDDTEPYFTGI 140
128 FAVEMVVMVALG-IFGKKCYLGDWNRDLPFIVAGMLEYS---LDLQNVSFSAVRTVR 183
141 FCEPAGIKIILALGFVPHKGYLNGWNVMDFVVVLGTILATAGTDFDLR-----TLRAVR 195
184 VLRLPRAINRVPSMRILVTLTLLDPLMGLNVLCCFFVFIFGIQVGVQLWAGLLNRCLF 243
196 VLRLPLVGLIPSLQVVKIMKAMPVLLQIGLLFFAILMFGILGLEFYMGKFKACF- 254
244 PENFSLPLVDLERYQTEDESPFCQPRENGMRSCSVPTLRGCGGGPPCGLDYE 303
255 -----PNSITDE-----PV-----GFPCCGKDP 273
304 AYNSSNTTCVNNQYNTCSAGHNPFKGAINDNIGYAMIAIFQVITLEGWVDIMYFV 363
274 ARQCDGDTFC---REYWP-----GNFGITFDNLFALLVFCIIMEGWTDILYNT 323
364 MD-AHSFYNYFVILLIIVGFFMINCLVVIATQSETQKRS-----QLMREQVRVF 416
324 NDAAGTNWLYFPLIIIGSFFMLNLVLGLSGEFAKERERVENRAFLKLARQOIE- 382
417 LSNASTLASFSEPGSGEELLYLYILRKAARLAQVRAAGVRVGLLSSAPLGGQET 476
383 -----RELNGYLEWIFKAEVLMAREDKNA-----EEK 410
477 QPSSSCSRSHRLSVHHLVHHHHHHHHHHLNGTFLRAPRASPEIQDRDANGSRRLMPP 536
411 SPLDVLRKAATKKSNDLIH----- 430

537 PSTPALSGAPGCAESVHSFYHADCHLEPVRCAQAPPSPSEASGRVTGSGKVPYTVHTS 596
431 ----- 430
597 PPEETLKEALVEVAASSGPPTLTSINIPPGPYSSMHKLELTQSTGACOSSCKISSPCLK 656
431 -----AEEGEDRFVDL-----CAVSGPPAR 450
657 ADSGACGPDSCPYCARAGAGEVELADREMPDSDSEAVVEFTQDAHQHSLDRPHSRQRSL 716
451 ASLKSQGTSESSYFR-----KEKMPF----- 473
717 GPDAEPSSVLAFWRLICDTFRKIVDSKYFGRGIMIAILVNTLSMGIEYHEQEELTNALE 776
474 -----FIRMVKAQSFYVVVLCVVALNTLCVAMVHNQPORLITALY 515
777 ISNIVTSLFALEMLKLLVYGPYKPNYINFDGVIVVISVWEIVGQ-----QGGGLS 831
516 FAEFVFLGLFTEMSLKMYGLGPRSPYFRSFCDFGVIVGSIFFVWMAAKPGTSGFIS 575
832 VLRTFRLMRVLKVRFLPALQRLQVLMTMDNVATPCLMLMLFIFISILGMLFGCKF 891
576 VLRALELLRIKVKYWNLSRLNVLLNSMKSIISLLFLFLFVIVFALLGLQLEGGQF 635
892 ASERDGDTLPRKPFDSLLNAIVTVFOILTCEDMKNVLYNGM-----ASTSSWAALYFIA 946
636 NFQDETPT-----TIFDTFPAAILTVFOLLTGEDNNAVMYHIGIESQGGVSGKGMSSFFYFV 691
947 LMTFCNVYLVNLLVAILVEGF-QAEISK-----REDASGQ-----LSCIQ 986
692 LTLFGNYLLNVFLAIVADNLANAQELTKDEEEMEAANQKALQKAKEVAEVSPPMSAAN 751
987 LEVDQGGDANKSESEPPFPSPDLGDRKCKALVSLGE-----HPELRK 1033
752 ISIAAQONSA-KARSVWEQASQLQLNLASCSALYSEMDPEERLYASTHVRPDMKT 810
1034 SLLPLLIH-----TAA2PMS-LPK-----STSTGLGEALGPASR 1067
811 HMDRPLVVEPGDGLRGVGSKEPTEATESADLPRHHRDRDRTSATAPAGEQD 870
1068 RTSSGS-----APGAAHEMKSPS-----ARSSPSWMSAASSWTSR-----RSSR 1110
871 RTESTETPREERARPRRSHSKETFCADTVRCESRRHRRGSPPEATEPRCHRAH 930
1111 NSL-----GRAPSLKERSPSGERRSLLSGE---GOESQDEEESSEERASAPGSHRUG 1162
931 HAQDSKEGVTVPL---VPKGERARHGRPTGTPREANNRPTRRRA-----RHK- 979
1163 SLEREAKSFDPLDTLOVPLGHLRTASGRGSAHQDCNGKSASGLARALRDPDPLD-- 1220
980 -----VPPTLQPP---EREAAEKESNPVEGD-----KETRNHQKPEPHCDLE 1018
1221 -----GDADDEGNLSK-----GE 1234
1019 AIAVTVGVLHMLPSTCLQKVEQDEADNQRNVTMGSPQSPDPTTVHVPVTLTGPGE 1078
1235 R-----VRWIRARLPACYLERSWSAYIFPQOSRRLC 1269
1079 TPVVPNGMNLQAEQKKEAEADVLRRGPRPVPYS-----SNFCLSPNLFRRFC 1131
1270 HRIITHKMFHVVLVILFNCITIAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTKV 1329
1132 HVIYTMRYLEMLVILVIALSIALAEDP-VRTDSFRNNALEYMDYIFTGFTCEMVIMK 1190
1330 VALGWCFOEAYLRSSWNVDLGLVLISVIDILVSMV-SDSGTKILGMLRVLRLTRP 1388
1191 IDLGLLHPGAYFRDLWNILD---FIWSSGALVAFAGSGSKGDINTIKSLRVLRLP 1246
1389 LRVISRAQGLKLVWETLMSLSKPIGNLWVICCAPIIFGILGVOLFKEGFFVCOGE--- 1444
1247 LKTIKRLPKLXPFVDSVNVSLKNVILITVNLPMFIFAVIALQVLFKGFYCTDESKEL 1306

1445 --DTRN--ITNKSCABASR-WVRHKYKPNFDNLGOALMSFLVLSKDGWVDIMYDGLDAV 1499
1307 ERDCRGYLDYEKEVEAQPQWKIDYFDHVDNVLWALLTLFTVSTGSGWVWLKHSVDAT 1366
1500 GVDQOQIMNHPMMLLYFISLLIYAFVFLVMFVGVVFNFKCRQHQEERARRREKR 1559
1367 YEEQSPGPFMELSILYVVFVFPFFVNFVALIITP-----QEQGDKVMSB--- 1417
1560 LRLEKKRKA-----QCKPY--YSDYSR--FRLLVHHLCTSHYLDLFTIGVIGLNVVTM 1610
1418 -CSLEKNERACIDFAISAKPLTRYMPQKQSFQYKWTWTFVSPFPFIMAMIALNTVL 1476
1611 AMEHYQOQILDEALKCNLYFTFVLESVEKLVAFGRFRFODRWNOLDLAVLLSIM 1670
1477 MMKYDAPYEYELMKCLNIVFTSMFSECKILKIAAGVLNFDADWVDFVTVLGSIT 1536
1671 GITLEEI-EVNASLPINPTIIRIMRVLRIARVLKLLKMAVMGRALLPTVMQALPQVNLG 1729
1537 DILVTEAETN-----NFNLSPLRLFRAARLIKLLAQGYTIRILLWTFVQSPKALPYVC 1591
1730 LLFMLLFFIIPAAAGVELFGDLECDTHPCBGLGRHATFRFGMAFLTLFRVSTGDNNGI 1789
1592 LLIAMLPFIYAIIGMQVFGNSALDD--TSINRHNFRFTPLQAIMLFRSATGEAWHEI 1648
1790 MKDTL--RDGD--QESTCYNTVTSPIYFVSFVLTAQFVLNVVVIAMVLMKHLBESKEAK 1844
1649 MSLCLNDRACDPHANSEC-GSDPAYFYFVSFIFLCSFLMLNLVAVIMONFEVLTLDSS 1707
1845 -----EEAELEAELE-----LEM-KTILSPQHSPLGSPFLMPGVEGP--- 1880
1708 ILGPHLHDEFIRVWAEYDPAACGRISYNDMEMLKMSPP--PLGL-----GKKCPARV 1758
1881 -----DSGDSKPKGALH-----PAAH----- 1896
1759 AYKELVRMNPISNEDMTVHTSTLMALIRTALEIKLAPADEMTVGKVAALMIFDYKQ 1818
1897 --ARSASH-----FSLGHPTM---OHPHTLPGDLLTYRKSGVSTHSLPN 1938
1819 NKTRDTHQAPGLSGOMQPVSLFPLKATLEQTPAVLRGARVFLRQKSAF-----SLSN 1874
1939 DSYN--CRHGSTABGLCHRGW-----GLPKAQSGSVL--SVHSQPADT 1978
1875 GGAIQTQESGSRSCPGRRGTQDALYEGRAPLERSHKEIPVQSGTLLVDVQWQ--- 1930
1979 SYIQLPKDAPHLLOP--HSAPTWTGTPKL-----PPGSRPLAQRFLRQAAIRTDSDL 2031
1931 NMTLRGPDGP--QPGLESQGRASMLRLAAETQAPAPNASPMKR-----S 1973
2032 VQIGLSRED--LLAEVSGSPPLARAYSWFGQSSQTAQOQHSRSHSKISKHMTPPAPCPG 2088
1974 ISTLAPDGTQLCSTVLDLRRPP-----SQASHHHHHRCHRRDK----- 2013
2089 PEPNWKGPPTRSLELDTLSWISGDLAP--PGQGEPPSPRDLKKCYSVAEQSQRR 2146
2014 KORSLEKP-----SLSDVEGASTAAAGPLPHGSGSTACRDRKQ---ERGRSQERR 2065
2147 -PTSWLDEQRHSTAVSC--LDSGS--QPHLGTDPG-----NLGGOPL 2184
2066 QPSSSSSEKORF---YSCDLRAGSPQLMPSLSHPTSPAAALEPAPHPQSGSGVNGSPL 2122
2185 -----GGPGSRPKKLSP-PSITIDPPES-----QGRPTTP--SPG----- 2217
2123 MSTSGAITPGRRGRRLPOTPLTPRPSITYKTANSPPVHFAOGSGPLPAPSPGRLSGLS 2182
2218 --ICLRRAPSSD-----SKDPLASGPPDSMAASPSPKKVLSL-----SGLSS 2259
2183 EHNALLQKPLSQPLAPGSRIGSDPYLGQRLDSEASHTUPEDTLTTEEAVATNSGRSS 2241

RESULT 7

S29236

calcium channel protein BII-1, brain - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)

C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: S29236
R;Nidome, T.; Kim, M.S.; Friedrich, T.; Mori, Y.
FEBS Lett. 308, 7-13, 1992
A;Title: Molecular cloning and characterization of a novel calcium channel from rabbit b
A;Reference number: S29236; MUID:92354772; PMID:1379552
A;Accession: S29236
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-2259 <NII>
A;Cross-references: UNIPROT:Q02343; EMBL:X67855; NID:g1472; PIDN:CAA48040.1; PID:g1473
C;Superfamily: voltage-dependent calcium channel protein alpha-1 chain
C;Keywords: transmembrane protein

Query Match 14.3%; Score 1697; DB 2; Length 2259;

Best Local Similarity 24.2%; Pred. No. 2.3e-95;

Matches 619; Conservative 362; Mismatches 848; Indels 730; Gaps 84;

QY 28 AGGRPGSGAEKDPGSDSEAGLPYPALA-----PV----- 59
DB 8 AGRPASGEGDSQG---RNLGTPVPASGSAAYKQSKAQRATMALYNPIPVQNCPT 64
QY 60 ---VFFYLSQDSRPSRCLRTVCNPPFERISMLVILLNCVTLGMFR--PCEDIACDSQRC 114
DB 65 VNRSLFIFGEDNIVRYAKKLIDWPPPEYMLATIANCIVLALEQHLPEDDKTPMSRR- 123
QY 115 RILOAPDDFIPAFVAVMMVMVALG-IFQKCYLGTWNRLDPFVIAGMLEYSLDLQN 173
DB 124 --LEKTEPYFIFGIFCFEAGIKIVALGFIFHKSYLRNGNMVDFIVVLSGLITAGATHFN 181
QY 174 --VSFSAVTVRVLRPLRAINRVPSMRILVTLDDTLPMGLGNVLLLCFFYFIFGIQVQV 231
DB 182 THVDLRTLRVRLRPLKLVSGIPSLQIVLKSIMKAMVPLQLGLLFFAILMFAIIGLE 241
QY 232 LWAGLLNRRCFLPENFSLPLSLVDLERYTYQTENEDESPPFICSPQRENQWRSRCSVPTLRGD 291
DB 242 FYSGLHRACFVNSGVL-----EGFDP-----PHPCGVQGC----- 273
QY 292 GGGGPPCGLDYRAYNSSNTTCVNNQYNTCSAGEHNPKGAINFNIGNIVAMTAIFQVI 351
DB 274 ----PAG--YE-----CKDW-----IGPNDGITQFDNILLFAVLTVPQCI 306
QY 352 TLGWDVIMYFVMDA-HSFYNYFIYFILLIIVGSEFMINLCIVVATOFSETKQESQLMR 410
DB 307 TMEGWTVTLVNTDAGATWNWLYFPLIIGSFVNLVGLVLSGSEFAKERERV----- 361
QY 411 EQRVFLSNASTLASPEPGSCYEELLYLVILRKAARLAQVSRRAAGVRVGLLSSPAP 470
DB 362 ENRRAFMK-----LRRQQQI----- 376
QY 471 LGGQETQPSSSCSRSHRRLSVHHLVHHHHHHHHLGNGTLRAPRASPEIQDRDANGSR 530
DB 377 -----ERELNGYR 384
QY 531 RLMLPPSTPALSCAPPGAESVHSFYHADCHLEPVRCQAPPPSPSPSEASGRVTGSGKVY 590
DB 385 AWI----- 387
QY 591 PTVHTSPPTLKEKALVEVAASSGPPTLSTLNIPPGPYSSMHKLELTQSTGACQSSCKI 650
DB 388 -----DKAEVMAEENKSGTSALEVLRRATIKRSTRTEAMTRDSSDEHCVDISSV 438
QY 651 SSPCLKADSGACGPDGCPYCARAGAGEVELADREMPDSDSEAVYFTQDAQHSDLRDPHS 710
DB 439 GTPLARASIKSAKVDGASY-----FRHKE----- 462
QY 711 RRQSLGPDAREPSVLAFWELICDTFRKIYDSKYFGRGIMAILVNLVLSMGIEVHEOPEE 770
DB 463 -----ELLRISVRHAVKQVFWYVLSLVALNTACVAIVHNNQPOW 503
QY 771 LTNALETSINIVFTSLFALEMLLKLIVGPGFYKPNVNIQFDGVIVLVSVMVEIQVQ----- 825
DB 504 LTHLLYYAEFLFGLFLELMSLRKMGCPRLYFHSSFNCFDFGVTVGSIQFEVWVAIFRPG 563

QY 826 QGGSLVLRTRFLMRVLKLVRELPAQOLQVLVMTMDVNAVFCMLLMFLFIFISILGMH 885
 DB 564 TSFGISVLRALRLRIFKITYKASLRNLVLSMSKSLIISLLFLFLFVIVFALLGWO 623
 QY 886 LFGCKFASERDGTLPDRKNFDSLLWAVTVFOILTOENKVKLYNGM-----ASTSSWA 940
 DB 624 LFGGRF-NFNDG--TPSANFDTPAAMTVFQILGEDWNEVYNGIRSQGVSGMWS 679
 QY 941 ALYPIALMTGNVYVFNLLVAILVEGF-QAEETSK-----REDASGSLCICQLPVDQSGD 995
 DB 680 AVYPIVLTFLGNTLLNVFLAIVDNLANAQELTKDQEBEEAFNQKHALQKAEV----VSL 1025
 QY 996 ANKSESPDPFSPSLDGGDKKCLAL-----VSL 1025
 DB 736 --SPMSAPNV--PSIERDRRRHHMSWEPSSHLRERRRRHHMSVMEQRTSLRRHMQ 791
 QY 1026 GEHPELAKSLPLLIHTAATPMG-----LPKSTGTGLCEALGPASRTSSS 1072
 DB 792 SSQELANKKEEAPPNNPLNPLNPLSPLNPLNAHPSLYRRPRME-GLAALGLEKCEEBEHR 850
 QY 1073 CSABPGAAHEMKSPS-ARSSPHSPWSA-----ASSWT-----SRRS 1108
 DB 851 GGSUKGALDCQSPSLUGRRP--PWLRPCHGNCPEALQETAGETVVTTFEDRARHRQS 908
 QY 1109 SRNSLGRAPSLKRRSPGERSLSLGBQESQDEESSEBERASPAGSDHRHGS-----1163
 DB 909 QRRSHRRVRTEAKESSASRS-RSVQESLDEGASTEGE-----DHEARGSHGKE 961
 QY 1164 ---LREAKSFDPDTLOVP-----GLHRTAS-----GRGSASEHQCNGKS 1203
 DB 962 PTIHEERAQDLRRRTSLMVPKGLAGLDEAGTPLVSSPEGVKEAPTEQHADGSG 1021
 QY 1204 ASGRL-----ARALR-----PDDPPL-----1219
 DB 1022 EPALLGHVQDVGRAISOEPDLSCVATTDKVTTESTDVTVAIPDAEPLVDSTVHVIGN 1081
 QY 1220 ---DGD-----DADDEGNLSKGERVRAWRARLPACYLERSDSAVIFFPQSRFL 1267
 DB 1082 KTDGEASPQEAEMKEAQETEKQKKRGPAGSKAWPHS-----SMFISTSNPIR 1134
 QY 1268 LCHRIITHQDFDVHVLVIFLNCITIAMERPKIDPHSAERIFLTLNSYIFAVFLAEMTV 1327
 DB 1135 ACHYVNVLRYPFMCILLVIAASSIALAAEDPVLNTSERNV-LRYDFYVTVGTFFEMVI 1193
 QY 1328 KVALGCMFGEQAYRSSNNVLDGLLVLSVIDI-LVSMVSDSGTKILGMLRVLRLTL 1386
 DB 1194 KMIDQGLILQDGSYFRDLWNILDFVVVVGALVAFALANALGNTKGRDITKSLRLVRL 1253
 QY 1387 RPLRVISRAQGLKLVVETLMSSLPIGNIWIICCAFFIIFGLVQLFKGKFFVC--QGE 1444
 DB 1254 RPLKTIKRLPKLKAVPDCVVTSLKNVNLIVVYKLFMFIFAVIAVQLFKGFFYCTDSK 1313
 QY 1445 DTRN-----ITNKSDECAEASVR-WVRHKYNFDNLGOALMSLFLVLSKDCWDIMVDGLD 1497
 DB 1314 DTEKECIGNVVDHEKNMEVKGEWKREHFEHYDNIWALLTLFTVSTGEGMPQVLOHSDV 1373
 QY 1498 AVGUDQOQIMNPNMMLLYFISLLIVAPFLVNMFGVVVENFHKCRQHEEEERREE 1557
 DB 1374 VTEEDGPRSSNRNEMSIFVTVVFPFFVFFVFNIFVALLIIF-----QSGDKMEE 1426
 QY 1558 KRLRLKEKKA-----QCKPY--YSDYSR--FRLLVHLCTSHVLDLFTIGVGLNVV 1608
 DB 1427 ---CSLEKNERACIDFAISAKPLTRYMPQNRHTFQYRVHVFVSPSEYTIMAMIALNTV 1483
 QY 1609 TMAMEHYQQOQILDEALKICNYITFVLESYKLVAGFRFFODRNOLDLAVLVS 1668
 DB 1484 VLMMKYTSAPCTEYALKYLNIAFTWVFSLECVLKVIAFQVNFYFRTWNIFFIVIGS 1543
 QY 1669 IMGITLBEIEVNASLPNPTIIRIMRLVRLIARVLKLLKMAVGNRALLDTVMQALPOVGNL 1728
 DB 1544 ITEIVLTDKLVNTTGFNMSPLKLFRA--ARLIKLRQGYTIRILLTVPQSKALPYV 1600

QY 1729 GLLFMILLFETFAALGVELFGDLECD-ETHPCEGLGRHATFRNFMGAPLTLFRVSTGDNVN 1787
 DB 1601 CLLIAMLFFIYALIGMVGFNIRLDESH-----INRHNFRSPFGSLMLLFRSATGEAWQ 1656
 QY 1788 GIMKDTLL--RDCC-----QESTCYNTVISPITYFVSFLTAQFVLVNVVAVLMLKHL 1836
 DB 1657 EIMLSCLGKGCEDTTPAGSQOQESERCGTDLAYVYVVSFFCSEFLMLMLFVAVIMDNF 1716
 QY 1837 EESNEAK-----EEAELEAELE-----LEMKTLSPQHPSPGLSGPFLWPG 1876
 DB 1717 EYLTRDSSILGPHHLDHFVRWAEYDRAACGRITHYEMVETLM-----SPPLGLG 1768
 QY 1877 VEGPDSPTSPKGAHPAAHARSASHFSLBHPHTMOPHTLPGPDLLTVKSGVSRHSL 1936
 DB 1769 KRCPSKVAVKELVLMNMPVAEDMTVHT--STLMALIRTALD-----IKIAKGGADROOL- 1821
 QY 1937 PNDSYMCHGSTAGSPLCHRWGL-----PKAQSGLSVSHSQPADTSYI-----1981
 DB 1822 --DSELOKETLAIWPHLSQKMLDLLVPMPKASDUTVGKIYAAMIMDYKQSKVKKQRRQ 1879
 QY 1982 LQLPKDAP--HLOPHSAP-----TWGTIPKLP-----PGRSPLAQRPLRRQ 2022
 DB 1880 LEEQKNAFMQFMEPSSLPQEIIANAKALPCLPQPPAGLGRGCGCPAMSPSQIFQLT 1939
 QY 2023 AAIRTD-----SLDVQGLGSRDLLAEVSGSPPLARAYSFW-----QGSSTQ 2065
 DB 1940 CMDPADDQFOEQRSVLVVTDPGSMRRSFSTIRD-----KRSSSWLEEFSEMERSSDNTY 1994
 QY 2066 AQHRSRHS--KISKHMTTPAPCPQEPNMGKGPETPRTASSLELDTLSWISGDLPLPGGQ 2123
 DB 1995 KBRRSYHSSLRLSAHL-----NSDSGHKSDTHRS-----GGR 2028
 QY 2124 BEPPSPR-----DLKKCYVEA-----QSCORRPTSWLDEQRHHSIAVCLDSGSGP 2170
 DB 2029 ERGRSKEREHLASDVSRCSSEERGAQADWDSPERHPSPSEGRSQS-----2076
 QY 2171 HLGTPSNLGGQPGGSRPKKLSPPSITIDPPES--QGPRTPPSPGICILRRAPSSD 2228
 DB 2077 -----PSR-----QGTGLSESSIPSVSDTSTPHSRRLQPPVPPKPRPLL--SYSSL 2122
 QY 2229 SKDPLASGPP-----DSMAASPPKPKVDLSLGLSSDP 2261
 DB 2123 KQQPSNFPADGSGSLASPALESQAQVGLPSSSDSP 2161

RESULT 8
 T31092
 probable voltage-gated sodium channel - Aiptasia pallida
 C:Species: Aiptasia pallida
 C:Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 09-Jul-2004
 C:Accession: T31092
 R:White, G.B.; Frahn, A.; Haddock, S.; Lamers, S.; Greenberg, R.M.; Anderson, P.A.V.
 submitted to the EMBL Data Library, January 1998
 A:Description: Structure of a putative sodium channel from the sea anemone Aiptasia palli
 A:Reference number: Z20975
 A:Accession: T31092
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: mRNA
 A:Residues: 1-1810 <WHI>
 A:Cross-references: UNIPROT:O44930; EMBL:AF041851; NID:G2791840; PID:G2791841; PIDN:AASB9;
 C:Genetics:
 A:Gene: Nai
 C:Superfamily: sodium channel protein

Query Match 14.2%; Score 1689; DB 2; Length 1810;
 Best Local Similarity 25.8%; Pred. No. 5, 3e-95;
 Matches 520; Conservative 343; Mismatches 721; Indels 428; Gaps 65;
 QY 78 VCNWFERISMVLNLCVTIGMFRPCEDIACQRCRILOAFDDFIF-AFFAVETVVKM 136
 DB 110 ITNQFFEFFILLTIIVNCIFLAL-----RDAPEQPEYFAAIYTFEMLKI 155
 QY 137 VALG-IFGKKCYKVLGDTWNRLDFFIVIAGMLEYSLDLQNVSFSAVRTVRLRLRAINRVP 195

A;Cross-references: UNIPROT:Q02343; EMBL:X67856; NID:g1474; PIDN:CAA48041.1; PID:g1475
C;Superfamily: voltage-dependent calcium channel protein alpha-1 chain
C;Keywords: transmembrane protein

Query Match 14.1%; Score 1681; DB 2; Length 2178;

Best Local Similarity 23.9%; Pred. No. 2.1e-94;
Matches 605; Conservative 366; Mismatches 811; Indels 752; Gaps 83;

Qy	28	AGRPGGSAEKDPSADSEAGLPYPALA-----PV-----	59	680	AVFIVLTLEGNVTLNVLAVLAVDNLANAQBLTKDEQEEBAFNQKHALQAKEV-----	735
Db	8	AAGRPASGEGSDQG---RNLGTPVPASGSAAYKQSAQARTWALYNPIPVQNCFT 64		Qy	996	ANKSESEDPFSPSLDGDGRKKCLAL-----VSL 1025
Qy	60	---VFYLSODSRPSRCLRTVCNWPFRISMVLVILNCVTLGMFR--PCEDIACDSQRC 114		Db	736	--SPMSAPNV--PSIERDRRRRHMSWMBFRSHLRERRRRHMSVWEORTSQLRHHQM 791
Db	65	VNRSLEFEGEDNIYVKAKLIDWPPPEYMLATIANCIVLALQHLPEDDKTPMSRR- 123		Qy	1026	GEHPLEKSLPLPLIITHAATPMS-----LPKSTSTGLGEALGPASRTSS 1072
Qy	115	RILQAFDFFIAPFAVEMVQWVALG-IFGKKCVLGDWNRLODFEIVAGMLBYSLDLQ 173		Db	792	SSQALNKEAPPWNPLNPLNPLNAHPSLYRRPRPMB-GLALGLEKEEESHVR 850
Db	124	--LEKTEPYFTIGFCFEAGIKIVALGFIFHKGSYLRNGWVMDFIIVLSGILATAGTF 181		Qy	1073	GSAPFGAAHEMKSPS-ARSSPHSPSA-----ASSWT-----SRSS 1108
Qy	174	--VSFSVRTVRLRPLRAINRVPMSRILVTLTLLDTPMLGNVLLCFFVFFIFGIVGQ 231		Db	851	GGSLKALDQCRSLSLGRREP--PMLARPCNCPALQOETAGGTVTTFEDRARHQS 908
Db	182	THVDLRTARVRLPLKLVSGIFSLQIVLKSIMKAMPVLLQIGLLFAIFAILFAIGLE 241		Qy	1109	SPNSLGRAPSLKRSPSGERRSLSGEQSQDESESEERASPAAGSDHRRHGS----- 1163
Qy	232	LMAGLLNRCLPENFSLPSVLDLERYQYOTENEDESPFICSDPRENGMRSRCSVPTLRGD 291		Db	909	QRRSRHRVTRTEAKSSASRS-RSVQSERSLDEGATEGER-----DHEARGSHGKE 961
Db	242	FYSGKLHRACFVNSGVL-----EGFDP-----PHPCGVQGC----- 273		Qy	1164	---LEREAKSSFDLPDLQVP-----GLHRTAS-----CGRSASEHQCNGKS 1203
Qy	292	GGGGPGCLDVEAYNSSNTTCVNNQYVNCISAGEHNPFKGAIFNFINIGYAMTAPQVI 351		Db	962	PTIHEERAQDLRRDLSLWPKVPSGLAGLDEAGTPLVLSPEGVGKEAAPTEQHADGSG 1021
Db	274	---PAG---YB-----CKDW-----IGPNDGITQFNILFAVLTVFQCI 306		Qy	1204	ASGRL-----ARALR-----PDDPPL----- 1219
Qy	352	TLEGWVDIMFYMDA-HGFYNIPIYILLIIVGSPMNLCLVVIATQSETKQRESQLMR 410		Db	1022	EPALLGHVOLVGRSAISOSEPDLSCTVATTDKVTTESTDVTVAIPDAEPLVDSTVWHIGN 1081
Db	307	TMEGWITVLYNTDAGATWNLVYIPLIIIGSFVNLVLVLGVLGSGFAKERERV----- 361		Qy	1220	--DGP-----DADDEGNLSKGERVRAIARLPACVLERDSASVIFPPQSRFL 1267
Qy	411	EQRVFLSNASTLASFSEPGSCYELLKYLVLKKAARLQAQVRAAGVRVGLSSPAP 470		Db	1082	KTDGEASPFQEAEMKEAQETEKQKERRPASGKAMPHS-----SMFISTNSPIRR 1134
Db	362	ENRAEFMK-----LRRQQOI----- 376		Qy	1268	LCRIITHMFDHVLVILFNCITIAMERPKIDPHSAERIFLTLSNIFYTFAVLAEMTV 1327
Qy	471	LGQQTQPSSSCSRRRLSVHLLVHHHHHHHHLNGTIRAPASPETQDRDANGSR 530		Db	1135	ACHYVNLRYFEMCTLLVIAASSIALAAEDPVLNTSENRV-LRYFDVFTGVTFEMVI 1193
Db	377	----- 387		Qy	1328	KVVALGWCPEQAYLRSSWNVLGDLVLSVIDI-LVSMVSDSGTKILGMLRVLRLRTL 1386
Qy	531	RLMLPPPTALSGAPPGAESVHSFYHADCHLEPVRQAPPPRSPSEASGRVTGSGKVY 590		Db	1194	KMIDQGLIILQDGSYFRDLWNILDFVVVVAFAALANALGNTKGRDITKTSRLVRLVL 1253
Db	385	AWI----- 397		Qy	1387	RPLRVTSRAQGLKVVETLMSLKGIGNIVVICCAFFIIFGILGVQLFKGKFFVVC--QGE 1444
Qy	591	PTVHTSPPTLKEKALVEVAASGPPTLTSLNIPPGYSSMHKLETSQACQSSCKI 650		Db	1254	RPLKTIKRLPKLAVPDCVVTSLKNVFNILVYKLFMFIFAVIAVOLPKGKFFYCTDSSK 1313
Db	388	-----DKAEVMLAENKNGTSALEVLRATIKRSRTEAMTRDSSDHCVDIISV 438		Qy	1445	DTEN-----ITNKSDEASYSR-WVRHYKNFDNI-GQALMSLFVLASDKDGNVDIMYDGLD 1497
Qy	651	SSPCLKADGACGPDSCPYCARAGAEVELADREMPSDSEAVYEFTQDAQHSDLRDPHS 710		Db	1314	DTKEKIGYVDEKKNMEVKGREWKEHFEHYDNIWALLTLFTVSTGEGMPQLQHSVD 1373
Db	439	GTPLARASIKSAKVDGASY-----FRKE----- 462		Qy	1498	AVGVDQOPIMNHNPMMLYIFISFLLIIVAFVLMVGVVVENFHKCRHQHEEERREE 1557
Qy	711	RQRSGLPDAEPSSVLAFWELICDTRFKIVDSKYFGRGIMAILVNLMSGLEYHEQPE 770		Db	1374	VTEEDGRPSRSNRMEMSIFVYVVFVFPFFVNFVALLIITP-----QEQDKWEE 1426
Db	463	-----RLLRISVRHA VKSQVYFVIVLSLVALNTACVAIVHNNQPOW 503		Qy	1558	KLRLREKKERKA-----OCKPY--YSDYSR--FRLLVHHLCTSHYLDLFTIGVGLNVV 1608
Qy	771	LTNALEISNIVFTSLFALEMLKLLVYGPFGYIKNPYNIPDGVIVVISWEIVGQ----- 825		Db	1427	---CSLEKNERACIDFAISAKPLTRYMPQNRHTFQVRVWHFVVPSPSEYTIMAMIALNTV 1483
Db	504	LTHLLYAEFLGLFLLEMSLKMVGMPRLYFHSFNCDFGVTVGSIFEVVWALFRPG 563		Qy	1609	TMAHEHYQQPQIILDEALKINYITFVIFULESVFKLVAFGRFFFOODRNQDLALVLLS 1668
Qy	826	QGGGLSVLRTPLRMVLKLVFLPALQOLVLMKTMNDVATFCMLMLFIFISILGMH 885		Db	1544	ITEVLVDSKLNTVTGNMFLKLFRA--ARLKLROQYTIIRILLTFTVQSKALPYV 1600
Db	564	TSFGISVLRALRLRIKITYWASLRNLVLSLMSKMSIISLLFLFLFVIVFALLGMQ 623		Qy	1729	GLLFMLAFFIPAAALGVELFGDLECD-ETHPCEGLRHATFRNFCMAFLTLFRVSTGDNW 1787
Qy	886	LFGCKFASERDGLTPDRKNFDSLMLIAIVTFQILTOEDWKNVLYNCM-----ASTSSWA 940		Db	1601	CLLIAMLFFIIVAIIGMQVFNIRLDEESH-----INRHNFRSPFGSLMLLFRGATGEAWQ 1656
Db	624	LFGGRF-NFNDG---TPSANEDTTPAAMTVFQILTGEDWNEVWYNGIRSQGGVSGMWS 679		Qy	1788	GIMKDTL--RDCD-----QESTCVNTVISPIYFVSFLTAQVFLVNVVIAVLMKHL 1836
Qy	941	ALYFIALMTFGNYVLFNLVAILVEGF-QAEISK-----REDASQQLSCIQLPVDQGGD 995		Db	1657	EIMLSCLGEKCEPDPTAPSQQESERCGTDLAVYFVSIFPFCFLMLLFLVAVIMDNF 1716
				Qy	1837	ESNSKEAK-----EEAELEAELE-----LEWKTLSPQHPSLGSPFFLWPG 1876

Db 1717 EYLTRDSSILGHHLDEFVRVWAEYDRAACGRHIIHYTEMVEMLTLM-----SPPLGLG 1768
Qy 1877 VEGPDSPSPKPGALHPAAHARSASHLSLEHTMQPHETELPGPDLLTVRKSGVSRTHSL 1936
Db 1769 KRCPSKVAIKLVLMNMPVAEDMTVHFT--STLMALIRTALD-----IKIAGGADROOL- 1821
Qy 1937 PNDSTYMCRHGSGTAEGPLHRCWGL-----PKAQSGSVLSVHSPADTSYI----- 1981
Db 1822 --DSELOKETLAIWPHLSQKMLDLLVPMKASDLTVGKIYAMIMDYKOSKVKKQRRQ 1879
Qy 1982 LOLPKDAP--HLLOPHSAP-----TWGTPKLP--PPGRSPLAQRPLRQAAIRTDSDLDV 2032
Db 1880 LEEQKNAFMQFMEPSLQBIILANAKALPCLPQGPFA----- 1917
Qy 2033 QGLGSRDLLAEVSGSPPLARAYSFWQSQSTQAQOHSRSKISKHMTTPAP-----C 2086
Db 1918 --GLGSRGCPA-----MSPLSPQIFQUTC 1940
Qy 2087 PGPEPNMGKPPETRSSLELDELTSWISGDLPLPGQBEPPSPDLKKCYVEAQSCORR 2146
Db 1941 MDPADDDQOP--QEQRSLVVD-----PGSMRKSFTIIRD--KRS 1976
Qy 2147 PWSLDE-----QRRHSIAVSC-----LDGSGOPHLGTDPSNLGGQPLGG*2186
Db 1977 SSSWLEEPSMERSDNTYKSRSSVHSSRLSAHRLNSDSGHK---SDTHRSGRERG- 2031
Qy 2187 PGSRPKKLSPTITDPPESQ-----PRTPSPGICLRRRAPSDSKDPIAS 2235
Db 2032 --RSKERHLLSADVSCSSEERGAQWDSPERHPSRSPSEG---RSQSPSRQGTGSLSE 2087
Qy 2236 GPPDSMAASPSPKK 2249
Db 2088 SSIFSVDSTSPRQ 2101

RESULT 10
C54972
voltage-dependent calcium channel alpha 1E - mouse
C:Species: Mus musculus (house mouse)
C>Date: 12-Apr-1995 #sequence_revision 12-Apr-1995 #text_change 09-Jul-2004
C:Accession: C54972
R:Williams, M.E.; Marubio, L.M.; Deal, C.R.; Hans, M.; Brust, P.F.; Philipson, L.H.; Mil
J. Biol. Chem. 269, 22347-22357, 1994
A:Title: Structure and functional characterization of neuronal alpha-1E calcium channel
A:Reference number: A54972; MUID:94350992; PMID:8071363
A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A:Molecule type: mRNA
A:Residues: 1-2272 <MIL>
A:Cross-references: UNIPROT:Q61290; GB:L29346; NID:9522330; PIDN:AAA59206.1; PID:9522331
A:Note: authors translated the codon AGG for residue 788 as lys, and CCT for residue 886
C:Superfamily: voltage-dependent calcium channel protein alpha-1 chain

Query Match 14.1%; Score 1681; DB 2; Length 2272;
Best Local Similarity 23.7%; Pred. No. 2.2e-94;
Matches 607; Conservative 375; Mismatches 844; Indels 740; Gaps 82;
Qy 30 GRPGSGAEKDPGSDSEAGLPYALAPVY----- 60
Db 11 GRPGSGDGSDS---QSRNRQGTPTVPASGPAAYKQSKAQRARTWALNPIVPRQNCFTVN 67
Qy 61 --FYLQSDSPRSWCLRTVCNPFERISMVLILNCVTLMFR--PCEDIACDSQRRI 116
Db 68 RSLFIFGEDNIVRYAKKLDMPPEFYMIATIIANCIVLALEQHLPEDDKTPMSRR--- 124
Qy 117 LOAFDDFIFAPFVEMVVMVALG-IFGKKCYLGDVTNRLDFFIVIAGMLEYSLDLON-- 173
Db 125 LEKTEPIFICFEAGIKIVAGLGFIFHKGYLRNGWMDPFIIVLSGILATATHENTH 184
Qy 174 VFSAVTRVRLRPLRAINRVPSMRILVTLLDLPMLGNVLLLCFFVFFIFGVQVLW 233
Db 185 VDLRALRAVRVRLPLKLVSGIPSIQIVLSIMKAWVPLQIGLLFFAILMFAIIGLEFY 244

Qy 234 AGLLNRCLFLENFSLPLSVLDLERYQYOTENDEDESPFICSPQRENCRMSRCSVPITLRGGG 293
Db 245 SGKLRACFMNNSGIL-----EGFDP-----PHPCGVOGC----- 274
Qy 294 GPPCGGLDIYAYNSSSNTTVCNNQYVYTCNSAGEHNPFKGAINFONIGVAMIAI FQVITL 353
Db 275 ---PAG--YE-----CKDW-----IGPNDGITQFDNIILFAVLTVEQCITM 309
Qy 354 EGWIDIMYFVMDA--HSFYNFYIFILLIIVGFFMINLCLVVIATOFSTKQRESQMLREQ 412
Db 310 EGWITVLYNTNDALGATNMWLYFIPLIIGSFFVLNLVLGVLGSEFAKERERV-----EN 364
Qy 413 RVRLSNASTLASFESEGCYBEELLYVILTRKAARLAQVSRAGVVRGLSSPAPLG 472
Db 365 RRAFMK-----LRRQQOI----- 377
Qy 473 QGETQPSSSCSRSHRRLSVHHLVHHHHHHHHHGLNGTLRAPRASPEIQORDANGSRRL 532
Db 378 -----ERELNGYRAW 387
Qy 533 MLPPPSTALSGAPPGGAESVHSFYHADCHLEPVRCQAPPPRSPSEASGRVTGSGKVYPT 592
Db 388 I----- 388
Qy 593 VHTSPPTLKEKALVEVAASSGPPTLTSLNIPGPYSSMHKLLTQSTGACQSSCKISS 652
Db 389 -----DKAEVNLAEENKNSGTSALEVLRRATIKRSRTTEAMTRDSDEHCVISSVGT 441
Qy 653 PCLKADSGACPDPCPCYCARAGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHSRR 712
Db 442 PLARASIKSYKVDGASY-----FRHKE----- 463
Qy 713 QRSIGPDAEPSSVLAFWRLICDTPRKIVDSKYFGRGIMAIILVNTLSMGIEYHQPBEELT 772
Db 464 -----RLLRISIRHMVKSQVFWIVLSVVALNTACTVAIVHHNQPMULT 506
Qy 773 NALISNIVFTSLPALEMLKLLVYGPFGYIKNPYNI FGVIVIVISWVEIVGO-----QG 827
Db 507 HLLYAEFFLGLGLFLEELMSKMGYGMPLYPHSHSNCFDFGVTVGTSIFEVVWAI PRPQTS 566
Qy 828 GGLSVLTFRLMRVLKVRFLPALQORQLVLMKMDNVATFCMLLMLFIFIFSLGHMLF 887
Db 567 FGISVLBALRLRIKTKYKWSLRNLVSLMSKMSIISLLFLFLFIVVFAALLGMLQ 626
Qy 888 GCKPASERDGTLPDRKXNFDLSLWAIYTVFQILQEDWNKLYNGM-----ASTSSWAAL 942
Db 627 GGRF-NFNDG---TPSANFDTFPAIIMTVFQILTGEDWNEVMYNGIRSGQGVSGMWSAI 682
Qy 943 YFIALMTFGNYVLNLLVAILVEGF-QAEISK-----REDASGQLSCIQLPVDQGGDAN 997
Db 683 YFIVLTFLGNYTLNVLFAIVADNLANAQBLTKDEQEBEEAFNQKHALQAKEV----- 736
Qy 998 KSSEPDFFSPSLDGDGRKKCLAL-----VSLGE 1027
Db 737 SPWSAPNM--PSTERDRRRHHHSMWEPFRSHLRERRRRHHHSMWERTSOLRRHMQSS 794
Qy 1028 HPELRKSLPLLIHTAATPMS--LPKSTSTGL-----GEALGPA-----SRRTSSS 1072
Db 795 QEALNKEEAPMNPPLNPLNPLSPLNLAHPSLYRRPRPIEGLALGLKCEBERISRG 854
Qy 1073 GSAB-----PGAHEMKSPPS-ARSSPHSPWSNASSWTS----- 1105
Db 855 GSLKGDIGLITSLDNRSLGKREP--PWLPRSCHGNCDDPTQEBAGGETVVTTFEDR 912
Qy 1106 ---RRSRNSLGRAPSLKRSRSGESQDSDEESSEERASAPAGSDHRRHG 1162
Db 913 ARHQSORRHRVRTEGKDSASAKS-RSASQERSLDEGVSVGEKEHPSHSHAKS 971
Qy 1163 SLEREAKSFDL--PDTLOVP---GL-----HRTASGRGSAHQDCNGK 1202
Db 972 PTTHEBERTQDLARTNSLWPRGSLVGALDEAETPLVQPOPELEVCKDAALTBQAEBS 1031
Qy 1203 SAS-----GRLARALRPD-----DPPLD----- 1220

Db 1032 SEQALLGVDVLDVGRGISEQSEPDLSCTANMOKATTESTSVTVVAIPDVLDVSTVNIS 1091
QY 1221 -----GDADDEGNLKGGER-----VRWIRARLPACYLBERDSWSAYIFFQPSR 1264
Db 1092 NKTDGEASPLKEAETKEEVEEKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK 1144
QY 1265 FRLCHRIITHKMPDHVVLVIFLNCITIAMERPKDPHSAERIFLTLNFIYTAFLAE 1324
Db 1145 IRRACHYIVNLRYPFEMCILLVIAASSIALAAEDPVLNTSERNKV-LRYFDYVFTGVFTFE 1203
QY 1325 MTVKVVALGCFGEOAYLRSSNNVLLGLLVLSVIDI-LVSMVSDSGTKILGMLRLRL 1383
Db 1304 MVIKMDQGLILQDSTFRDLNLLDFVVGALVAFALANALGTNGRDIKIKSLRLV 1263
QY 1384 RTRPLRVISRAOGLKLVETLMSLSKPIGNIVVICAPFIIFGILGVQLFKGKFFVC-- 1441
Db 1264 RVLRPLTKIKELPKLKAFCVCTVSLKNVFNILVYKLFMFIFAVIAVQLFKGKFFCYTD 1323
QY 1442 QGEDTRN-----ITNKSDCAEASR-VWRHKNFNGLGOALMSFLVASKDGWVDIMYD 1494
Db 1324 SSKOTEKECIGNYDHEKNKMEVKGREWKHEFHIDNIWALLTLFTVSTGEGWPQVLOH 1383
QY 1495 GLDAVGVDQOIMNHNPMWLLYFISFLIIVAFFVNNFVGVVNFHFKRQHQBEEFARR 1554
Db 1384 SVDTEEDRGSRNRMEMSIFYVYVFPVFPFVFVNFVLIITP-----QEOGDKM 1436
QY 1555 REEKRLRLKKRKA-----CKPY--YSDYSR--FRLVHLHCTSHYLDLFTIGVL 1605
Db 1437 MEE---CSLEKNACIDFAISAKPLTRYMPQNRRHTQYRWMHFPVSPSEYTIMAMIAL 1493
QY 1606 NVVTWAMEHYOQQLIDALACINVIYFVLSVFKLVAFGRFRFQDRWNOLDIAV 1665
Db 1494 NTVLWMIKYIYAPCTYELALKYLIATFNWFSLECVLKVIAFGELNYFRDTWNLFDFTV 1553
QY 1666 LLSIMGITLEEVNASLPIPTIIRIMVRLRIARVLKLMKVMGMRALLDTVWQALPOV 1725
Db 1554 IGSITEIILTSKLVNTSGFNMSFLKLFRA---ARLIKLRQGYTIRILLWTFVQSPKAL 1610
QY 1726 GNGLGLFMLLPFIIPALGVLEFGDLECD-ETHPCGEGRHATFRNFGMAFLTLFRVSTGD 1784
Db 1611 PYVCLLIAMLFYIAYIAGQVFNKLDDESH-----INRHNFRSFGSLMLLFRSATGE 1666
QY 1785 NNNGIMKOTL--RDCQBSTC-----YNTVISPIYFVSFVLTAQFVLNVIIVLM 1833
Db 1667 AQEIMLSLCKEGCEPTTAPSGQNESERCTDLAYVYVFSIFFCFSFLMLNLFVAVIM 1726
QY 1834 KHLBSNKBAK-----EEAELEAELE-----LEMKTLSPQHSPLGSPFL 1873
Db 1727 DNFEYLTDRSSILGPHHLDDEFVRVWAEDRAACGRHITYEMEMLTLM-----SPPL 1778
QY 1874 WPGVEGPDSPDKPCALHPAAHARSASHFSLEHPTMOPHTLPGLPDLTLVRKSGVSRT 1933
Db 1779 GLGKCPKSVKAVKRLVLMNFMVAEDMTVHFT--STLMALIRTALD-----IKIAGGADQ 1832
QY 1934 HSLPNDSYMCRHGSTAEGPLGRHGMGL-----PKAOGSVLSVHSPADTSYI----- 1981
Db 1833 QL---DSELQKETLAIWPHLSQKMLDLVPMPEKASDLTVGKIYAAMIMDIYKOSKVKQ 1889
QY 1982 ---LQLPKADP--HLLOPHSAP-----TWGTTIPKLP-----PGRSPLAORPL 2019
Db 1890 RQGLEEKQKAPQRMPESSLPOETIANAKALFYLOQDPVSGLSGRSGVPSMSPLOEI 1949
QY 2020 -----RQAAIRTDSDVQGLSR-----EDLLAEVGSPPPLA 2053
Db 1950 FQLACMDPADDOFQOQSLVITDPSSMRSSTIRDKRSNSSLWEFSMERSSENTYKS 2009
QY 2054 RAYFWGQOSTOAOQH-----SRSHKISKHMTTP----- 2083
Db 2010 RRRSY--HSSLRLSAHRLNSDSGHKSDTHRSGRGRGRSKRKHLLSPVSRCSNEERG 2067
QY 2084 -AFPCGPEPNWGGPPETRS-----SLE-----LDTELSWISGDLLPPGQBE 2126

Db 2068 QADWESPERRQSRSPSEGRSQTNRQGTGSLSESSIPSIISTSTPRSRRLP-----VP 2123
QY 2127 PSPRLKKCYVSAQSCQRRPTSMWLDQRRHSIAVSCLDGSGPHLGTDPNGLGQPLGG 2186
Db 2124 PKPRELLLSYSSU-----MRHTGSGISPPDGSE-----GGSPLAS 2157
QY 2187 PGSREPKK-LSPPGSITIDPPSQQRTP---PSPGICLRRRAPSSD 2228
Db 2158 QALESNSACLTSSNSLHPQOQHPSPOHYISEPYLALHEDSHASD 2203
RESULT 11
A54972
voltage-dependent calcium channel alpha 1B-3 - human
C:Species: Homo sapiens (man)
C>Date: 12-Apr-1995 #sequence_revision 12-Apr-1995 #text_change 09-Jul-2004
R:Accession: A54972
R:Williams, M.E.; Marubio, L.M.; Deal, C.R.; Hans, M.; Brust, P.F.; Philipson, L.H.; Mil
J. Biol. Chem. 269, 22347-22357, 1994
A:Title: Structure and functional characterization of neuronal alpha-1E calcium channel
A:Reference number: A54972; MUID:94350992; PMID:8071363
A:Accession: A54972
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-2270 <WIL>
A:Cross-references: UNIPROT:Q15878; GB:I29385; NID:9495869; PIDN:AAAS9205.1; PID:9495870
C:Superfamily: voltage-dependent calcium channel protein alpha-1 chain
Query Match 14.0%; Score 1665; DB 2; Length 2270;
Best Local Similarity 24.2%; Pred. No. 2.1e-93;
Matches 620; Conservative 386; Mismatches 814; Indels 744; Gaps 90;
QY 31 RPOGSAEKDPCGASAEGLPYPALA-----PV----- 59
Db 11 RPOGSGDSD---QSRNRQGTVPASGQAAAYKQTKAQRMTALYNPIPVQNCFTVNR 67
QY 60 VPFYLSQDSRPSWCLRTVCNPFERISMLVILLNCVTILGMPF--PCEIACDSORCRIL 117
Db 68 SLFIFGEDNIVRKIAKLLIDWPPFFEMILATIANCIVLALQHLPEDDKTPMSRR--L 124
QY 118 QAFDDDFIAFFAVEMVVMKVVALG-IFGKKYIGDTNRNLDFFIVTIVAGMLEYSLDLQN--V 174
Db 125 EKTEPYFIFGFCFAGIKIVALGFIFKGSYLRNGWNVMDFIWVLSGILATAGTHTNTHV 184
QY 175 SPFAVTVRVLRLRAINRVPNMRILVTLTLLDPLMGNVLLCRFPVFIIGVGVOLWA 234
Db 185 DLRTLAARVRLRLKLVSGIPSLQIVLKSIMKAWPPLQLGLLFFAILMFIALLGLEFYS 244
QY 235 GLLRNRCFLPNFSLPLSVDLERYOTENEDESFPFICSQPRENGMRSRSPVTLRGDGG 294
Db 245 GKLRACFMNNSGIL-----EGFDP-----PHPCGVQGC----- 273
QY 295 GPPCGLDYEAYNSSNTTCVNNQYVTCNCSAGEHNFPGKAINPDNIGYAWIAIIFOVITLE 354
Db 274 --DAG--YE-----CKDW-----IGPNDGITQFDNLIIFAVLTVFQCITME 309
QY 355 GWVDIMYFVMDA-HSEYNYFIYILLIIVGSEFFMINICLVVIATQFSETKQES-----Q 407
Db 310 GWITVLYNTNDALCATWNWLIYFIPLIIGSFVNLVILVLSGSEFAKERERVENRRAFMK 369
QY 408 LMREQRVRLSNASTLASFSEPGSCYVEELKYLYILRKAARLAQVSRAGVRVGLSS 467
Db 370 LRQOQIE-----RELNGYRAWIDKABEVMABENKQAG----- 403
QY 468 PAPLGGQETQSSCSRSRRLSVHVLVHHHHHHHHHGLNGTLAPRASPIQDRDAN 527
Db 404 -----TSALEVLRRATI-----KRSTEAMTIDS- 427
QY 528 GSRRLMLPPSTPALSGAPPGGAESVHSFYHADCHLEFVRCPQAPPPRSPSEASGRTVSG 587
Db 428 -----SDEH----- 431
QY 588 KYPTVHTSPPEPTLKEKALVEVAASSGPTLISLNIPPGPGYSMHKLETFQSTGACQSS 647

C>Date: 12-Apr-1995 #sequence_revision 12-Apr-1995 #text_change 24-Sep-1999
C/Accession: B54972
R/Williams, M.E.; Marubio, L.M.; Deal, C.R.; Hans, M.; Brust, P.F.; Philipson, L.H.; Mil
J. Biol. Chem. 269, 22347-22357, 1994
A/Title: Structure and functional characterization of neuronal alpha-1E calcium channel
A/Reference number: A54972; MUID:94350992; PMID:8071363
A/Accession: B54972
A/Status: Preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: mRNA
A/Residues: 1-2251 <MIL>
A/Cross-references: GB:129384; NID:G495867; PID:AAA59204.1; PID:G495868
C/Superfamily: voltage-dependent calcium channel protein alpha-1 chain

Query Match 14.0%; Score 1663.5; DB 2; Length 2251;
Best Local Similarity 24.2%; Pred. No. 2.6e-93;
Matches 617; Conservative 383; Mismatches 815; Indels 735; Gaps 89;

Qy 31 RPPGSAEKDPGSADEAGLPYALA-----PV----- 59
Db 11 RPPSGDGDSD--OSNRQGTTPVSPASQAAYKQTKAQRATMALYNPIPVQNCFTVNR 67

Qy 60 VFFYLSQDSRRSCLRTVCNPFERISMLVILLNCVTLGMFR--PCEDIAQDSQRCIL 117
Db 68 SLFIFGEDNIVRKYAKKLDWPPPEYMLATIIANCIVLALEQHLPEDDKTPMSRR--L 124

Qy 118 QAFDDPIFAPAVEMVKNVALG-IFGKKCYLGDWRLDFFIVIAHMLEYSLDLQN--V 174
Db 125 EKTEPYFIFGFCFAGIKVALGFIHKGSYLRGNVMDFIVVLSGILATAGTHFNTHV 184

Qy 175 SFSARVTVRLPURLRNVPSMILVTLGLDLPMLGNVLLLCFFVFFIGIVGVOLWA 234
Db 185 DLRLTRAVRULRPLKVGSPISQIVLKSINKAMVPLQIGLLFFAILMPAIIIGLEFYS 244

Qy 235 GLLRNRCFLPNFSLPLSLVDLERYIYQYOTENEDSPFICQPRENGMRSRCSVPTLRGDGG 294
Db 245 GKLHRCFMNSGIL-----EGFDP-----PHPCGVQC----- 273

Qy 295 GPPCGLDYEAYNSSNTTCWNNOYNTCSAGENPFPKGFNAINFONIGVAMTAIQTITLE 354
Db 274 --PAG--YE-----CKDW-----IGPNDGITQFONILFAVLTVPCITME 309

Qy 355 GWVDIMYFVMDA-HSFYNFIYFILLIIVGSPFMNLCLVWITATOFSETKRES-----Q 407
Db 310 GWTVTLNTDNLGATWNWLFIFLIIGSFVNLVLGVLSGSEFAGERKERVNRAPMK 369

Qy 408 LMREQRVFLSNASTLASFSPGSCYBELLKYLVIYILKAAARLQAQVRAAGVRVGLSS 467
Db 370 LRRQQIE-----RELNGYRAWIDKAEVMLAEENKAG----- 403

Qy 468 PAPLGGQETQSSCSRSRRLSVHLVHHHHHHHHYHLNGTLRPRASPEIQDRDAN 527
Db 404 -----TSALEVLRRATI-----KRSRTAMTRDS- 427

Qy 528 GSRLMLPPPSTPALSGAPGGAESVHSFYHADCHLEPVRVCAQPPRSPSPASGRVTGSG 587
Db 428 -----SDEH----- 431

Qy 588 KVPYTVHTSPPTLKEKALVEVAASSGPPTLSLNIIPPGPYSSMHKLETTQSTGACQSS 647
Db 432 -----CVDI 435

Qy 648 KTSPPCLKADSGAGDPCPYCARAGAGEVELADREMPDSDSEAVYFTODAQSILRD 707
Db 436 SSVGTPLARASIKSAKVDGVS-----FRHKE----- 462

Qy 708 PHSRQRSLGDAEPSSVLAFWRLICDTFRKIVDSKYFGRGIMTALVNTLSMGIEVHEQ 767
Db 463 -----RLRISIRHMVSKQFYTWIIVLSLVALNACVAIVHHNQ 500

Qy 768 PEELTNALIEISNIVTSLFALEMLLKLIVGPFYKPNVNIIDGVVWISVWBIQV-- 825
Db 501 POWLTHLLYAEFLFLGLFLEMSLKMVGMPRLYFHSSFNCFDFTGVTVGSIFEVVWAIF 560

Qy 826 ---QGGGLSVLRFLMRVLKLVFLPALQRLQVLMKTMNDVATFCMLMLFIFPSIL 882
Db 561 RPTGTFGISVLRALLRLRIKITYWASLRNLVSLMSMKSIISLLFLFLFVVFALL 620

Qy 883 GMHLFGCKFASERDGTLPDRKNFDSLLWAIVTFQILTOEDMNKVLNMG-----ASTS 937
Db 621 GMQLFGGRF-NFNDG---TPSANEDTFPAALMTVFQILTGEDWNEVMYNGIRSGQGVSSG 676

Qy 938 SWAALYFIALMTFQNYVFLNLLVAILVEGF-QAEIEISK-----REDASQLSCIQLPVDSQ 992
Db 677 MWSAIYFIVTLTFCNYTLLNVLAVIAVDNLANAQELTKDEQEEBAFNQKHALQAKEV- 735

Qy 993 GGDANKSEBPDFFPSLDGDDKCKCLAL-----VSLGEHPELRK----- 1033
Db 736 -----SPMSAPNM--PSIERRRRRHMSVWEQRTSQLRKHMQSSQALNREAPTWP 788

Qy 1034 -----SLAPPLIITHAATPMSLPKSTSTGLGALGPA-----SRTSSSGS-----AE 1076
Db 789 LNPLNPLSSLNPLNAHP-----SLYRPRALIEGLALGALKEKFEERISRGSLKGDGD 843

Qy 1077 PGAAHEMKSPSARSSPHSPWSA-----ASWTSRSSR 1110
Db 844 RSSALDNRQTPSLGQREPPWLPARPCHGNCDDPTQOEAGGGEAVVTFEDRARHRQRSSR 903

Qy 1111 NSLGR-----APSLKRSPSGERSL--LSGEGESQD-----EESSEEBERASPA 1155
Db 904 HRRVTSKGSSASRSRSGESQERSLDEAMTEGKDEHLELGNHGAKEPTIOEBRA----- 959

Qy 1156 SDHRHRSGLEREAKSSF-----DLPTQLVQPLGHRHTASGRGSASBHQDCNGKSAS--- 1205
Db 960 QDLRTNLSLVSRGSLAGGLDEADTFLVPHPELE---VGKHVVLTQEPEGSEQALL 1016

Qy 1206 -----GLARALRPD-----DPLDG----- 1221
Db 1017 GNVOLDGRVTSSEPDLSCTITANTKATTESTSVTVAIPDVPDLVDVSTVHISNKTGDE 1076

Qy 1222 -----DDADDEGNLSKGERVRAWRARIPACYLERDSAYIFPQSRFLACH 1270
Db 1077 ASPLKEAIREDEEBEVEKKQKKEK-RETGKAMVPHS-----SMFISTTNPIRRACH 1128

Qy 1271 RIITHKMFDFHVLVIIIFLNCITIAMERPDKIDPHSAERIFLTLSNVIPTAVFLAEMTVKV 1330
Db 1129 YIVNLRVFCILLIVIAASSIALAAEDPVLNSENKV-LRYFDYVFTGVTFEVIKMI 1187

Qy 1331 ALGCMFGEQAYLRSSNVNLDGLVLSVIDI-LVMSVSDSGTKILGMRLRLRLTLRPL 1389
Db 1188 DOGLILQDGSYFRLWNILDFVWVGALVAFALANALGTNGRDIKTIKSLRVLRLRPL 1247

Qy 1390 RVISRAOGLKLVETLMSLKPIGNIVVICAPFIIIFGILGVLPKGFVVC--QGEDTR 1447
Db 1248 KTIKRLPKLKAVIDCVVTSLNQVFNILIVYKLFMFIFAVIAVQLFKGKFFYCTDSSKDPTE 1307

Qy 1448 N-----ITNKSACAASR-YWRHKYNFONLQALMSLFLVASKDGKVDIMYDGLDAVG 1500
Db 1308 KECIGNYVDHEKKNWEKVGREWEKEHEHYDNI-IWALLTLFTVSTGEGMPQLQHSVDYTE 1367

Qy 1501 VDOQPIMNHNPMMLLYFISFLLIIVAFVFLNMFVGVVENFHKCRHOHEEBEERREKRL 1560
Db 1368 EDGRPSRSNRMEMSIFVYVWVFPVFPFVFIIVFALIIITF-----QEQDKWME--- 1417

Qy 1561 RLLEKKERKA-----QCKPY--YSDYSR--FRLAVHHLCTSHYLDLFTITGVIGLNVTMA 1611
Db 1418 CSLEKNRACIDFAISAKPLTRYMPQNRHTFYQYRVHFWVSPSEYTIMAMIALNTVILM 1477

Qy 1612 MEHYQQOQILDEALKICNYIFTVIFVLESVKLVAFGRFRFQRWNLDAIIVLLSIMG 1671
Db 1478 MKYSACTVELALKYLNIAFTAVFSLECVLKVIAFGFLNVRFRDWNIFDFTIIGSITE 1537

Qy 1672 ITLEEIEVNASLPINPTIIRIMRVLRIARVLKLNKAVGMRRALLDTVWQALPQVGNLGL 1731
Db 1538 IILTDSKLVNTSGFNMSFLKFR-----ARLIKLRQGVTTIRILLTWFVQSPKALPYVCLL 1594

Qy 1732 FMLLFFFAALGVLEFGDLECD-BTHPCBGLGRHATFRNFGMAFLTLFRVSTGDNWNGIM 1790

1595 IAMLFFIYALIGMOVGNKLDSEH-----INRHNFRSFFGSLMLLFRSATGEAWQBEIM 1650
1791 KOTL--RDCQESTC-----YNTVISPIYFVSFVLTAQVLNVNVIAMVLMKHLEES 1839
1651 LSCLGKGCBDTAPSGQNERCOTDLAYVYVSFIFFCSFLMLNLFEVIMONFEYL 1710
1840 NKEA-----EAELEAELE-----LEMKTLSPQSPHPLSGSPFLMPGVEG 1879
1711 TRDSILGPHHLEDFVWVAEYDRAACGRHYHTEMVEMTLM-----SPLGLGKRC 1762
1880 PDSDPSPKALHPAAHARSASHFSLEHPTMQDHPTELPGDPLLVKRGVSRTHSLPND 1939
1763 PSKAYKELVLMNMPVAEDMTVHFT--STLMALIRALTALD-----IKIAGGADRQOL--D 1813
1940 SYMCRHGSSTAEGPLCHRGWGL-----PKAQSGLSVLSVHQSQADTSYI-----LQL 1984
1814 SELQKETLAIWPHLSQKMLDLLVMPKASDLTVOKIYAAWIMWYKQSKVKKQROOLEE 1873
1985 PKDAP--HLLQPHSAP-----TWGTIPKLPP-----PGRSPLAORPLRQAAI 2025
1874 QKNAPMFORMESPSSLPQELIANAKALPYLOQDPVSGLSGRGYPMSPLSPQDIFOLACM 1933
2026 RTDLSVVOGLSREDLLAEVSGSPPLARAYS-----FWGOSSTOAAQOHSR 2071
1934 --DPADDGQFQERQSLV--VTDP--SMRRSFSTTRDKRNSWLEEFMSERSSENTYKSR 1988
2072 SHSKISKHMTTPAPCPGEPNWKGPPTETRSLELDT--ELSWISG-----DLLPGGQEPP 2127
1989 RRS-----YHSSLALSAHLNSDSCHKSDTHPSGGRERR 2023
2128 SPR-----DLKKYVSEAGSCRRPTSWLDEQRHSIAVCLDSGSOPLGTDPSNLG 2180
2024 SKERKHLSPDVSRNSEE-----RGTQADWESPERRORSRPS--EGRSQ-----TPNR-- 2070
2181 GQPLGPGSRPKKLSPPSITIDPPES--QGPRTPPSPGICLR-----RRAPS----- 2226
2071 ----QGTGSLSSPSVSDTSTPRSRRLQPPVPPKPRPLLSYSLIRHAGSISPPADG 2126
2227 SPSKDFLASGPPDSMAA-----SPSPKK 2249
2127 SEBGSPLTSALESNNAWLTSSNSPHPOQ 2156

RESULT 14
A47447
calcium channel protein alpha-1 chain (variant doe-1) - electric ray (Discopyge ommata)
C:Species: Discopyge ommata
C:Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: A47447
R:Horne, W.A.; Ellinor, P.T.; Inman, I.; Zhou, M.; Tsien, R.W.; Schwarz, T.L.
Proc. Natl. Acad. Sci. U.S.A. 90, 3787-3791, 1993
A:Title: Molecular diversity of Ca(2+) channel alpha 1 subunits from the marine ray Discopyge
A:Reference number: A47447; MUID:93248175; PMID:7683405
A:Accession: A47447
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-2223 <HOR>
A:Cross-references: UNIPROT:P56699
A>Note: sequence extracted from NCBI backbone (NCBI:P130671)
C:Superfamily: voltage-dependent calcium channel protein alpha-1 chain

Query Match 13.9%; Score 1656; DB 2; Length 2223;
Best Local Similarity 24.2%; Pred. No. 7.3e-93;
Matches 595; Conservative 385; Mismatches 811; Indels 668; Gaps 89;

35 GSAEKDPSADSEAGLPPAL--APV-----VFFVLSQDSRPSWCLRTVCNWP 82
44 GAAQGSAGFKQTRAQARTALYNPIPVHNCILTANKSLFLFGEDNIVKRSARVIEWPP 103
83 FERISMLVILLNCVTLGMFR--PCEDIACDSQRCRIIOAFDDFIAPFAVEMVVMVALG 140
104 FEYMLATILIANCVVLALEQLPNGD--KTPMAKSLQETPEYPIGIFCFEAGIKIVALG 160

Qy 141 -IFGKCYLGDTWNRLLDFFIVTAGMLEYSLDLQNVSFSAVRTVRLRPLRAINRVPSMRI 199
Db 161 FVPHKSYLRGNWVDFIVLSEGL--ATAATHFNRLRLRAVRLRPLKLVSGIPSLQI 218
Qy 200 LVTLLDTPMLGNVLLLCFFVFFIFGVQVQVWAGLNRNCFELPENFSLPLSVDLERY 259
Db 219 VLKSIKAMPVLLQIGLLFFAILMEFIIIGLEFYKGLHRTCYTDDAAAEEDLQF-- 274
Qy 260 QTENEDESPICSQPRENGMRCSCSVPTLRGDGGGPPCGCLDYEAYNSSNTTCVNMNQY 319
Db 275 -----PCGTQEPTRLCPNGTVCSYV-- 294
Qy 320 YTNCAGEHNPFGKAINFDNIGYAWIAIQVITLEGWVDIMYFMDA--HSFYNFIFILL 378
Db 295 -----IGNDGITQFDNILFALLTVFCITMEGWTTILYNTD DALGAMWNLVFIPL 346
Qy 379 IIVGSFMINICLVVIATOFSETKQES-----OLMREORVRFLSNASTLASFSEPGSC 432
Db 347 IIGSFFVNLVLGVGEFAKERHVENRRSFLKLRQOIE----- 389
Qy 433 YEELLKYLVIYILRKAARLAQVSRAGVRYGLLSSPALGGQETQPSSSCSRRRLSVH 492
Db 390 --RELNGYRANIDKAEVWMLLEENKAGEKSAL----- 420
Qy 493 HLVHHHHHHHHYHNGTTLRAPASPEIQDRDANGSRRLMLPPSTPALSGAPPGAES 552
Db 421 -----HVLRRATIKKR----- 432
Qy 553 VHSFYHADCHLEPVRCAQPPRSPSEASGRTVGSGKVYVTVHTPPPETLKEKALVEVA 612
Db 433 -----MEMIQTES-----SEDOYTRISS 450
Qy 613 SSGPPTLSLNPFGPYSSMHKLLTQSTGACQSCCKISSPCLKADSGACGPDSPCYCAR 672
Db 451 VGSPLARASI-----KSTKLLEGSS----- 470
Qy 673 AGAGEVELADREMPDSDSEAVVEFTODACHSLDRDPHSRRQSLGPDAPESVLAFWRLI 732
Db 471 -----YFRKE-----RML 479
Qy 733 CDTFRKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPELTWNALEISNIVFTSLPALEML 792
Db 480 RISIRHMKSHAFYIWLGLVALNTVCVAVVHYDQPLMLSNFLYYAEFTFLGLFSEFPL 539
Qy 793 KLVYGPFGYKPNYNIYFDGVIVLSVWEIV-----GOQGGLSVLRFLMRVLKLVRF 847
Db 540 KMYGCGPRLYFHSSFCFCGVIGSIFDVVWTLIRPETSFGISVLRLRLRIFKITKY 599
Qy 848 LPALQRLVVMKTMNDVATFCMLMLFIFISILGMHLFGCKFASERDGTLPDRKNFD 907
Db 600 WASLRLNVLSLMSMKSIISLLFLFLFVFWFALLGMQLFGQGFEE--GTFP--TNFD 655
Qy 908 SLLWAVTVFOILLTQDWNKVLVNGWAS-----TSSWAALYFTALMTFGNYVLNLLVAI 962
Db 656 TFPAAIITVFOILTGEDWNEVMYNGIKSKQGVNSGWSVYFVLTFLFGNYTLNVLAI 715
Qy 963 LVEGF-QAERISK-----REDASGQLSCIQ-----LPVDSQGGDANKSE----- 1000
Db 716 AVDNLANAQELTKEEQEEBAINQKHALQAKVSPMSAFGFESTERFRHKKHMSIWEA 775
Qy 1001 -----SEPDFFSLDG-DGDRKK-----CLALVSLGCEHPELRKSLPLP 1039
Db 776 RTSQLRRMQMSREALFTDALQLEGSRFRRHRSRIFEAESLRLAEQQAESHQGEV 835
Qy 1040 LIHTAATPMSLPKSTGCLGALGPASRRTS-----SSGSAEPFGAAHEMKSPSA 1089
Db 836 GRREAFKRSRLNS-----WQAPGDKKSSSIKVNQGGRALGRSVEAGASFRMAEPIRA 890
Qy 1090 RSPSHSPW-----SAASSWTSRRSRSLGR-APSLKERSPSG--ERRSLLSGEQ 1137
Db 891 RRRYSLYKARWGLSESAETSLSRPGKNGEGRLLQOLCEEQSGQLTQTPVWDAGQ 950

QY 1138 ES-----ODEBESSEERASPAHSRRHRSGLERE-----AKSSFDLPD----- 1176
Db 951 MKAFSWQGBEHSSEWNTPTDVTDD-PSGNGLEKESGRTPENGKEESANTSEQVNEQSNWL 1009
QY 1177 TLQV-----POLHRTASGRGSASEHQ-----DCNGKSASGLARALRPDPDPLD-- 1220
Db 1010 NLQNLQOATPDRELTTGTTRDTKDQKQEQTEIDVDCEN-----TETPMDSL 1056
QY 1221 ---GDDADDEGSKGRVRAWIRARLPACVLERDSWSAYIPFQPSRFLRLCHRIITHKM 1277
Db 1057 VTFGNAYSSSSSVKDEBKSS---KAIIPYT-----SMFLFRKTNPIRRVCHPVLNRY 1106
QY 1278 FDHVLVLIIFLNCITTIAMERKIDPHSAERIFLTLNVIPTAVFLAEMTVKVAALGWCFCG 1337
Db 1107 FEMCILIVIAASSVALAEDP-IKDSARNQVLFYDFYVTFGTFFEWIKMIDIGLVFH 1165
QY 1338 EOAYLRSSWNVDGLLVLSVIDI-LVSMVSDSGTKILGMLRLVRLRLTLRLPLRAVISAQ 1396
Db 1166 EGSYFRDVMNILDPIVVGALVAFATNLIGSSGKDINTIKSLRVLRLPLKTKRLP 1225
QY 1397 GLKLVETLMSLKPIGNVIVVCCAPFIIFGILGVQLFKGKFFVQCGEDTRNITNKSQCA 1456
Db 1226 KLRVAFDVCVTSKLVNFIIVYKLFMFIFAVIAVQLFKGKFFYC--TDSSKMT-KQDC- 1281
QY 1457 EASYRWVRHK-----YNFDNLGOALMSLFLVLASKDGVDMYDGLDAVGVDQO 1504
Db 1282 RGQVLYRQRTKLSIENGNTVTFHYDNVVMALLTFTVSTGEGWPQLQHSVDVTEADQG 1341
QY 1505 PIMNHNPMWLLYFISLLIVAFVFLNMVFGVVVFNHFKCHQOHEEBARREKRLRLE 1564
Db 1342 PIPGNRMEMSIFYIVYVFPVFPFVFNIFVALIITP-----QEQDKMLEES--SLE 1391
QY 1565 KKRKA-----QCKPY--YSDYSR--FRLLVHLLCTSHYLDLFTGTGVLGNVMTAMEHY 1615
Db 1392 KNERACIDFAISAKPLTRYPNQRTQYRWQFWQSPSFEYTLITMALNTVLMVMKHH 1451
QY 1616 QQQILDEALKICNYITVFLVLESVKLVAFGRFRFQDEBNQDLAIALLSIMGITLE 1675
Db 1452 SPPGFGASVKLMMIAFTITFTLECIILKIATGFLNYFRDSWNVDFVTVVGSISEIIVT 1511
QY 1676 EIE---VNASIPINPTIIRIMRVLIARVLKLMVGMRAALLDVMQALPQVGNLGLLF 1732
Db 1512 ECNLKFVNL-----FLKLFRAARLIKLRQGITIRILLWTFVQSPKALFYVCLLI 1562
QY 1733 MLUFFIFAALGVLEFGLDETHPCBGLGHATFRNFGMAFLFLRVSTGDNWNGIMKD 1792
Db 1563 AMLFFIYAIIGMQLFGNIGLDDHTP---INRHNHFTFPAALMLLFRSATGESQOEIMLA 1619
QY 1793 TL--RDGD--QESTCYNTVISPIFYVSVFLTAQFVLNVNVIATVLMKHLBESNKEAK---- 1844
Db 1620 CLSGKECEGTREPSG-GTDVAIFYVSVFIFLCSFLMLNLFVAVIMDNFVYLTRDSSILGP 1678
QY 1845 ---EAELEAELE-----LEMKT-LSPQPHSLGSPFLWPG-----VE 1878
Db 1679 HHLDEFVVAWEYDRAACGRHITMDYQMLTMSF---PLGLGKCKPSKVAYKRLVLMN 1734
QY 1879 GPQSPD-----SPKPGALHPAAHARSA-----SHFSLBHPTMQPHTELPQGD 1922
Db 1735 MPVTEDKTVHTSTLMGLIRLTALQIKLARGADKQQLDAELRKEIMTIWPHLSQ-KTLDL 1793
QY 1923 L-----TVKSGSVRTHSL-----PNDSYMCRGSTAGPLGHR----- 1956
Db 1794 LVPMTHTYSDLTGVGIYAMIMIMDYKQSNKKYQKLQEQSRTFMFQMEASSLPQIIS 1853
QY 1957 -GWLKPAQSGSVLSVHSPADTSTVILQLPKDAPHLQLPHSAPTGW-TIPKLPFGPSPL 2014
Db 1854 STKGLPLVLTGTGPDVDSR-SEFTPLVPL---PVMFQOGRSTSSQGEIHKQRKPELKKI 1909
QY 2015 AQR-----PLRRQA-AIRTDSDVQGLSGSLDLAELVSGSPFPPLARAYSFWGQSTQ 2065
Db 1910 KLEYPHYGHVLPDENQRAVSMPLREIE---SAED-----TSPLKRSU-----STP 1952
QY 2066 AQHSRSHSKISKMTTPAPCPGPE---PNWKGKP--PETRSLSLELDTLSWISGDLPLP 2120

Db 1953 AAHSNS-TWLNEXSLERA---GPEDLYKRSRRLPPSRSS-----N 1992
QY 2121 GGQEPSPRDLKKCYVBEAQSCORRPTSMLEQRRHSIAVSLDSGQPHLGTDPNSLG 2180
Db 1993 AGSRERCRSRERKHLSPERSVCS-----TGQCAH-----PSQHRGLD-QRLS 2034
QY 2181 GQPLGGPGSRPKKLLSPSITIDPPESQGRTPPSGICLRRRAPSDSKD-PLASGPP 2238
Db 2035 RSPSPGYSHRPRBOVN-SSVSESPVSSGTSPPKQG---ORQLPQTPSKRPLVSVSP 2089
RESULT 15
A37490
voltage-dependent calcium channel alpha 1E - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 24-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A37490
R;Soong, T.W.; Stea, A.; Hodson, C.D.; Dubel, S.J.; Vincent, S.R.; Snutch, T.P.
Science 260, 1133-1136, 1993
A;Title: Structure and functional expression of a member of the low voltage-activated ca
A;Reference number: A37490; MUID:93262464; PMID:8388125
A;Accession: A37490
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-2222 <SOO>
A;Cross-references: UNIPROT:Q07652; GB:L15453; NID:g310082; PIDN:AAA40855.1; PID:g310083
A;Experimental source: brain
A;Note: sequence extracted from NCBI backbone (NCBI:P132101)
C;Superfamily: voltage-dependent calcium channel protein alpha-1 chain
Query Match 13.9%; Score 1651.5; DB 2; Length 2222;
Best Local Similarity 23.6%; Pred. No. 1.4e-92;
Matches 591; Conservative 374; Mismatches 831; Indels 707; Gaps 77;
62 FYLSQDSRPRSWCLRTVCNPFWRISMLVILLNCVTLMGPR--PCEDIACDSQRCILQA 119
21 FIGEDNIVRYAKKLIDWPFPEYMIATIANCIVLALBQHLDEDDKTPNSRR---LEK 77
120 FDDFIFAFFAVEMVVMKVALG-IFGKKCYLGDWTNRDLDFIVIAGMLEYSLDLQN--VSF 176
78 TEPYFIGIFCFEAGIKIVLGFIFHKSYLRNGWNVMDFIVLSGILATAGTHTFNTHVDL 137
177 SAVRTVRLPLRAINRVPMSRLVTLTLLDPLMGNVLLLCFFVFFIGVIGVQLWAGL 236
138 RTLRAVRLPLKLVSGIPSLQIVLKSIMKAWPELLQIGLLFFAILMFAILGFEYSKG 197
237 LRNRCFLPENFSLPSVDLERYTYQTEDESPFICSPRENGMRSRCSVPTRLRGDGGGP 296
198 LHRACFMNNSGIL-----EGFDP-----PHPCGVQGC----- 224
297 PCGLDYEAYNSSNTTCVNNQYITNCSAGEHNPPFKGAINPDNITGYAMIAIFQVITLEGW 356
225 PAG--YE-----CKDW-----IGPNDGITQFDNILFAVLTVFQCITMBGW 262
357 VDIMYFMDA-HSPYNIYFILLIIVGSPMINCLVVIATQPSQETQKBSQLMRQVR 415
263 TTLYNTNDALGATWNLWYFIPLIIIGSFFVLNLVLGVLGSEFAKERERV-----ENRRA 317
416 FLSNASTLASFSEPGSCYSELKLVYLILKARLARLAQVSRAGVRVGLLSSPAPLGQE 475
318 FMK-----LRQQOI----- 327
476 TOPSSSCSRSHRRLSVHHLVHHHHHHHHHHLGNTLAPRASPEIQDQDANGSRRLMLP 535
328 -----ERELNGYRAWI-- 338
536 PPSTPALSGAPPGGAESVHSFYHADCHLEPVRCQAPPRSPSEASGRVTGSGKVPVTH 595
339 ----- 338
596 SPPPETLKEALVEVAASSGPPTLTSLNIPGPVSSMHKLELTOSTGACQSSCKISSPCL 655

Db	339	----	DXAEVWLA	BEKNKNGST	SALEVL	VRLEATTIKR	TEAMTRDSD	SDSEHCVD	SISSVGTPLA	394																																	
Qy	656	KADSGACG	DPSCPYCAR	GAGEVELA	DREMPDSD	SEAVYFTQD	AQHSDLRDP	PHRRORS	715																																		
Db	395	RASIKSTK	VDGASY	-----	PHKE	-----	-----	-----	413																																		
Qy	716	LGPDAEPSS	VLAFWRLLI	CDTFRKIV	DSKYFGRG	IMIALI	AVNTLSWG	IEVHEQPELTNAL	775																																		
Db	414	-----	RLRISIRHM	VKSQVY	WIVUSVA	INTACVAI	VHHNQPMWL	THLL	459																																		
Qy	776	EISNIVFTS	LFALEMLL	KLVIVG	PGFYIK	PNYINFD	GVIVIS	WVEIVGQ	830																																		
Db	460	YIAEFLGL	FLLEMSLK	MYMGPR	LYPHSS	FNCFD	FGVTVGS	IFEVVWAI	PRGTSFI	519																																	
Qy	831	SVLRTFLMR	VLKVRPL	PALQRL	VLVLMKT	WDNVA	TCMLML	FIPIFSIL	GMLFGCK	890																																	
Db	520	SVLRALRL	LRIFRIT	TYWASLR	NLVLSM	SKSIIS	LFLFLFL	FIVVFP	ALLGMLQFGR	579																																	
Qy	891	FASERDGT	LPRDKN	FDLSLL	WAIVTV	FQILTO	DNMKNLY	NGW----	ASTSMAALYFI	945																																	
Db	580	F- FN DDG	---TPS	ANDFT	TPAALMT	VFOILT	GEDN	WVNGIR	SOGGVSSG	WSAIYFI	635																																
Qy	946	ALMTFGNY	LVNLLVAIL	VEGF-Q	ABEISK-	---RED	ASQJSC	QLPVD	OSGGDANKSE	1000																																	
Db	636	VLTLFGNY	TLNVFLA	IVADNL	ANAQELT	KDEQEBE	EAFNQ	HALQAK	AEV-----	SPM	689																																
Qy	1001	SEDPFSPS	LDGDGR	KKCLAL	-----	-----	-----	-----	-----	VSLGEHPE	1030																																
Db	690	SAPNM-	-PS	TERRRR	HHMSW	PESSHU	RERRHH	MSW	WEQRTS	QLRRHM	QMSQEA	747																															
Qy	1031	LRKSLPL	LIHTA	ATPMS	-----	-----	-----	-----	-----	-----	-----	1076																															
Db	748	LNKEEA	PPMPLN	PLNPLS	PLNPA	NHPSLY	RPRPIE	GLALGL	EKECEER	ISRG	SSL	807																															
Qy	1077	PGAHEW	KSPPS	AKSPHS	-----	-----	-----	-----	-----	-----	-----	1104																															
Db	808	KGDTGGIT	SVLNDQ	RSPLSG	KREPPML	PRSCH	GNCDPT	QOET	GGGT	VVTF	PEDRARHQ	867																															
Qy	1105	SRSSRNL	GRAPSL	KRSPS	GBERRSL	TCEGOS	ODEE	SEES	PEERAS	PAGS	PHRRGSL	1164																															
Db	868	SORSRH	RVNTE	KESAS	ASRSR	-----	SASQ	RS	LD	EGVS	ID	GEKEHE	FQSSHR	KEPT	923																												
Qy	1165	EREAKS	FDL--	PD	TLOVP--	GL-----	-----	-----	-----	-----	-----	-----	-----	-----	1204																												
Db	924	IHEERTQ	DLRRT	NSLW	PRGSL	VGALDE	AEATPL	VQPO	PELV	GVGK	DAAL	TEQ	AE	SGSSE	983																												
Qy	1205	SGRLA	-----	RALR	DDPPL	-----	-----	-----	-----	-----	-----	-----	-----	-----	1219																												
Db	984	QALLAD	VQLD	VGRGIS	QSEPDLS	CMTMM	KAT	TESTS	VTVAI	PDVD	PLVD	SVIV	NI	SNK	1043																												
Qy	1220	-DGD	DA-----	DD	BNLS	KGBER	-----	VR	AWIR	ARLP	PAC	YLER	D	WS	SA	YIF	PPQSR	FRLL	1267																								
Db	1044	TDGEAS	PLKEA	ETKEE	EEVEK	KQK	KEK	ETG	KAMV	PHS-----	-----	-----	-----	-----	-----	-----	-----	-----	SM	FIST	TP	PIRK	1096																				
Qy	1268	LCHRIITH	KMDH	VULV	IIFL	NCITIA	MER	KPID	PHSA	ERI	PLT	LSNY	I	ETA	FL	EA	MTV	1327																									
Db	1097	ACHVIVN	LYFEM	CILLIV	AASS	IALA	AE	PVL	TNS	ERNK	V- RY FD	VY	FT	VT	FT	TE	WVI	1155																									
Qy	1328	KVALG	WCFG	COAYL	RRSS	NVLD	GLL	V	LIS	VIDI	-LV	SMV	S	D	S	G	T	K	L	G	M	L	R	V	L	R	T	L	1386														
Db	1156	KNID	GLLI	QGS	FR	DLN	ILDF	VVVV	GA	VA	FAL	ANAL	G	T	N	K	R	D	I	K	T	K	S	L	R	V	L	V	L	1215													
Qy	1387	RPLRV	ISAQ	GLK	V	VE	T	M	S	S	K	P	I	G	N	V	V	I	C	A	P	I	I	F	G	I	L	G	V	Q	L	F	K	G	K	F	F	V	C	-----	QGE	1444	
Db	1216	RPLKTI	KRLPK	LA	V	Q	C	V	W	T	S	L	N	V	F	L	I	V	Y	K	F	M	F	I	A	V	A	V	Q	L	F	K	G	P	F	F	C	T	D	S	S	K	1275
Qy	1445	DTRN	-----	IT	N	S	D	C	A	E	A	S	V	R	-W	R	H	K	N	F	D	N	I	G	A																		

Qy	1558	KRLRLLEKRRKA	-----OCKPY--YSDYSR--FRLLVHHLCTSHVLDLFTICVGLNVV	1600
Db	1389	---CSLEKNERACIDFAISAKPLTRVMPQNRHTFQVRVWHFVVVSPSEYTIMAMIALNTV	1445	
Qy	1609	TMAMEHVQOPOILDEALKICNYITFTVIFVLESFKLVAFCRRFFQDRWNQLDLAIVLLS	1668	
Db	1446	VLMKMYISAPWTYELALKYINTAFTWVFSLECVLKVIAFGFLNYFRDTWNIPDFITWIGS	1505	
Qy	1669	IMGITIEEIVNASLPINPFTIRIMRVLRIARVLKLLKMAVGMKALLDVTMOALPOVGNL	1728	
Db	1506	ITEIILTDSKLVNTSGFNMFLKLFRA---ARLIKLRQGYTIRILLTWFVQFKALPYV	1562	
Qy	1729	GLIFMLLFFIFPAALGVELDGLCED-ETHPECEGLGRHATFRNFGMAFLTLFRVSTGDNWN	1787	
Db	1563	CLLIAMLFFYIYALIGOVFNCKILDBESH-----INRHNFRSFGSLMLLFRSATGEAWQ	1618	
Qy	1788	GIMKDTL--RDCDOESTC-----YNTVISPFIYFVSFLVTAQFVLNVVIAVLMKHL	1836	
Db	1619	EIMSLCGERKCEPDITAPSGQNESERCGTDLAVVYFVSFIFPCSFLMLNLFVAVIMDNF	1678	
Qy	1837	EEGNKEAK-----EEAELEAELE-----LEMKTLSPQHPSPGSPPLWPG	1876	
Db	1679	EYLTRDSSILGPHHLDEFVRVWAEYDRAACGRITHYTEMYLEMTLM-----SPPGLG	1730	
Qy	1877	VEGPDSPDSPKPGALLHPAAHARSASFHSLEHPMQHPTELPGLDILLTVKSGVSRTHSL	1936	
Db	1731	KRCPSKVAYKRLVLMNPFVAEDMTVHT--STLMALIRTALD-----IKIAGGDROQL-	1783	
Qy	1937	PNDSYMCRHGSTATGEPGLGHRGWGL-----PRAQSGSVLSVHSHQPADTSYI-----	1981	
Db	1784	--DSELQKETLAIWPHLSQKMLDLLVMPWKASDLTVGKIYAAMIMDYIKQSKVKKQROQ	1841	
Qy	1982	LOLPKDAP--HLLOPHGAP-----TWGTIPKLP-----PGRSPLAQRPL---	2019	
Db	1842	LEEKNAPMFQMEPSSLPQEIISNAKALPYLOQDPVSGLSGRSGVPSMSPLSQEIPQL	1901	
Qy	2020	-----RQAAIRTDLSLDVOGLGR-----EDLLAEVSGPSPPLARAY	2056	
Db	1902	ACMPDADGQFOEQOQSLVTTDPSMRRSFTIRDKRSNSSWLBEFSMERSENITYKSRRR	1961	
Qy	2057	SFWQCSSTOAOQH-----SRSHKISKIMTTP-----AP	2085	
Db	1962	SY--HSSLRLSAHLNLSDSHGKSDTHRSGCGRGRSKERKHLIISPDVSRNCNSEERGTOAD	2019	
Qy	2086	CPGPEPNWGKPPPTRS-----SLE-----LDTELSWTSGLDLPPEGQEEPPSP	2129	
Db	2020	WESPERRQSRSPSEGRSQTPNRQGTGLSSSIPISDTSTPRKSRQLPP-----VPPKP	2075	
Qy	2130	RDLLKKCVSVEAQSCORRPTSMWLDQCRSHSIASVCLDSGSOPLHGTDPFNLGGQPLGGPGS	2189	
Db	2076	RPLLSYSGL-----MRHTGGISPPPDGSE-----GGSPLASQAL	2109	
Qy	2190	RPKKK--LSPPSITIDPPESQGRPT-----PSPGICLRRRAPSSD	2228	
Db	2110	FSNSACTTESNSLHPQOOGHPSPOHYISEPYLALHEDSHASD	2152	

Search completed: April 13, 2005, 16:40:40
Job time : 87 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 13, 2005, 16:01:41 ; Search time 276 Seconds
(without alignments)
4204.244 Million cell updates/sec

Title: US-09-611-257A-37

Perfect score: 11904

Sequence: 1 MDEEDGAGAESQPRSFM.....PKDVLSLGLSDPADLDP 2266

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 03.*

1: uniprot_sprot.*

2: uniprot_trenbl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	11815.5	99.3	2377	1 CCAG HUMAN	O43497 homo sapien
2	11133.5	93.5	2295	2 Q9WU72	Q9WU72 mus musculus
3	11111	93.3	2288	2 Q9WU88	Q9WU88 rattus norv
4	10945	91.9	2254	1 CCAG RAT	O54898 rattus norv
5	10913	91.7	2248	2 Q6PFV8	Q6PFV8 mus musculus
6	6573	55.2	1389	2 Q6ZPX4	Q6ZPX4 mus musculus
7	6217.5	52.2	2359	1 CCAH RAT	Q9eq60 rattus norv
8	6210	52.2	2353	1 CCAH HUMAN	Q95180 homo sapien
9	6176.5	51.9	2365	1 CCAH MOUSE	Q88427 mus musculus
10	5496.5	46.2	2223	1 CCAI HUMAN	Q9p0x4 homo sapien
11	5383	45.2	1835	1 CCAI RAT	Q9z0y8 rattus norv
12	4836	40.6	1994	2 Q7Z6S8	Q7z6s8 homo sapien
13	4200.5	35.3	1762	2 Q7PQV4	Q7pqv4 anopheles g
14	4180	35.1	2893	2 Q9W433	Q9W433 drosophila
15	3855	32.4	1837	2 Q967R4	Q967r4 caenorhabdi
16	3845.5	32.3	1852	2 Q7Z002	Q7z002 caenorhabdi
17	3828.5	32.1	1844	2 Q7YZR6	Q7yzt6 caenorhabdi
18	3823	32.1	1885	2 Q7Z003	Q7z003 caenorhabdi
19	3683.5	30.9	1460	2 Q80TJ2	Q80tj2 mus musculus
20	2925.5	24.6	1418	2 Q7JBP4	Q7jbp4 caenorhabdi
21	2866	24.1	1942	2 Q869H0	Q869h0 lymnaea sta
22	2089	17.5	1211	2 Q8MQ95	Q8mq95 caenorhabdi
23	1746.5	14.7	2339	1 CCAB HUMAN	Q90975 homo sapien
24	1740.5	14.6	2333	2 Q89089	Q89089 rattus norv
25	1732.5	14.6	2327	1 CCAB MOUSE	O55017 mus musculus
26	1729.5	14.5	2331	2 Q9TTA4	Q9tta4 bos taurus
27	1722	14.5	2336	1 CCAB RAT	Q92294 rattus norv
28	1712.5	14.4	541	2 Q6PE92	Q6pe92 mus musculus
29	1710	14.4	2339	1 CCAB RABIT	Q95152 oryctolagus
30	1697.5	14.3	2357	2 Q9PUM6	Q9pum6 gallus gall
31	1697	14.3	2259	1 CCAE_RABIT	Q92343 oryctolagus

32	1689	14.2	1810	2	O44930	O44930 aiptasia pa
33	1688.5	14.2	2295	2	Q923K6	Q923k6 rattus norv
34	1685	14.2	2346	2	Q9PW47	Q9pw47 gallus gall
35	1683	14.1	2332	2	Q9PW45	Q9pw45 gallus gall
36	1681	14.1	2272	1	CCAE MOUSE	Q61290 mus musculus
37	1666.5	14.0	2312	1	CCAE HUMAN	Q15878 homo sapien
38	1664.5	14.0	1891	2	O970I7	O970i7 stylophora
39	1664.5	14.0	2321	2	Q9PUM4	Q9pum4 gallus gall
40	1662	14.0	2182	2	Q9PUM5	Q9pum5 gallus gall
41	1657	13.9	1847	2	Q6RKB0	Q6rkb0 brachydanio
42	1656	13.9	2223	1	CCAE DISOM	P56699 discopyge o
43	1654	13.9	2304	2	Q9BMO4	Q9bmq4 blattella g
44	1651.5	13.9	2222	1	CCAE RAT	Q07652 rattus norv
45	1649.5	13.9	2171	2	Q9PW46	Q9pw46 gallus gall

ALIGNMENTS

RESULT 1

ID	CCAG HUMAN	STANDARD;	PRT;	2377 AA.
AC	O43497; Q94770; Q9NYU4; Q9NYU5; Q9NYU6; Q9NYU7; Q9NYU8;			
AC	Q9NYU9; Q9NYV0; Q9NYV1; Q9UHN9; Q9UHP0; Q9ULU6; Q9UNG7; Q9V5T2;			
AC	Q9V5T3;			
DT	15-JUL-1999 (Rel. 38, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	05-JUL-2004 (Rel. 44, Last annotation update)			
DE	Voltage-dependent T-type calcium channel alpha-1G subunit (Voltage-			
DE	gated calcium channel alpha subunit Cav3.1) (Cav3.1c) (NBR13).			
GN	Name=CCNALG; Synonyms=KIAA1123;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING (ISOFORMS 4 AND 5).			
RC	TISSUE=Brain;			
RX	MEDLINE=20014446; PubMed=10548410; DOI=10.1016/S0304-3940(99)00716-8;			
RA	Mittman S., Guo J., Agnew W.S.;			
RT	"Structure and alternative splicing of the gene encoding alpha1G, a			
RT	human brain T calcium channel alpha subunit."			
RL	Neurosci. Lett. 274:143-146(1999).			
RN	[2]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RC	TISSUE=Brain;			
RX	MEDLINE=20115462; PubMed=10648811; DOI=10.1016/S0014-5793(99)01756-1;			
RA	Cribbs L.L., Gomora J.C., Daud A.N., Lee J.-H., Perez-Reyes E.;			
RT	"Molecular cloning and functional expression of ca(v)3.1c, a T-type			
RT	calcium channel from human brain."			
RL	FEBS Lett. 466:54-58(2000).			
RN	[3]			
RP	SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING (ISOFORMS 1-2 AND 6-13).			
RC	TISSUE=Brain;			
RX	MEDLINE=20158909; PubMed=10692398; DOI=10.1074/jbc.275.9.6090;			
RA	Montell A., Chemin J., Bourinet E., Mennesier G., Lory P.,			
RT	"Molecular and functional properties of the human alpha1G subunit that			
RT	forms T-type calcium channels."			
RL	J. Biol. Chem. 275:6090-6100(2000).			
RN	[4]			
RP	SEQUENCE FROM N.A. (ISOFORM 14).			
RA	Kishi F.;			
RL	Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.			
RN	[5]			
RP	SEQUENCE OF 550-2377 FROM N.A. (ISOFORM 13).			
RC	TISSUE=Brain;			
RX	MEDLINE=22158633; PubMed=12168954;			
RA	Nakajima D., Okazaki N., Yamakawa H., Kikuno R., Ohara O., Nagase T.;			
RT	"Construction of expression-ready cDNA clones for KIAA genes: manual			
RT	curation of 330 KIAA cDNA clones."			
RL	DNA Res. 9:99-106(2002).			
RN	[6]			

FT	TRANSMEM	151	170	S3 of repeat I (Potential).	
FT	DOMAIN	171	175	Extracellular (Potential).	
Query Match					
Best Local Similarity 95.2%; Pred. No. 0;					
Matches 2264; Conservative 1; Mismatches 1; Indels 111; Gaps 2;					
Qy	1	MDEEDGAGAEESQPRSFRLNDLSGAGGPGPGSAEKDPGSADSAEGLPYPALAPV	60		
Db	1	MDEEDGAGAEESQPRSFRLNDLSGAGGPGPGSAEKDPGSADSAEGLPYPALAPV	60		
Qy	61	FFYLSQDSRPSWCLRTVCPNPFERISMLVTLNVCVLGMFRPCEDIACDSQRCRIIQAF	120		
Db	61	FFYLSQDSRPSWCLRTVCPNPFERISMLVTLNVCVLGMFRPCEDIACDSQRCRIIQAF	120		
Qy	121	DDFIAPFAVEMVVMVALGIFGKKCYLGDWTNRLLDFFIVIAAGMLEYSLDLQNVFSFAVR	180		
Db	121	DDFIAPFAVEMVVMVALGIFGKKCYLGDWTNRLLDFFIVIAAGMLEYSLDLQNVFSFAVR	180		
Qy	181	TVRVLRPLRAINRVPNRILVTLTLLDPLMGNVLLLCFFVFFIFGIVGQVLMAGLNR	240		
Db	181	TVRVLRPLRAINRVPNRILVTLTLLDPLMGNVLLLCFFVFFIFGIVGQVLMAGLNR	240		
Qy	241	CFLPENSLPLSVDLERYOTENEDSPFICSPRENGMRSCRVPTLRGDGGGPPCGL	300		
Db	241	CFLPENSLPLSVDLERYOTENEDSPFICSPRENGMRSCRVPTLRGDGGGPPCGL	300		
Qy	301	DYEAYNSSNTTCVMNQYTNCSAGBNPKGAINFDNIGYAMIAIFQVITLGGWYDIM	360		
Db	301	DYEAYNSSNTTCVMNQYTNCSAGBNPKGAINFDNIGYAMIAIFQVITLGGWYDIM	360		
Qy	361	YFVMDAHSFNYFIYFILLIIVGSFMINCLVVIATQFSETKQRESQMRQVRFLSNA	420		
Db	361	YFVMDAHSFNYFIYFILLIIVGSFMINCLVVIATQFSETKQRESQMRQVRFLSNA	420		
Qy	421	STLASFEPGSCYBELLYVILRKAARLAQVSRAGVRVGLSSPAPLGGQETOPSS	480		
Db	421	STLASFEPGSCYBELLYVILRKAARLAQVSRAGVRVGLSSPAPLGGQETOPSS	480		
Qy	481	SCSRSHRRLSVHILVHHHHHHHHYHLNGTGLRAPRASPEIQDRDANGSRRLMPPSTP	540		
Db	481	SCSRSHRRLSVHILVHHHHHHHHYHLNGTGLRAPRASPEIQDRDANGSRRLMPPSTP	540		
Qy	541	ALSGAPGGAESVHSFYHADCHLBPVRCQAPPPRSPSEASGRTVGSKVPTVHTSPPE	600		
Db	541	ALSGAPGGAESVHSFYHADCHLBPVRCQAPPPRSPSEASGRTVGSKVPTVHTSPPE	600		
Qy	601	TLKEKALVEVAASGPPTLSLNPFGPYSSMHKLLTQSTGACQSSCKISSPCLKADSG	660		
Db	601	TLKEKALVEVAASGPPTLSLNPFGPYSSMHKLLTQSTGACQSSCKISSPCLKADSG	660		
Qy	661	ACGPDSCPYCARAGAGEVELADREMPDSDSEAVYFTQDAQHSDLRDPHRRQRSLGPD	720		
Db	661	ACGPDSCPYCARAGAGEVELADREMPDSDSEAVYFTQDAQHSDLRDPHRRQRSLGPD	720		
Qy	721	EPSSVLAFWRLICDTFRKIVDSKYFGRGIMAILVNTLSMGIEYHQPPELTNALEISNI	780		
Db	721	EPSSVLAFWRLICDTFRKIVDSKYFGRGIMAILVNTLSMGIEYHQPPELTNALEISNI	780		
Qy	781	VFTSLFALEMLLKVLYGPGYIKNPYNIPOGVLVLSVWEIVCOQGGSLVLTFFLMR	840		
Db	781	VFTSLFALEMLLKVLYGPGYIKNPYNIPOGVLVLSVWEIVCOQGGSLVLTFFLMR	840		
Qy	841	VKLVRFLPALORQLVLMKTMNDVATFCMLLMFLIFIFSLGNMHLFGCKFASERDGTLL	900		
Db	841	VKLVRFLPALORQLVLMKTMNDVATFCMLLMFLIFIFSLGNMHLFGCKFASERDGTLL	900		
Qy	901	PDRKNFDSLLWAIIVTVFQILTQEDWNKVLYNGMASTSSWAALYFIALMTFGNYVFLNLLV	960		
Db	901	PDRKNFDSLLWAIIVTVFQILTQEDWNKVLYNGMASTSSWAALYFIALMTFGNYVFLNLLV	960		
Qy	961	AILVEGFOABEISKREDASGQLSCIQLPVDSQGDANKSSEPPDFSPSLDGDGRKKCL	1020		

Db	961	AILVEGFOABEISKREDASGQLSCIQLPVDSQGDANKSSEPPDFSPSLDGDGRKKCL	1020		
Qy	1021	ALVSLGHPBLRKSLLPPLIIHTAATPMSLPKSTSTGLGALGPASRRRTSSSGSAEPGAA	1080		
Db	1021	ALVSLGHPBLRKSLLPPLIIHTAATPMSLPKSTSTGLGALGPASRRRTSSSGSAEPGAA	1080		
Qy	1081	HEMKSPPSAESSPHSPMSAASSWTSRBSRNSLGRAPSLKRRSPSGRRSLLSGEGQESQ	1140		
Db	1081	HEMKSPPSAESSPHSPMSAASSWTSRBSRNSLGRAPSLKRRSPSGRRSLLSGEGQESQ	1140		
Qy	1141	DEBESSEERASPAQSDHRRHRSLEERAKSFDLPDTPQLVPLHRTASGRSASEHODCN	1200		
Db	1141	DEBESSEERASPAQSDHRRHRSLEERAKSFDLPDTPQLVPLHRTASGRSASEHODCN	1200		
Qy	1201	GKSASGRALARALPDDPPLDGDADDDEGNLSKSERVNAWIRARLPACCLERDSWSAIFP	1260		
Db	1201	GKSASGRALARALPDDPPLDGDADDDEGNLSKSERVNAWIRARLPACCLERDSWSAIFP	1260		
Qy	1261	PQSRFRLLCHRIITHKMPDHVVLVIIPLNCITITAMERPKIDPHSAERIFLTSNYIETAV	1320		
Db	1261	PQSRFRLLCHRIITHKMPDHVVLVIIPLNCITITAMERPKIDPHSAERIFLTSNYIETAV	1320		
Qy	1321	FLAEMTVKVVVALGWCGEQAYLRSSMNVDGLLVLISVIDILVSMVSDSGTKILGMLRVL	1380		
Db	1321	FLAEMTVKVVVALGWCGEQAYLRSSMNVDGLLVLISVIDILVSMVSDSGTKILGMLRVL	1380		
Qy	1381	RLLRTRPLRVIIRAQGLKLVETLMSLPIGNIVVICAPFIIFGILGVQLPKGFV	1440		
Db	1381	RLLRTRPLRVIIRAQGLKLVETLMSLPIGNIVVICAPFIIFGILGVQLPKGFV	1440		
Qy	1441	COGEDTRNITNKSDCAEASVYRVRHKKYFNFNGLQALMSLFLVASKDQWVDIMYDGLDAVG	1500		
Db	1441	COGEDTRNITNKSDCAEASVYRVRHKKYFNFNGLQALMSLFLVASKDQWVDIMYDGLDAVG	1500		
Qy	1501	VDQOPIMNHNPMWLLYFISPELLIVAFVLMFVGVVVENFHKCRHQHQBEEAREERKRL	1560		
Db	1501	VDQOPIMNHNPMWLLYFISPELLIVAFVLMFVGVVVENFHKCRHQHQBEEAREERKRL	1560		
Qy	1561	RRLEKRR-----KAQCKPYYSYDSYRFRLLVHHLCTSHYLDLFTGV	1602		
Db	1561	RRLEKRRNLMDDVITAGSSASASAEQAQCKPYYSYDSYRFRLLVHHLCTSHYLDLFTGV	1602		
Qy	1603	IGLVNVTMAHEHYQOQOILDEALKICNYIFTVIFVLESVKLVAFGRRFPQDRWNOLDL	1662		
Db	1621	IGLVNVTMAHEHYQOQOILDEALKICNYIFTVIFVLESVKLVAFGRRFPQDRWNOLDL	1680		
Qy	1663	AIVLLSTMGITLLEEIVNASLNPITIRIIRVLRIRARVLKLMVGMARALLDTVMQAL	1722		
Db	1681	AIVLLSTMGITLLEEIVNASLNPITIRIIRVLRIRARVLKLMVGMARALLDTVMQAL	1740		
Qy	1723	POVGNLGLLPMLLFFIPAAALGVLEFGDLECDETHPCCEGLGRHATFRNFGMAFLTLFRVST	1782		
Db	1741	POVGNLGLLPMLLFFIPAAALGVLEFGDLECDETHPCCEGLGRHATFRNFGMAFLTLFRVST	1800		
Qy	1783	GDWNGIMKDTLRDCDOESTCYNTVISPPIYFVSFVLTAQFVLVNVVITAVLMKHLEESNKE	1842		
Db	1801	GDWNGIMKDTLRDCDOESTCYNTVISPPIYFVSFVLTAQFVLVNVVITAVLMKHLEESNKE	1860		
Qy	1843	AKEEAELEAELEEMKTLSPQHPSPGSPFLWPQVEGPDSPDKPGALHPAAHARSASH	1902		
Db	1861	AKEEAELEAELEEMKTLSPQHPSPGSPFLWPQVEGPDSPDKPGALHPAAHARSASH	1920		
Qy	1903	FSLEHPT-----	1909		
Db	1921	FSLEHPTDRQLFDTISILLIQGSLEWELKLMDELACGPGQSPAPSPAPSLGSDDPQIPLAE	1980		
Qy	1910	-----MQHPTELPGDILLTVKSG	1929		
Db	1981	MEALSITSETSVSPSCSLATDDBSLPDDMHTLLLSALESNNQHPTELPGDILLTVKSG	2040		
Qy	1930	VSRTHSLPNDSYMCRHGSTAEGLGHRGWGLPKAQSGSVLSVHSQADTTSYIQLPKDAP	1989		
Db	2041	VSRTHSLPNDSYMCRHGSTAEGLGHRGWGLPKAQSGSVLSVHSQADTTSYIQLPKDAP	2100		

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QY 1990 HLIOPHSAPTGWIPKLPGRSPLAQRPLRQAARTDSDLYOGLGSREDLLAELVSGPS 2049
Db 2101 HLIOPHSAPTGWIPKLPGRSPLAQRPLRQAARTDSDLYOGLGSREDLLAELVSGPS 2160
QY 2050 PPLARAYSFVWGQSTQAQHSRSHKISKHMTTPAPCPGPEPNWKGPPETRSSLELDT 2109
Db 2161 PPLARAYSFVWGQSTQAQHSRSHKISKHMTTPAPCPGPEPNWKGPPETRSSLELDT 2220
QY 2110 LSWISGDLPLPGGQEPSPRDLKCKYVSAQSCQRRPTSWLDEQRHSHIANVCLSDSGSQ 2169
Db 2221 LSWISGDLPLPGGQEPSPRDLKCKYVSAQSCQRRPTSWLDEQRHSHIANVCLSDSGSQ 2280
QY 2170 PHLTGDSNLSGGPLGPGSRPKKLSPPSITIDPPESQGPRTPPSPGICLRRRAPSSDS 2229
Db 2281 PHLTGDSNLSGGPLGPGSRPKKLSPPSITIDPPESQGPRTPPSPGICLRRRAPSSDS 2340
QY 2230 KDPLASGPPDSMAASPSPKDVLSSLGSLSDPADLDP 2266
Db 2341 KDPLASGPPDSMAASPSPKDVLSSLGSLSDPADLDP 2377

RESULT 2
Q9WUT2
ID Q9WUT2 PRELIMINARY; PRT; 2295 AA.
AC Q9WUT2;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Voltage-gated calcium channel, alpha-1-G subunit.
GN Name=Cacna1g;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=99189326; PubMed=10087148;
RA Klugbauer N., Marais E., Lacinova L., Hofmann F.;
RT "A T-type calcium channel from mouse brain.";
RL Pfluegers Arch. 437:710-715(1999).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to the calcium channel alpha-1 subunits
CC family.
DR EMBL; AJ012569; CAB40793.1; -.
DR MGD; MGI:1201578; Cacna1g.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR GO; GO:0005886; C:plasma membrane; IDA.
DR GO; GO:0005245; F:voltage-gated calcium channel activity; IDA.
DR InterPro; IPR001682; Ca/Na_pore.
DR InterPro; IPR002111; Cat_channel_TripI.
DR InterPro; IPR002077; Ca_channel_alpha.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR005820; M+channel_nlg.
DR InterPro; IPR005445; TVDCCalpal.
DR Pfam; PF00520; Ion_trans_4.
DR PRINTS; PR00167; CACHANNEL.
DR PRINTS; PR01629; TVDCCALPAL.
KW Calcium; Calcium channel; Calcium transport; Calcium-binding;
KW Ion transport; Ionic channel; Transmembrane; Transport;
KW Voltage-gated channel.
SQ SEQUENCE 2295 AA; 253957 MW; FE817D054ED26984 CRC64;

Query Match 93.5%; Score 11133.5; DB 2; Length 2295;
Best Local Similarity 93.3%; Pred. No. 0;
Matches 2142; Conservative 32; Mismatches 91; Indels 31; Gaps 5;

QY 1 MDEEDGAGAESGQPRSMFLNDLSGAGRGPCSAKXDPGSADSEAEGLPYALAPV 60
Db 1 MDEEDGAGAESGQPRSMFLNDLSGAGRGPCSAKXDPGSADSEAEGLPYALAPV 60
QY 61 FFYLSQDSRPSWCLRTVCNPFERVSNMLVILLNCVTLGMFRPCEDACDSQRCRILOAF 120
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Db 61 FFYLSQDSRPSWCLRTVCNPFERVSNMLVILLNCVTLGMFRPCEDACDSQRCRILOAF 120
QY 121 DDFIFAFPAVEMVVMVALGIFGKKCYLGDWTNRLDFFIAGLMLEYSLDQNVSFSAVR 180
Db 121 DDFIFAFPAVEMVVMVALGIFGKKCYLGDWTNRLDFFIAGLMLEYSLDQNVSFSAVR 180
QY 181 TVRVLRLPRLAENRVPSEMRILVTLLDTPMLGNVLLLCFFVFFIFGIVGVLMAGLLNR 240
Db 181 TVRVLRLPRLAENRVPSEMRILVTLLDTPMLGNVLLLCFFVFFIFGIVGVLMAGLLNR 240
QY 241 CFLPENFSLPLSVLERYOTENEDSPFICOSPENGMRSCRSVPTLRGGGGPPCGL 300
Db 241 CFLPENFSLPLSVLERYOTENEDSPFICOSPENGMRSCRSVPTLRGGGGPPCGL 300
QY 301 DYEANSSNTTVCNNNOYTCNSAGEHNPFGAINFDNIGYAMIAIFQVITLEGWVDM 360
Db 301 DYEANSSNTTVCNNNOYTCNSAGEHNPFGAINFDNIGYAMIAIFQVITLEGWVDM 360
QY 361 YFVMDAHSFYNFYFILLIIVGSPFMINCLVVIATQFSETKQESQMRQVRFLNSA 420
Db 361 YFVMDAHSFYNFYFILLIIVGSPFMINCLVVIATQFSETKQESQMRQVRFLNSA 420
QY 421 STLASFSPGSCYEELLKVLVYLKKAARLAQVSRAAGVRVGLLSSPAPLGGGTQPS 480
Db 421 STLASFSPGSCYEELLKVLVYLKKAARLAQVSRAAGVRVGLLSSPAPLGGGTQPS 480
QY 481 SCSRSRRLSVHHLVHHHHHHHHYHLGNTGLRAPSPASPEIQDRDANGSRRLMLPPSTP 540
Db 481 SCSRSRRLSVHHLVHHHHHHHHYHLGNTGLRAPSPASPEIQDRDANGSRRLMLPPSTP 540
QY 541 ALSGAPPGAESVHSFYHADCHLEVPVCOAPPPSPSEASGRTVSGVGKYPVTVHTSPPE 600
Db 541 TPGSGPPRGAEVHSFYHADCHLEVPVCOAPPPSPSEASGRTVSGVGKYPVTVHTSPPE 600
QY 601 TLKEKALVEVAASSGPPITLSLNIPPGVSSMHKLETTQSTGACOSSCKISPCAKADSG 660
Db 601 MLKXALVEVAPSPGPPITLTENIPPGPSSMHKLETTQSTGACHSSCKISSPCSADSG 660
QY 661 ACPGSPCYCARAGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDDHSRQRSLGDDA 720
Db 661 ACPGSPCYCARAGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDDHSRQRSLGDDA 720
QY 721 EPSSVLAFWRLICDTPRKIVDSKYFGRGMIAILVNTLSMGIYHEQPEELTNALEISNI 780
Db 721 EPSSVLAFWRLICDTPRKIVDSKYFGRGMIAILVNTLSMGIYHEQPEELTNALEISNI 780
QY 781 VFTSLFALEMLKLLVYGPFGYIKNPYNIFDGVIVISVWEIVGQGGGLSVLRTFLMR 840
Db 781 VFTSLFALEMLKLLVYGPFGYIKNPYNIFDGVIVISVWEIVGQGGGLSVLRTFLMR 840
QY 841 VLKLVFLPALORQLVLMKTDNVATFCMLMLFIFISILGMHLFGCKFASERDGDTL 900
Db 841 VLKLVFLPALORQLVLMKTDNVATFCMLMLFIFISILGMHLFGCKFASERDGDTL 900
QY 901 PDRKNFDSLILWAIVTVFQILITQEDMNKVLNGMASTSSWAALFYFIALMTFGNYVFNLLV 960
Db 901 PDRKNFDSLILWAIVTVFQILITQEDMNKVLNGMASTSSWAALFYFIALMTFGNYVFNLLV 960
QY 961 AILVEGFQABEISKREDASQSLSCIQLPVDQSGDANKSESPDPSPSLDGDGRKKCL 1020
Db 961 AILVEGFQABEISKREDASQSLSCIQLPVDQSGDANKSESPDPSPSLDGDGRKKCL 1020
QY 1021 ALVSLGHEPRLKSLPLLIHTAATPMSLPKSTSTGLGEALGPASRRRTSSSGSAPFGAA 1080
Db 1021 ALVSLGHEPRLKSLPLLIHTAATPMSLPKSTSTGLGEALGPASRRRTSSSGSAPFGAA 1080
QY 1081 -HEMKSPPSARSPPHSPWSAASWTSSRSRSLGRAPSLKRRSPSGERRSLLSGCGQES 1139
Db 1081 -HEMKSPPSARSPPHSPWSAASWTSSRSRSLGRAPSLKRRSPSGERRSLLSGCGQES 1140
QY 1140 QDEESSESEERASPGSDHHRGSLREAKSSFDLPTLTQVPCLHRTASGRGASDHQC 1199
Db 1140 QDEESSESEERASPGSDHHRGSLREAKSSFDLPTLTQVPCLHRTASGRGASDHQC 1199
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Db 1141 QDEBESSEDRASPAQSDHRRHGRSLERAKSSFDLPTDLOVPLGLHRTASGRSSASEHQDC 1200
Qy 1200 NGKASGRLALAPDDPPLDGDADDDEGNLSKGERVRAWTRAKLPACYLERDSWSAYIF 1259
Db 1201 NGKASGRLALTRADDPLDGDADDDEGNLSKGERLAWVRARLAPACRERDSWSAYIF 1260
Qy 1260 PPOSRFLLCHRIITHKMFDFHVLVIFLNCITITAMERPKIDPHSAERIFLTLGNYLFTA 1319
Db 1261 PPOSRFLLCHRIITHKMFDFHVLVIFLNCITITAMERPKIDPHSAERIFLTLGNYLFTA 1320
Qy 1320 VFLAEMTVKVALWCFCGEQAYLRSSNMVNLGLLVLISVIDILVSMVSDSGTKILGMLRV 1379
Db 1321 VFLAEMTVKVALWCFCGEQAYLRSSNMVNLGLLVLISVIDILVSMVSDSGTKILGMLRV 1380
Qy 1380 LRLRLRPLRVLISRAQGLKLVETLMSLKPIGNVVICAPFIIFGILGVQLFKGKPF 1439
Db 1381 LRLRLRPLRVLISRAQGLKLVETLMSLKPIGNVVICAPFIIFGILGVQLFKGKPF 1440
Qy 1440 VCOGEDTRNITNKSDCAEASVRWRHRYKYNFNLGALMSLFLVASKOGWVDIMYDGLDVA 1499
Db 1441 VCOGEDTRNITNKSDCAEASVRWRHRYKYNFNLGALMSLFLVASKOGWVDIMYDGLDVA 1500
Qy 1500 GVDQOPIMNHNPMMLLYFISPLLVAFFVLMFVGVVNFHFKRQHQEERARRRBEKR 1559
Db 1501 GVDQOPIMNHNPMMLLYFISPLLVAFFVLMFVGVVNFHFKRQHQEERARRRBEKR 1560
Qy 1560 LRLLEKRR-----KAQCKPYSDYSRFLRLVHLCTSHY 1594
Db 1561 LRLLEKRRSKEKQWADMLDLDDVITASGSSAASEAQCKPYSDYSRFLRLVHLCTSHY 1620
Qy 1595 LDLEITGVIGLVNVTMAHEVQOQOILDEALKICNYITFTVIFVLESFVKLVAFGRFRFFQ 1654
Db 1621 LDLEITGVIGLVNVTMAHEVQOQOILDEALKICNYITFTVIFVLESFVKLVAFGRFRFFQ 1680
Qy 1655 DRWNQDLALVLLSIMGITLIEEIEVNASLPINPTIIRIMRVLRIRARVLLKLMKAVGHRAL 1714
Db 1681 DRWNQDLALVLLSIMGITLIEEIEVNASLPINPTIIRIMRVLRIRARVLLKLMKAVGHRAL 1740
Qy 1715 LDTVMQALPQVNGILGLFMLLFFIPAALGVLEFGLDECDETHPCCEGLGRHATFRNFGWAF 1774
Db 1741 LDTVMQALPQVNGILGLFMLLFFIPAALGVLEFGLDECDETHPCCEGLGRHATFRNFGWAF 1800
Qy 1775 LTLFRVSTGDNWNGIMKDTLDCDOESTCYNVTLSPIYFVSFVLTAQFVLNVVIVLMLK 1834
Db 1801 LTLFRVSTGDNWNGIMKDTLDCDOESTCYNVTLSPIYFVSFVLTAQFVLNVVIVLMLK 1860
Qy 1835 HLEESNKEAEAELEAELEEMTKLSPQHPSPGLSPPLWPGVGPDSPOSPPKPCALHPA 1894
Db 1861 HLEESNKEAEAELEAELEEMTKLSPQHPSPGLSPPLWPGVGPDSPOSPPKPCALHPA 1920
Qy 1895 AHARSASH- FSLHPTWQHPHTELP---GPDLLTVRKSGVSRTHSLPNDSTYMRHGSTAE 1950
Db 1921 AHIGAASSGFSLEHPTWVPHTEGFPVPLGPDLLTVRKSGVSRTHSLPNDSTYMRHGSTAE 1980
Qy 1951 GPLGHRGWLPAKQSGVLSVHSOPADTSYILOPKDAPHLLQPHSAPTWTIIPKLPPPG 2010
Db 1981 RSLGHRGWLPAKQSGVLSVHSOPADTSYILOPKDAPHLLQPHSAPTWTIIPKLPPPG 2040
Qy 2011 RSLPAQRLRQAARITSDLDVQGLGSRDLEAEVSGSPPLARAYSFWGSSSTQAQOHS 2070
Db 2041 RSLPAQRLRQAARITSDLDVQGLGSRDLEAEVSGSPPLARAYSFWGSSSTQAQOHS 2100
Qy 2071 RSHSKI SKHMTTPAPCPGEPNWKGPPTETRSLSLELDTLSWISGDLPLPGQGEPEPSR 2130
Db 2101 GSQSKVSKHRLPAPCPGLEPSWAKDQETHSSLELDTLSWISGDLPLPGQGEPEPSR 2159
Qy 2131 DLKCYVSAEQSCORRPTSWLDEORRHSAVSCLDSDSGPHLGTDPNGLGQPLGGFGSR 2190
Db 2160 DLKCYVSAEQSCORRPTSWLDEORRHSAVSCLDSDSGPHLGTDPNGLGQPLGGFGSR 2219
Qy 2191 PKKLSPPSITIDPPESQGPRTTPSPGICLRRRAPSDSDSKDPLASGPPDMSAASPSPKKD 2250
Db 2220 PKKLSPPSISIDPPESQGPRTTPSPGICLRRRAPSDSDSKDPLASGPPDMSAASPSPKKD 2279

RESULT 3

Q9WUB8 ID AC Q9WUB8 PRELIMINARY; PRT: 2288 AA.
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE T-type calcium channel isoform.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Pancreas;
RX MEDLINE=20081696; PubMed=10615950;
RA Zhuang H., Bhattacharjee A., Hu P., Zhang M., Goswami T., Wang L.,
RA Wu S., Berggren P.O., Li M.,
RT "Cloning of a T-type Ca2+ channel isoform in insulin-secreting
cells.";
RL Diabetes 49:59-64(2000).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (by similarity).
CC -!- SIMILARITY: Belongs to the calcium channel alpha-1 subunits
CC family.
DR EMBL; AF125161; AAD26858.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005891; C:voltage-gated calcium channel complex; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0005245; F:voltage-gated calcium channel activity; IEA.
DR GO; GO:0006816; P:calcium ion transport; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR InterPro; IPR001682; Ca/Na pore.
DR InterPro; IPR002111; Cat channel TrpL.
DR InterPro; IPR002077; Ca channel_alpha.
DR InterPro; IPR005821; Ion trans.
DR InterPro; IPR005820; M+channel_nlg.
DR InterPro; IPR005445; TVDCCALPHA1.
DR Pfam; PF00520; Ion trans; 4.
DR PRINTS; PR00167; CACHANNEL.
DR PRINTS; PR01629; TVDCCALPHA1.
DR KMW Calcium; Calcium channel; Calcium transport; Calcium-binding;
DR KMW Ion transport; Ionic channel; Transmembrane; Transport;
DR KMW Voltage-gated channel.
SQ SEQUENCE 2288 AA; 253476 MW; B89DBB5A1D81757F CRC64;
Query Match 93.3%; Score 11111; DB 2; Length 2288;
Best Local Similarity 93.3%; Pred. No. 0;
Matches 2135; Conservative 35; Mismatches 95; Indels 24; Gaps 5;
Qy 1 MDEEDGAGAEESQSPRSFMRLNDLSGAGRGPGSAEKDPGSAESAEGLYPALAPV 60
Db 1 MDEEDGAGAEESQSPRSFTQLNDLSGAGRGQPGSTKDPGSAESAEGLYPALAPV 60
Qy 61 FFYLSQDSRRSRCLRTVCNPFERISMLVILLNCVTLGMFRPCEDTACDSQRCRILOAF 120
Db 61 FFYLSQDSRRSRCLRTVCNPFERISMLVILLNCVTLGMFRPCEDTACDSQRCRILOAF 120
Qy 121 DDFTFAFVAVMVVMVALGIFGKKCYLGDTWNRDLDFVIAGLMLEYSLDLQNVFSFAVR 180
Db 121 DDFTFAFVAVMVVMVALGIFGKKCYLGDTWNRDLDFVIAGLMLEYSLDLQNVFSFAVR 180
Qy 181 TVRLVRLPRAINRVPVNRILVTLTLLDTPMLGNVLLLCFFVFFIFGIVGVQLWAGLLNR 240
Db 181 TVRLVRLPRAINRVPVNRILVTLTLLDTPMLGNVLLLCFFVFFIFGIVGVQLWAGLLNR 240
Qy 241 CFIIPENFSLPSVDLERYOTENEDESPPFICSQPRENGMSCRSVPTLRGDDGGGPGCL 300

Db 241 CFLPENFSLPLVDLEFYQTENEDESPFICSQPRENGMBCRSVPTLRGEGGGPPCSL 300
Qy 301 DYBAYNSSNTTCVNNQYVYTNCSAGEHNPFGKAINPDNIGYAWIAIFQVITLEGWVDM 360
Db 301 DYETINSSNTTCVNNQYVYTNCSAGEHNPFGKAINPDNIGYAWIAIFQVITLEGWVDM 360
Qy 361 YFVMDAHSFYNYFYIILLIIVGFFMINCLVVIATQFSETKORESQLMREQVRFLSNA 420
Db 361 YFVMDAHSFYNYFYIILLIIVGFFMINCLVVIATQFSETKORESQLMREQVRFLSNA 420
Qy 421 STLASFSEPGSCYBELLYLYILRKAARLAQVSRAGVRLGLSPAPLGOETQPS 480
Db 421 STLASFSEPGSCYBELLYLYILRKAARLAQVSRAGVRLGLSPAPLGOETQPS 480
Qy 481 SCBSHRRLSVHHLVHHHHHHHHYHNGTILRAPRASPEIQORDDANGSRLMLPPSTP 540
Db 481 SCTSHRRLSVHHLVHHHHHHHHYHNGTILRAPRASPEIQORDDANGSRLMLPPSTP 540
Qy 541 ALSGAPPGGAESVHSFYHADCHLEPVRCQAPPPRSPSEASGRVTGSGKVYPTVHTSPPE 600
Db 541 TPGSGPPRGAEVHSFYHADCHLEPVRCQAPPPRSPSEASGRVTGSGKVYPTVHTSPPE 600
Qy 601 TLKEKALVEVAASGPPTLSLNIIPGYPYSSMKLLETQSTGACQSSCKISSCLKADSG 660
Db 601 ILKDKALVEVAPSGPPTLSLNIIPGYPYSSMKLLETQSTGACHSSCKISSCSKADSG 660
Qy 661 ACGPDSCPYCARAGAVEVADREMPDSDSEAVYFTQDAQHSDLRDPHS-RRQSLGPD 719
Db 661 ACGPDSCPYCARAGAVEVADREMPDSDSEAVYFTQDAQHSDLRDPHSRRQSLGPD 720
Qy 720 AEPSSVLAFAWRLICDTRFKIVDSYKFGRGIMAILVNTLSMGIEYHEQPEELTNALEISN 779
Db 721 AEPSSVLAFAWRLICDTRFKIVDSYKFGRGIMAILVNTLSMGIEYHEQPEELTNALEISN 780
Qy 780 IVFTSLFALEMLKLIVTGPYIKNPNIPDGVIVISWEIVGQGGGLSVLRFLM 839
Db 781 IVFTSLFALEMLKLIVTGPYIKNPNIPDGVIVISWEIVGQGGGLSVLRFLM 840
Qy 840 RVKLVRFLPALQOLVLMKTMONVATFCMLLMFIFIFISILGMHIFGCKFASERDGT 899
Db 841 RVKLVRFLPALQOLVLMKTMONVATFCMLLMFIFIFISILGMHIFGCKFASERDGT 900
Qy 900 LPDRKNFDSLWALVTVFQILTOEDWNKVLVNGMASTSSWAALYFIALMTFGNVLENLL 959
Db 901 LPDRKNFDSLWALVTVFQILTOEDWNKVLVNGMASTSSWAALYFIALMTFGNVLENLL 960
Qy 960 VAILVEGFOAEISKREDASQOLCQIPVDQSGDANKSESEPDFFSPSLDGDGRKKC 1019
Db 961 VAILVEGFOAEISKREDASQOLCQIPVDQSGDANKSESEPDFFSPVDGGRKKR 1020
Qy 1020 LALVSLGHPHBLKSLPLIHTAATPMSLPKSTSTGLGALGPASRRRTSSSGSAPGA 1079
Db 1021 LALVALGHEAELKSLPLIHTAATPMSLPKSSSTGVGEALGSGRRRTSSSGSAPGA 1080
Qy 1080 A-HEMKSPPSARSSPHSPWASASWTSRRSRNSIGRAPSLKRRSPGERRSLLSGGOE 1138
Db 1081 AHHEMKSPPSARSSPHSPWASASWTSRRSRNSIGRAPSLKRRSPGERRSLLSGGOE 1140
Qy 1139 SODEEESSEERASPAGSDHHRGSLEREAKSFDLPDTLOVGLHRTASGRSASBHQD 1198
Db 1141 SODEEESSEERASPAGSDHHRGSLEREAKSFDLPDTLOVGLHRTASGRSASBHQD 1200
Qy 1199 CNGKSASGLARALPDDPFLDGDADDEGNLSKGERVRAWIRALPACYLERSWSAYI 1258
Db 1201 CNGKSASGLARALPDDPFLDGDADDEGNLSKGERIQAWVRSLPACCRERDSWSAYI 1260
Qy 1259 PPQSRFLLCHRIITHKMFHVLVLIIFLNCITIAMERPKIDPHSAERIFLTLSNYFT 1318
Db 1261 PPQSRFLLCHRIITHKMFHVLVLIIFLNCITIAMERPKIDPHSAERIFLTLSNYFT 1320
Qy 1319 AVFLAEMTVKVALGWCFOEQAFLRSSWNVLDGLVLISVIDILVMSVDSGTKILGMLR 1378
Db 1321 AVFLAEMTVKVALGWCFOEQAFLRSSWNVLDGLVLISVIDILVMSVDSGTKILGMLR 1380

Qy 1379 VLRLRLTLRLRVRISRAOGLKLVVETLMSLKPIGNIIVVICAPFIIFGILGVQFKGKF 1438
Db 1381 VLRLRLTLRLRVRISRAOGLKLVVETLMSLKPIGNIIVVICAPFIIFGILGVQFKGKF 1440
Qy 1439 FVCOGEDTRNITNKSDCABEASRWVRHKNYFNPDNLQALMSLFLVASKDQWDMYDGLDA 1498
Db 1441 FVCOGEDTRNITNKSDCABEASRWVRHKNYFNPDNLQALMSLFLVASKDQWDMYDGLDA 1500
Qy 1499 VGVDQOOPMNHPNMLLYFISFLLIIVAFVLMFVGVVFNHFKCRQOESEERREBEK 1558
Db 1501 VGVDQOOPMNHPNMLLYFISFLLIIVAFVLMFVGVVFNHFKCRQOESEERREBEK 1560
Qy 1559 RLRLLEKRR-----KAQCKPYYSYDSRFRLLVHHLCTSHYLDLFT 1600
Db 1561 RLRLLEKRRMLDLDVIASGSSASASEAQCKPYYSYDSRFRLLVHHLCTSHYLDLFT 1620
Qy 1601 GVIGLVNVTMAEHVQOPOILDEALKICNYIPTVIVLESVPKLVAFGRFPFQDRMQL 1660
Db 1621 GVIGLVNVTMAEHVQOPOILDEALKICNYIPTVIVFESVPKLVAFGRFPFQDRMQL 1680
Qy 1661 DLAIIVLLSTMGITLLEEIEVNASLPINPTIIRIMRVLRIARVLKILKMAVGMALLDTVMQ 1720
Db 1681 DLAIIVLLSTMGITLLEEIEVNASLPINPTIIRIMRVLRIARVLKILKMAVGMALLDTVMQ 1740
Qy 1721 ALPOVGNLGLLFWLFFIIPAAALGVLELFGDLECDETHPCGELGRHATFRNFGMAFLTLFRV 1780
Db 1741 ALPOVGNLGLLFWLFFIIPAAALGVLELFGDLECDETHPCGELGRHATFRNFGMAFLTLFRV 1800
Qy 1781 STGDWNGIMKDTLRDCOESTCYNTVISPVIYFVSFVLTAQFVLNVVIAVLMKHESEN 1840
Db 1801 STGDWNGIMKDTLRDCOESTCYNTVISPVIYFVSFVLTAQFVLNVVIAVLMKHESEN 1860
Qy 1841 KEAKEAEAELEEMKTLSPQHPSPGSPPLPMPGVEGSPDPSPKPAALPAHARS 1900
Db 1861 KEAKEAEAELEEMKTLSPQHPSPGSPPLPMPGVEGSPDPSPKPAHPTTAHIGAA 1920
Qy 1901 SHFSLEHPTMQHPTEL-----GPDLLTVKSGVSRTHSLPNDSYMCRGSGTAEGPLGHRG 1957
Db 1921 SGFSLEHPTMQHPTEL-----GPDLLTVKSGVSRTHSLPNDSYMCRGSGTAEGPLGHRG 1980
Qy 1958 WGLPKAQSGLSVSHSQPADTSTVILQPKDAPHLQPHSAPTWTGTIPKLPFGSPSLAQ 2017
Db 1981 WGLPKAQSGLSVSHSQPADTSTVILQPKDAPHLQPHSAPTWTGTIPKLPFGSPSLAQ 2040
Qy 2018 PLRQAAIRTDSDVQGLGREDLLAEVSGSPPLARAYFWGQSGSTOQOHSRSHSKIS 2077
Db 2041 PLRQAAIRTDSDVQGLGREDLLAEVSGSPPLARAYFWGQSGSTOQOHSRSHSKIS 2100
Qy 2078 KMTTPAPCGEPBNWKGPPETRSLELDTELWSISGDLPPGGOEPPSPDLAKKYS 2137
Db 2101 KHRLPAPCGEPBNWKGPPETRSLELDTELWSISGDLPPGGOEPPSPDLAKKYS 2159
Qy 2138 VEAQSCORRPTSLDQRRHSIAVSCLDGSGOPHLGTDPSNLGGQPLGGPGRPKKLSP 2197
Db 2160 VETQSCRRFPGLDQRRHSIAVSCLDGSGOPHLGTDPSNLGGQPLGGPGRPKKLSP 2219
Qy 2198 PSTIDPPESQGBRTPPSPGICLRRRAPSDSKDPLASGPPDPMASAPKDVLSGL 2257
Db 2220 PSTIDPPESQGBRTPPSPGICLRRRAPSDSKDPLASGPPDPMASAPKDVLSGL 2279
Qy 2258 SSDPADLDP 2266
Db 2280 SSDPTMDP 2288

RESULT 4

CCAG RAT
ID CCAG RAT STANDARD; PRT; 2254 AA.
AC OS4898;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)

QY	61	FFYLSQDSRPSRCLRTVCNPFERISMLVILNCVTLGMFPCEDICADSORCILQAF	120
Db	61	FFYLSQDSRPSRCLRTVCNPFERISMLVILNCVTLGMFPCEDICADSORCILQAF	120
QY	121	DDFIFAPFAVMVQWVALGIFGKKCYLGDWTNRLOFFIVIAWGLVSYSLDLQNVFSVR	180
Db	121	DDFIFAPFAVMVQWVALGIFGKKCYLGDWTNRLOFFIVIAWGLVSYSLDLQNVFSVR	180
QY	181	TVRLRLRLRAINRVPMSRIILVLLDTPMLGNVLLLCFFVFFIFGIVGVQWAGLLNR	240
Db	181	TVRLRLRLRAINRVPMSRIILVLLDTPMLGNVLLLCFFVFFIFGIVGVQWAGLLNR	240
QY	241	CFLPENFSLPLSDLEYYQTEDESPFTCSOPRENGMRSCSVTLRGDGGGPPCGL	300
Db	241	CFLPENFSLPLSDLEYYQTEDESPFTCSOPRENGMRSCSVTLRGDGGGPPCGL	300
QY	301	DYENYSSNTTCVNNQYVYTCNSAGHNPFGKAINFDNIGYAWIAIFOVITILEGWDIM	360
Db	301	DYETYNSSNTTCVNNQYVYTCNSAGHNPFGKAINFDNIGYAWIAIFOVITILEGWDIM	360
QY	361	YFVMDAHSFYNYFIYFILLIIVGSPFMINCLVLIATQFSETKQRESQLMREQVRFLSNA	420
Db	361	YFVMDAHSFYNYFIYFILLIIVGSPFMINCLVLIATQFSETKQRESQLMREQVRFLSNA	420
QY	421	STLASFSBPGSCYBELLKYLVIILKKAARLAQVSRAGVRVGLSSPAPLGGQETQPS	480
Db	421	STLASFSBPGSCYBELLKYLVIILKKAARLAQVSRAGVRVGLSSPAPLGGQETQPS	480
QY	481	SCSRSHRLSVHLLVHHHHHHHVLGNGTLRAPRASPEIQDRDANGSRRLMPPSTP	540
Db	481	SCTRSHRLSVHLLVHHHHHHHVLGNGTLRVPRASPEIQDRDANGSRRLMPPSTP	540
QY	541	ALSGAPPGBASVHSFYHADCHLSPVRCQAPPPSPSEASGRTVGSKVYPTVHTSPPE	600
Db	541	TPSGPPRGAESVHSFYHADCHLSPVRCQAPPPSPSEASGRTVGSKVYPTVHTSPPE	600
QY	601	TLKEKALVEVAASGPPTLTSLNTPPGPYSSMHLLETQSTGACQSSCKISSPCLKADSG	660
Db	601	ILKDKALVEVAPSGPPTLTSLNTPPGPYSSMHLLETQSTGACHSSCKISSPCKADSG	660
QY	661	ACGPDSCPCYCARAGAGEVELADREMPDSDSEAVYFTODAOHSDLRDPHS-RRORSIGPD	719
Db	661	ACGPDSCPCYCARAGAGEVELADREMPDSDSEAVYFTODAOHSDLRDPHSRRORSIGPD	720
QY	720	ABPSSVLAFWRLICDTFRKIVDSKYFGRGIMAILVNTLSMGIEVHEQPELTNALEISN	779
Db	721	ABPSSVLAFWRLICDTFRKIVDSKYFGRGIMAILVNTLSMGIEVHEQPELTNALEISN	780
QY	780	IVFTSLFALEMLLKLIVYGPFGYIKNPYNIIFDGVIVWISVMEIVGQOQGGLSVLRTRFLM	839
Db	781	IVFTSLFALEMLLKLIVYGPFGYIKNPYNIIFDGVIVWISVMEIVGQOQGGLSVLRTRFLM	840
QY	840	RVLKLVRLPALQRLVLMKTDNVNATFCMLMLFIPIFSLGNHLCGCKFASRDGDT	899
Db	841	RVLKLVRLPALQRLVLMKTDNVNATFCMLMLFIPIFSLGNHLCGCKFASRDGDT	900
QY	900	LPDRKNFDSLALVAITVFOILLTQEDWNKVLVNGMASTSSWAALYFIALMTFGNYVLFNLL	959
Db	901	LPDRKNFDSLALVAITVFOILLTQEDWNKVLVNGMASTSSWAALYFIALMTFGNYVLFNLL	960
QY	960	VAILVEGFGQAEISKREDASGQLSCTQLPVDGQGDANKSESEPDPFSPSLDGDGRKK	1019
Db	961	VAILVEGFGQAEISKREDASGQLSCTQLPVDGQGDANKSESEPDPFSPSLDGDGRKK	997
QY	1020	LALVSLGEHPELRKSLPLLIHTAATPMSLPKSTGTGLGEALGPASRRRTSSGSAEPGA	1079
Db	998	LALVSLGEHPELRKSLPLLIHTAATPMSLPKSTGTGLGEALGPASRRRTSSGSAEPGA	1057
QY	1080	A-HEMKSPPSARSPHSPWASAASWTSSRRSNLGRAPSLKRRSPSGRRRSLSGEQE	1138
Db	1058	AHEMKSPPSARSPHSPWASAASWTSSRRSNLGRAPSLKRRSPSGRRRSLSGEQE	1117
QY	1139	SQDEESESSEERASPGSDHRRHRSGLEREAKSFDLPDTLOVPLGHLRTASGRSASHQD	1198
Db	1118	SQDEESESSEERASPGSDHRRHRSGLEREAKSFDLPDTLOVPLGHLRTASGRSASHQD	1177
QY	1199	CNGKSASGRLARALRPPDDPDLGGDDADDEGNLSKGERVRAWIRARLPACVLERDSWYAI	1258
Db	1178	CNGKSASGRLARALRPPDDPDLGGDDADDEGNLSKGERIQAWVRSRLPACCRERDSWYAI	1237
QY	1259	FPQSRFRLLCHRIITHKMPDHVVLVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFT	1318
Db	1238	FPQSRFRLLCHRIITHKMPDHVVLVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFT	1297
QY	1319	AVFLAEMTVKVALGWCFCGEQAYLRSNNVLDGLLVLSVIDILVSVSDSGTKILGWL	1378
Db	1298	AVFLAEMTVKVALGWCFCGEQAYLRSNNVLDGLLVLSVIDILVSVSDSGTKILGWL	1357
QY	1379	VLRLRTLRPLRVISRAOGLKLVVETLMSLKPIGNIWIICCAFFIIFGILGVLFKGF	1438
Db	1358	VLRLRTLRPLRVISRAOGLKLVVETLMSLKPIGNIWIICCAFFIIFGILGVLFKGF	1417
QY	1439	FVCOGEDTRNITNKSDCAEASYRWRHKNYFNDNLGOALMSLFLVASKDGWDIMYDGLDA	1498
Db	1418	FVCOGEDTRNITNKSDCAEASYRWRHKNYFNDNLGOALMSLFLVASKDGWDIMYDGLDA	1477
QY	1499	GVDOQOPIMNHPMMLLYPISFLLIVAFVLMFVGVVFNHFKROHOBEEARREK	1558
Db	1478	GVDOQOPIMNHPMMLLYPISFLLIVAFVLMFVGVVFNHFKROHOBEEARREK	1537
QY	1559	RURLEKKRR-----KAQCKPYYSYRFRLLVHHLCTSHYLDLFTIGVGLNVVMTA	1611
Db	1538	RURLEKKRRSKEKQMAEAKQPYYSYRFRLLVHHLCTSHYLDLFTIGVGLNVVMTA	1597
QY	1612	MEHYQOQILDBALKICNYIIFTVIFLESVKLVAFGFRFPQDRWNOLDLAILLSLTMG	1671
Db	1598	MEHYQOQILDBALKICNYIIFTVIFLESVKLVAFGFRFPQDRWNOLDLAILLSLTMG	1657
QY	1672	ITLEEVNVAIPINPTIIRIMRVLRARVLLKXWAVGMRALDVTVMQALPQVGNLGLL	1731
Db	1658	ITLEEVNVAIPINPTIIRIMRVLRARVLLKXWAVGMRALDVTVMQALPQVGNLGLL	1717
QY	1732	FMLLFFIIFALGVFELGDLCEDETHPCBGLGHATFRNFGMAFLTLFRVSTGDNWNGIMK	1791
Db	1718	FMLLFFIIFALGVFELGDLCEDETHPCBGLGHATFRNFGMAFLTLFRVSTGDNWNGIMK	1777
QY	1792	DTLRDQDQESTCNYTIVSPIYFVSFVLTQAQVFLVNVVIAVLMKLEESKEAEAELEA	1851
Db	1778	DTLRDQDQESTCNYTIVSPIYFVSFVLTQAQVFLVNVVIAVLMKLEESKEAEAELEA	1837
QY	1852	ELEEMKTLSPQPHSPGLSPFLMPGVGPDSPDPSKPGALHPAAHARSASHFSLEHPTMQ	1911
Db	1838	ELEEMKTLSPQPHSPGLSPFLMPGVGPDSPDPSKPGALHPAAHARSASHFSLEHPTMQ	1897
QY	1912	PHTELP---GPDLLTVRKSGVSRTHSLPNDSYMCHSGSTAGPLGHRGWLKPAQSGSV	1968
Db	1898	PHTELP---GPDLLTVRKSGVSRTHSLPNDSYMCHSGSTAGPLGHRGWLKPAQSGSV	1957
QY	1969	LSVHSQPADTSYLQPKDAPHLLQPHSAPTWTGTPKLPPLPPGSRPLAQRLRQAIRTD	2028
Db	1958	LSVHSQPADTSYLQPKDAPHLLQPHSAPTWTGTPKLPPLPPGSRPLAQRLRQAIRTD	2017
QY	2029	SLDVQGLSREDLLAEVSGSPPLARAYSPWGSSTQAQOHSKSHSKI SKHMTPPAPCPG	2088
Db	2018	SLDVQGLSREDLLAEVSGSPPLARAYSPWGSSTQAQOHSKSHSKI SKHMTPPAPCPG	2077
QY	2089	PEPNWKGPPETRSLSLELDTLWSIGDLAPPGQEPSPRDLKKCYSVAEQSCORRPT	2148
Db	2078	LEPSWAKDPPETRSLSLELDTLWSIGDLAPPGQEPSPRDLKKCYSVAEQSCORRPT	2136
QY	2149	SWLDEQRHRSIAVSLDSSQPHLGTDPNLGQOPLGGPSRPPKXKLSPSPSIDPPESQ	2208
Db	2137	SWLDEQRHRSIAVSLDSSQPHLGTDPNLGQOPLGGPSRPPKXKLSPSPSIDPPESQ	2196
QY	2209	GPRTPPPGICLRRRARRSSDKDPLASGPPDPSMAASPSPKDVLISLGLSDPADLDP	2266


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QY 1260 PPOSRELLCHRIITHKDFHVVLLVILFNLCITIAMERPKIDPHSAERIFLTLNVIYFTA 1319
Db 1221 PPOSRELLCHRIITHKDFHVVLLVILFNLCITIAMERPKIDPHSAERIFLTLNVIYFTA 1280
QY 1320 VFLAEMTVKVALGWCFCGEQAYLRSSNMVLDGLLVILISVIDILVMSVDSGTKILGMLRV 1379
Db 1281 VFLAEMTVKVALGWCFCGEQAYLRSSNMVLDGLLVILISVIDILVMSVDSGTKILGMLRV 1340
QY 1380 LRLRLTLRPLRVISRAQGLKLIVETLMSSLKPIGNIVWICCAFFIIFGLIQLFKGKFF 1439
Db 1341 LRLRLTLRPLRVISRAQGLKLIVETLMSSLKPIGNIVWICCAFFIIFGLIQLFKGKFF 1400
QY 1440 VCGEDTRNTKNSDCAEASRYRWKYNFNDLGOALMSLFVLASXGQWVDIMYDGLDAV 1499
Db 1401 VCGEDTRNTKNSDCAEASRYRWKYNFNDLGOALMSLFVLASXGQWVDIMYDGLDAV 1460
QY 1500 GVDQQTIMNHPWMLLYFISFLIIVAFFVLNMFVGVVNFHFKCRQHQEERARRBEKR 1559
Db 1461 GVDQQTIMNHPWMLLYFISFLIIVAFFVLNMFVGVVNFHFKCRQHQEERARRBEKR 1520
QY 1560 LRLEKKRR-----KAQCKPYSDYSRFRLLVHHLCTSHVLDLFIITG 1601
Db 1521 LRLEKKRRMLDDVVIASGSSAASAEQAQCKPYSDYSRFRLLVHHLCTSHVLDLFIITG 1580
QY 1602 VIGLNVVTMAEHVYQOQIILDEALKICNYIFTVIFVLESVFKLVAFGRFRFFQDRWNQLD 1661
Db 1581 VIGLNVVTMAEHVYQOQIILDEALKICNYIFTVIFVLESVFKLVAFGRFRFFQDRWNQLD 1640
QY 1662 LAIVLLSIMGITLBEIEVNASLPINPTIIRIMRVLRIRARVLKLLKWAQGNRALLDVTMOA 1721
Db 1641 LAIVLLSIMGITLBEIEVNASLPINPTIIRIMRVLRIRARVLKLLKWAQGNRALLDVTMOA 1700
QY 1722 LPQVGNIGLLFMILLFFFAALGVELFGLDCEDETHPCCEGLGRATFRNFGMAFLTLFRVS 1781
Db 1701 LPQVGNIGLLFMILLFFFAALGVELFGLDCEDETHPCCEGLGRATFRNFGMAFLTLFRVS 1760
QY 1782 TGDNNWNGIMKDTLRDCQESTCYNTVISPITYFVSFLVTAQFVLNVVIVAVLMKHLESNK 1841
Db 1761 TGDNNWNGIMKDTLRDCQESTCYNTVISPITYFVSFLVTAQFVLNVVIVAVLMKHLESNK 1820
QY 1842 EAKEEAELEAELEEMTKLSPQHSPLGSPFLMPGVEGDPSPSPKPGCALHPAARASAS 1901
Db 1821 EAKEEAELEAELEEMTKLSPQHSPLGSPFLMPGVEGVNSPSPKPGAPHTTAHTGAAS 1880
QY 1902 H-FSLEHPTWOPHTLP---GPDLLTVRKSGVSRTHSLPNDSTVMCRHGSTAEGPLCHRG 1957
Db 1881 SGFSLEHPTWOPHTLP---GPDLLTVRKSGVSRTHSLPNDSTVMCRHGSTAEGPLCHRG 1940
QY 1958 WGLPKAQSGLSVLSVHSPADTSYILQPKDAPHLLQPHSAFTWGTITPKLPPPGCRSPLAQR 2017
Db 1941 WGLPKAQSGLSVLSVHSPADTSYILQPKDAPHLLQPHSAFTWGTITPKLPPPGCRSPLAQR 2000
QY 2018 PLRQQAIRTDLSLVQGLSREDLLAEVSGSPPLARAYAFWQSGSSTQAQHSRSHKIS 2077
Db 2001 PLRQQAIRTDLSLVQGLSREDLLAEVSGSPPLARAYAFWQSGSSTQAQHSRSHKIS 2060
QY 2078 KHMTPPAPCPGPEPNWKGPPETRSLSLELDELTSWISGDLPLPGQOEPEPSPRDLKKCY 2137
Db 2061 KHIRLPAPCPGLEFSWAKDPETHSSLELDELTSWISGDLPLPGQOEPEPSPRDLKKCY 2119
QY 2138 VEAQSCORRPTSWLDEQRHHSIAVSCLDGSGQPHLGTDPNLSGQPIGGPGSRPKKLSLP 2197
Db 2120 VEAQSCORRPTSWLDEQRHHSIAVSCLDGSGQPHLGTDPNLSGQPIGGPGSRPKKLSLP 2179
QY 2198 PSITIDPESQPRTPSPGICLARRAPSPDSKDLASGPPDMSAASPSPKVDLSLSGL 2257
Db 2180 PSITIDPESQPRTPSPGICLARRAPSPDSKDLASGPPDMSAASPSPKVDLSLSGL 2239
QY 2258 SSDPADLDP 2266
Db 2240 SSDPFDLDP 2248
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RESULT 6
Q6ZPX4
ID Q6ZPX4 PRELIMINARY; PRT: 1389 AA.
AC Q6ZPX4;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE MKIAA1123 protein (Fragment).
CN Name=MKIAA1123;
OS Mus musculus (Mouse);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX PubMed=14621295;
RA Okazaki N., Kikuno R., Ohara R., Inamoto S., Koseki H., Hiraoka S.,
RA Saga Y., Nagase T., Ohara O., Koga H.;
RT "Prediction of the coding sequences of mouse homologues of KIAA gene:
RT III. the complete nucleotide sequences of 500 mouse KIAA-homologous
RT cDNAs identified by screening of terminal sequences of cDNA clones
RT randomly sampled from size-fractionated libraries.";
RL DNA Res. 10:167-180(2003).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to the calcium channel alpha-1 subunits
CC family.
DR EMBL; AK129294; BAC98104.1; -.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR GO; GO:0005886; C:plasma membrane; IDA.
DR GO; GO:0005245; F:voltage-gated calcium channel activity; IDA.
DR InterPro; IPR001682; Ca/Na_pore.
DR InterPro; IPR002111; Cat channel TrpL.
DR InterPro; IPR002077; Ca channel TrpL.
DR InterPro; IPR005821; Ion trans_alpha.
DR InterPro; IPR005820; M-channel_nlg.
DR Pfam; PF00520; Ion trans_3.
DR PRINTS; PR00167; CACHANNEL.
DR KEGG; Calcium channel; Calcium transport; Calcium-binding;
KW Ion transport; Ionic channel; Transmembrane; Transport;
KW Voltage-gated channel.
FT NON_TER 1
SQ SEQUENCE 1389 AA; 153067 MW; DA31535CA3C03B10 CRC64;

Query Match 55.2%; Score 6573; DB 2; Length 1389;
Best Local Similarity 92.0%; Pred. No. 7.8e-291;
Matches 1279; Conservative 25; Mismatches 62; Indels 24; Gaps 5;

QY 900 LPDRKNFDSLLWAIIVTVFOILTQEDWNKVLNMGMASTSSWALYFTALMTFGNYVLFNLL 959
Db 1 LPDRKNFDSLLWAIIVTVFOILTQEDWNKVLNMGMASTSSWALYFTALMTFGNYVLFNLL 60
QY 960 VAILVEGFOAEIISKREDASGQLSCIQLPVDQSGGDANKSESEPDPFSPSLDGDGRKKC 1019
Db 61 VAILVEGFOAEIISKREDTSQGLSCIQLPVDQSGGDANKSESEPDPFSPVDGDGRKKR 120
QY 1020 LALVSLGEHPELRKSLPLPLIITHATPMSLKPSTSTGLGEALGPASRTSSGSGSAEPGA 1079
Db 121 LALVALGHESELKSLPLPLIITHATPMSLKPSSSTGVGEALGSGSRSTSSGSAEPGT 180
QY 1080 A-HEMKSPSARSSPHSPMSAASSWTSRRSSNSLGRAPSLKRRSPSGRRSLLSGEGQE 1138
Db 181 AHHEMKSPSARSSPHSPMSAASSWTSRRSSNSLGRAPSLKRRSPSGRRSLLSGEGQE 240
QY 1139 SQDEESSSEERASPAGSDHRRHGRSLERAKSGSFDLPDTLQVPLHRTASGRGSAEHQD 1198
Db 241 SQDEESSSEEDRASPAGSDHRRHGRSLERAKSGSFDLPDTLQVPLHRTASGRGSAEHQD 300
QY 1199 CNGKSASGRILARLPDPPPLDGDADDDEGNLSKGRVNAVIRARLPACVLERDSWSAYI 1258
Db 301 CNGKSASGRILARLPDPPPLDGDADDDEGNLSKGRVNAVIRARLPACCRERDSWSAYI 360
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QY 1259 FPQSRRLCHRIITHKMFHDVVLVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFT 1318
Db 361 FPQSRRLCHRIITHKMFHDVVLVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFT 420
QY 1319 AVFLAETVKVVALGWCFCGQAYLRSSWNVLGDLIIISVIDIIVSMVSDSGTKILGMLR 1378
Db 421 AVFLAETVKVVALGWCFCGQAYLRSSWNVLGDLIIISVIDIIVSMVSDSGTKILGMLR 480
QY 1379 VLRLRLRLRLVLSRAQGLKLVVETLMSSLKPTGNIWVCCAPFIIFGILGVOLFPGKF 1438
Db 481 VLRLRLRLRLVLSRAQGLKLVVETLMSSLKPTGNIWVCCAPFIIFGILGVOLFPGKF 540
QY 1439 FVCGEDTRITNKSDCAEASRYRVRHKYFNDNLGQALMSLFLVLSKDGWVDIMYDGLDA 1498
Db 541 FVCGEDTRITNKSDCAEASRYRVRHKYFNDNLGQALMSLFLVLSKDGWVDIMYDGLDA 600
QY 1499 VGVDDQPPIMNHNPMMLLYFISFLIIVAFFVLNMFVGVVFNFKCRQHQEERREK 1558
Db 601 VGVDDQPPIMNHNPMMLLYFISFLIIVAFFVLNMFVGVVFNFKCRQHQEERREK 660
QY 1559 RLRLLEKRR-----KAQCKPYSDYSRFRLLVHHLCTSHYLDLFIIT 1600
Db 661 RLRLLEKRRMLDDVIAAGSSASAASEAQCKPYSDYSRFRLLVHHLCTSHYLDLFIIT 720
QY 1601 GVIGLNVVTWAMEHYQOQILDEALKICNIYFTVIFVLESVKLVAFGRFRFODRNQOL 1660
Db 721 GVIGLNVVTWAMEHYQOQILDEALKICNIYFTVIFVLESVKLVAFGRFRFODRNQOL 780
QY 1661 DLAIIVLSINGITLLEEVNASLPINPTIIRIMVLRIRARVLLKLLKMAVGRALLDVTMQ 1720
Db 781 DLAIIVLSINGITLLEEVNASLPINPTIIRIMVLRIRARVLLKLLKMAVGRALLDVTMQ 840
QY 1721 ALPOVGNLGLLMLLFFIPALGVLEFGLDECDTHPCGELGRHATPRNFGMAFLTFRV 1780
Db 841 ALPOVGNLGLLMLLFFIPALGVLEFGLDECDTHPCGELGRHATPRNFGMAFLTFRV 900
QY 1781 STGDNWNGIMKOTLRDCDQSTCNTVTSPIYFVSFVLTAQFVLNVVIAVLMKHLEEN 1840
Db 901 STGDNWNGIMKOTLRDCDQSTCNTVTSPIYFVSFVLTAQFVLNVVIAVLMKHLEEN 960
QY 1841 KEAKEAELEAELELEMKLTSPHSPGLSGPFLMPGVEGSDPSPKPGALHPAAHARS 1900
Db 961 KEAKEAELEAELELEMKLTSPHSPGLSGPFLMPGVEGSDPSPKPGALHPAAHARS 1020
QY 1901 SH-FLSEHPTMQPHTLP---GPDLLTVRKSGVSRTHSLPNDSYMCRHGSTAGPILGHR 1956
Db 1021 SSGFSLSEHPTMQPHTLP---GPDLLTVRKSGVSRTHSLPNDSYMCRHGSTAGPILGHR 1080
QY 1957 GWGLPKAQSGLSVHSOPADTSVILQPKDAPHLQPHSAPTWTGTPKLPGRSLAQ 2016
Db 1081 GWGLPKAQSGLSVHSOPADTSVILQPKDAPHLQPHSAPTWTGTPKLPGRSLAQ 1140
QY 2017 RPLRQAAITDSDLVQGLSREDLLAEVSGSPPLARAYSFWGQSTQAOQHSRSHKI 2076
Db 1141 RPLRQAAITDSDLVQGLSREDLLAEVSGSPPLARAYSFWGQSTQAOQHSRSHKI 2120
QY 2077 SKMTTPAPCGPEPNWKGKPPETRRSLDLTSLWISGDLPLPGGQEPSPRDLKKCY 2136
Db 1201 SKMTTPAPCGPEPNWKGKPPETRRSLDLTSLWISGDLPLPGGQEPSPRDLKKCY 1259
QY 2137 SVEAQSCORPSTWLDQRHSTAVSLDGSQPHLGTDPNLCGQPLGGPGRPKKLS 2196
Db 1260 SVEAQSCORPSTWLDQRHSTAVSLDGSQPHLGTDPNLCGQPLGGPGRPKKLS 1319
QY 2197 PPSITIDPPSQGPRTPPSGICLRRRAPSDDSKDPLASGPPDSMAASPSPKDDLSLSG 2256
Db 1320 PPSITIDPPSQGPRTPPSGICLRRRAPSDDSKDPLASGPPDSMAASPSPKDDLSLSG 1379
QY 2257 LSSDPAIDLDP 2266
Db 1380 LSSDPAIDLDP 1389

RESULT 7
CCAH RAT STANDARD; PRT; 2359 AA.
AC Q9EQ60;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Voltage-dependent T-type calcium channel alpha-1H subunit (Voltage-gated calcium channel alpha subunit Cav3.2).
GN Name=Cacnalh;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX PubMed=11073957; DOI=10.1074/jbc.M008215200;
RA McRory J.E., Santi C.M., Hamming K.S.C., Mezeyova J., Sutton K.G., Baillie D.L., Stea A., Snutch T.P.;
RT "Molecular and functional characterization of a family of rat brain T-type calcium channels.";
RL J. Biol. Chem. 276:3999-4011(2001).
CC -I- FUNCTION: Voltage-sensitive calcium channels (VSCC) mediate the entry of calcium ions into excitable cells and are also involved in a variety of calcium-dependent processes, including muscle contraction, hormone or neurotransmitter release, gene expression, cell motility, cell division and cell death. The isoform alpha-1H gives rise to T-type calcium currents. T-type calcium channels belong to the "low-voltage activated (LVA)" group and are strongly blocked by nickel and mibefradil. A particularity of this type of channels is an opening at quite negative potentials, and a voltage-dependent inactivation. T-type channels serve pacemaking functions in both central neurons and cardiac nodal cells and support calcium signaling in secretory cells and vascular smooth muscle. They may also be involved in the modulation of firing patterns of neurons which is important for information processing as well as in cell growth processes.
CC -I- SUBCELLULAR LOCATION: Integral membrane protein.
CC -I- TISSUE SPECIFICITY: Expressed in brain.
CC -I- DOMAIN: Each of the four internal repeats contains five hydrophobic transmembrane segments (S1, S2, S3, S5, S6) and one positively charged transmembrane segment (S4). S4 segments probably represent the voltage-sensor and are characterized by a series of positively charged amino acids at every third position.
CC -I- PTM: In response to raising of intracellular calcium, the T-type channels are activated by CaM-kinase II.
CC -I- SIMILARITY: Belongs to the calcium channel alpha-1 subunits family.

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DR EMBL; AF290213; AAC35187.1; -;
DR RGD; 68943; Cacnalh.
DR InterPro; IPR001682; Ca/Na pore.
DR InterPro; IPR02111; Cat_channel_TrpL.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR005820; N+channel_nlg.
DR InterPro; IPR005445; TVDCCALpha1.
DR Pfam; PF00520; Ion_trans_4.
DR PRINTS; PR01629; TVDCCALPHA1.
KW Calcium channel; Glycoprotein; Ion transport; Ionic channel;
KW Multigene family; Phosphorylation; Repeat; Transmembrane;
FT REPEAT 87 422 I.
FT REPEAT 776 1015 II.
FT REPEAT 1292 1569 III.

Db 1100 SRSSSSVDPQLG-DKSLASLSSSCTPGPNSAGSSRRSSWNSLGRAPSLKRNQCG 1158
Qy 1127 ERSLLSGEOESODEESEEERAS-----PAGSDHRRHGRSLERAKSSFDL-- 1174
Db 1159 ERESLLSGEGKGTDDDE--AEDSRPSTGTHPGSPGPRATPLRAESLDH--RSTLDLCP 1214
Qy 1175 --PDTLQVPGHRTASRGSSASGHODCNGKSASGRALARLPDPPLDGDADDEGNLSK 1232
Db 1215 PRPAALPTKPH-----DCNQKVALPSEFFLRIDSHKEDAAEFDDIEDSC 1261
Qy 1233 GERVRAMIRARLPACYLERSWSAYIFPPQSRFRLLCHRIITHGMFDHVVLVIFLNCIT 1292
Db 1262 CFRHLKVLPEYAPOWCERSRESWALYLPQPNRLRVSCQVIAHKMFHVVVLVIFLNCIT 1321
Qy 1293 IAMERPKIDPHSABRIFLTSNYIFTAVFLAEMTVKVALGCEGOAYLRSSWNVLDDL 1352
Db 1322 IALERPDIIDPGSTERAFSLSNYIFTAIFVVMVMKVALGLLWGEHAYLQSSWNVLDDL 1381
Qy 1353 LVLSIVDILSVNVSDDGKILGLMLRVLRILRLPLRVISRAOGLKLVVETLMSLKPI 1412
Db 1382 LVLVSLVDIIVAMASAGAKILGLRVLRVLRPLRVISRAPGLKLVVETLMSLRPI 1441
Qy 1413 GNIWICAFPIIGILGVOLFKGKFFVCOGEDTRNITNKSDCAEASYRVWRHKYKFNDL 1472
Db 1442 GNVILICAFPIIGILGVOLFKGKFFYCEGDTNRNITTKAECHAHYRVWRHKYKFNDL 1501
Qy 1473 GOALMSLFLVASKDGVYDIIYDGLDVGVDQOPIIMNHPNMLLYFISFLLIIVAFVLMNF 1532
Db 1502 GOALMSLFLVSSKDGWNIWYDGLDVGIDQOQVONHNPWMLLYFISFLLIIVAFVLMNF 1561
Qy 1533 VGVVVENFHKCRHQEABEAREEKLRLKRRKAKQCKPYSDYSRFLLVHHLCTS 1592
Db 1562 VGVVVENFHKCRHQEABEAREEKLRLRRRRKARPPYADYSHTRRSHSCTS 1621
Qy 1593 HYLDLFTIGVGLNVVWMAHEHYOQPOLDEALKICNYIFTVIVLSEVFKLVAFGRFR 1652
Db 1622 HYLDLFTIFCINVTMSHEYNQPSLDEALKICNYFTIVFPAALKLVAFGRFR 1681
Qy 1653 FQDRWNOLDLAILLSIMGITLEBIEVNASLPINPTIIRIMRVLRIRARVLKLMQAVGM 1712
Db 1682 FQDRWNOLDLAILLSIMGIALEBIEMNAALPINPTIIRIMRVLRIRARVLKLMQAVGM 1741
Qy 1713 ALLDTVMQALPOVGNLGLFMLFFPIPAALGVELFGDCEDETHPCBGLGRHATFRNFM 1772
Db 1742 ALLDTVMQALPOVGNLGLFMLFFPIPAALGVELFGLECEDNPNCEGLSRHATFTNFM 1801
Qy 1773 AFLTLFRVSTGDNWNGIMKDTLRDC---DOESTCYNTVIGPIYFVSFVLTAAQFVLNVVI 1829
Db 1802 AFLTLFRVSTGDNWNGIMKDTLRCTREDKHCLSYLPALSPVFTVFMVAQFVLNVVV 1861
Qy 1830 AVLKMLEENKKEAEAELEAELEMLEKTLSPQPSPLGSPFLWPGVEGPDSPDKPG 1889
Db 1862 AVLKMLEENKKEAREDAEMDAEIELEM----- 1889
Qy 1890 ALHPAAHARSASHFSLHEPTWQPHPT--ELPG-----PDLLTVRKSGVSRTHSLPNDSYM 1942
Db 1890 -----AQGTAQPPPTAQESQGTQPDTPNLLVVRKVSVRMLSLPNDSYM 1934
Qy 1943 CRHGSTAEGPLHGRWGLP-----KAQSGVLSVHSQPADTSYIOLPKDAPHLQLPHS 1996
Db 1935 FRVAPAAAPHSH-----PLQEVEMETVGTGVTSAHSPPLEPRASFQVPSAA-----S 1982
Qy 1997 APTWTGTIP--KLPPPG--RSLPAQRPLRQAAIRTDSLD--VQGLSGREBLLAEVSGPSP 2050
Db 1983 SPARVSDPLCALSPRGTPRSLSLKILCRQEAHSESLGKGVDDVGG--DSIPDYTEPAE 2040
Qy 2051 PLARAYFWG-----QSSTQAQOHSRSHSKISKHMTTPAPCPGPRNWKGPET 2100
Db 2041 NMSTSOASTGAPRPPCPSPRPSVTRKHTFGQRCISSR--PPT-----LGDEA 2088
Qy 2101 RSSLELDTLSWISGDLPL-----PGGOEERP-----SPRDLKKCVSYBAQSCOR 2145

Db 2089 EAADPADEEVSHITSSAHPWATEPHSPASPTASPVKGTMGSGDRPRRFSVDQAQSFLD 2148
Qy 2146 RPTSWLDQRHRIASVCLDSGQPHLGTDPNSLGGQPLG-----GPSRPPKKLSPP 2198
Db 2149 KP-GRPDAQORSSVVE---LDNG-ESHLES-----GEVGRASELEPALGSRKKKQASPP 2197
Qy 2199 SITIDPP-ESQGRTPSPSP---GICLRRRPPSSDSK-----DPLASGPP 2238
Db 2198 CTSIEPTKDEGSRPPAEGGNTTLRRTPSCAALHRDCPEPTGPGTGCDPVAKGER 2257
Qy 2239 DSMAASPPSPKOVLSLGLSSDPADL 2264
Db 2258 WQQA---SCRAEHLTVNFAPEPLDM 2280
RESULT 8
CCAH HUMAN
ID _CCAH HUMAN STANDARD; PRT; 2353 AA.
AC 095180: Q95802; Q8WWI6; Q96016; Q96RZ9; Q9NY4; Q9NYV5;
DT 15-JUL-1999 (Rel. 38, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Voltage-dependent T-type calcium channel alpha-1H subunit (Voltage-gated calcium channel alpha subunit Cav3.2) (Low-voltage-activated calcium channel alpha 3.2 subunit).
DE Names: CACNA1H; (Human).
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Heart;
RX MEDLINE=98333998; PubMed=9670923;
RA Cribbs L.L., Lee J.-H., Yang J., Satin J., Zhang Y., Daud A.N., Barclay J., Williamson M.P., Fox M., Rees M., Perez-Reyes E.; "Cloning and characterization of alpha1H from human heart, a member of the T-type Ca2+ channel gene family."; J. Neurochem. 72:791-799 (1999).
RL Circ. Res. 83:103-109 (1998).
RN [2]
RP REVISIONS.
RA Cribbs L.L., Lee J.-H., Yang J., Daud A.N., Perez-Reyes E.; Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Thyroid carcinoma;
RX MEDLINE=99127945; PubMed=9930755;
RA Williams M.E., Washburn M.S., Hans M., Urrutia A., Brust P.P., Prodanovich P., Harpold M.M., Stauderman K.A.; "Structure and functional characterization of a novel human low-voltage activated calcium channel."; J. Neurochem. 72:791-799 (1999).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=21096910; PubMed=11157797; DOI=10.1093/hmg/10.4.339; Daniels R.J., Feden J.F., Lloyd C., Horsley S.W., Clark K., Tufarelli C., Kearney L., Buckle V.J., Doggett N.A., Flint J., Higgs D.R.; "Sequence, structure and pathology of the fully annotated terminal 2 Mb of the short arm of human chromosome 16."; Hum. Mol. Genet. 10:339-352 (2001).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Testis;
RX MEDLINE=21864207; PubMed=11751928; DOI=10.1074/jbc.M105345200; Jagannathan S., Punt E.L., Gu Y., Arnould C., Sakka D., Barratt C.L., Publicover S.J.; "Identification and localization of T-type voltage-operated calcium channel subunits in human male germ cells. Expression of multiple isoforms."; J. Biol. Chem. 277:8449-8456 (2002).
RN [6]
RP SEQUENCE OF 86-817 FROM N.A.

RA Cobley V.E.;
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP SQUENCE OF 424-661 AND 838-2373 FROM N.A. (ISOFORM 1).
 RA Mittman S.; Agnew W.S.;
 RT "Organization and alternative splicing of CACNA1H".
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Voltage-sensitive calcium channels (VSCC) mediate the
 CC entry of calcium ions into excitable cells and are also involved
 CC in a variety of calcium-dependent processes, including muscle
 CC contraction, hormone or neurotransmitter release, gene expression,
 CC cell motility, cell division and cell death. The isoform alpha-1H
 CC gives rise to T-type calcium currents. T-type calcium channels
 CC belong to the "low-voltage activated (LVA)" group and are strongly
 CC blocked by nickel and mibefradil. A particularity of this type of
 CC channels is an opening at quite negative potentials, and a
 CC voltage-dependent inactivation. T-type channels serve pacemaking
 CC functions in both central neurons and cardiac nodal cells and
 CC support calcium signaling in secretory cells and vascular smooth
 CC muscle. They may also be involved in the modulation of firing
 CC patterns of neurons which is important for information processing
 CC as well as in cell growth processes.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms=2;
 CC Name=1; Synonyms=ALH-a;
 CC IsoId=095180-1; Sequence=Displayed;
 CC Name=2; Synonyms=ALH-b;
 CC IsoId=095180-2; Sequence=VSP_000949;
 CC Isoform 2 seems to be testis-specific.
 CC -1- DOMAIN: Each of the four internal repeats contains five
 CC hydrophobic transmembrane segments (S1, S2, S3, S5, S6) and one
 CC positively charged transmembrane segment (S4). S4 segments
 CC probably represent the voltage-sensor and are characterized by a
 CC series of positively charged amino acids at every third position.
 CC -1- PTM: In response to raising of intracellular calcium, the T-type
 CC channels are activated by CaM-kinase II.
 CC -1- SIMILARITY: Belongs to the calcium channel alpha-1 subunits
 CC family.
 CC -1- CAUTION: AT-AC pre mRNA splicing gives rise to the isoform 1 shown
 CC in this entry. The additional 20 amino acids found in the Ref.4
 CC and Ref.6 sequences are due to a misunderstanding of the real type
 CC of splicing mechanism involved.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; AF051946; AAC67239.3; -
 CC EMBL; AF073931; AAD17668.1; -
 CC EMBL; AE006466; AAK61268.1; ALT_SEQ.
 CC EMBL; AJ420779; CAD12646.1; -
 CC EMBL; AL031703; CAC42094.1; ALT_SEQ.
 CC EMBL; AF223562; AAF60162.1; -
 CC EMBL; AF223563; AAF60163.1; -
 CC EMBL; HGNC:1395; CACNA1H.
 CC MIM; 607904; -
 CC GO; GO:0005891; C: voltage-gated calcium channel complex; TAS.
 CC GO; GO:0008332; P: low voltage-gated calcium channel activity; TAS.
 CC GO; GO:0008236; P: muscle contraction; TAS.
 CC GO; GO:0007520; P: myoblast fusion; TAS.
 CC GO; GO:0008016; P: regulation of heart rate; TAS.
 CC GO; GO:0006810; P: transport; TAS.
 CC InterPro; IPR001682; Ca/Na_pore.
 CC InterPro; IPR002111; Cat_channel_TrpL.
 CC InterPro; IPR005821; Ion_trans.
 CC InterPro; IPR005820; M_channel_nlg.
 CC InterPro; IPR005445; TVDCCALPH1.
 DR PFam: PF00520; Ion trans; 4.
 DR PRINTS: PR01629; TVDCCALPH1.
 KW Alternative splicing; Calcium channel; Calcium-binding; Glycoprotein;
 KW Ion transport; Ionic channel; Multigene family; Phosphorylation;
 KW Repeat; Transmembrane; Voltage-gated channel.
 FT REPEAT 87 422 I.
 FT REPEAT 779 1018 II.
 FT REPEAT 1281 1558 III.
 FT REPEAT 1602 1863 IV.
 FT DOMAIN 1 100 Cytoplasmic (Potential).
 FT TRANSMEM 101 119 S1 of repeat I (Potential).
 FT DOMAIN 120 139 Extracellular (Potential).
 FT TRANSMEM 140 160 S2 of repeat I (Potential).
 FT DOMAIN 161 169 Cytoplasmic (Potential).
 FT TRANSMEM 170 184 S3 of repeat I (Potential).
 FT DOMAIN 185 193 Extracellular (Potential).
 FT TRANSMEM 194 212 S4 of repeat I (Potential).
 FT DOMAIN 213 232 Cytoplasmic (Potential).
 FT TRANSMEM 233 253 S5 of repeat I (Potential).
 FT DOMAIN 254 294 Extracellular (Potential).
 FT TRANSMEM 395 419 S6 of repeat I (Potential).
 FT DOMAIN 420 793 Cytoplasmic (Potential).
 FT TRANSMEM 794 814 S1 of repeat II (Potential).
 FT DOMAIN 815 827 Extracellular (Potential).
 FT TRANSMEM 828 849 S2 of repeat II (Potential).
 FT DOMAIN 850 855 Cytoplasmic (Potential).
 FT TRANSMEM 856 874 S3 of repeat II (Potential).
 FT DOMAIN 875 882 Extracellular (Potential).
 FT TRANSMEM 883 906 S4 of repeat II (Potential).
 FT DOMAIN 907 917 Cytoplasmic (Potential).
 FT TRANSMEM 918 938 S5 of repeat II (Potential).
 FT DOMAIN 939 990 Extracellular (Potential).
 FT TRANSMEM 991 1015 S6 of repeat II (Potential).
 FT DOMAIN 1016 1290 Cytoplasmic (Potential).
 FT TRANSMEM 1291 1313 S1 of repeat III (Potential).
 FT DOMAIN 1314 1331 Extracellular (Potential).
 FT TRANSMEM 1332 1352 S2 of repeat III (Potential).
 FT DOMAIN 1353 1362 Cytoplasmic (Potential).
 FT TRANSMEM 1363 1382 S3 of repeat III (Potential).
 FT DOMAIN 1383 1396 Extracellular (Potential).
 FT TRANSMEM 1397 1418 S4 of repeat III (Potential).
 FT DOMAIN 1419 1428 Cytoplasmic (Potential).
 FT TRANSMEM 1429 1452 S5 of repeat III (Potential).
 FT DOMAIN 1453 1529 Extracellular (Potential).
 FT TRANSMEM 1530 1555 S6 of repeat III (Potential).
 FT DOMAIN 1556 1617 Cytoplasmic (Potential).
 FT TRANSMEM 1617 1637 S1 of repeat IV (Potential).
 FT DOMAIN 1638 1651 Extracellular (Potential).
 FT TRANSMEM 1652 1673 S2 of repeat IV (Potential).
 FT DOMAIN 1674 1680 Cytoplasmic (Potential).
 FT TRANSMEM 1681 1699 S3 of repeat IV (Potential).
 FT DOMAIN 1700 1713 Extracellular (Potential).
 FT TRANSMEM 1714 1737 S4 of repeat IV (Potential).
 FT DOMAIN 1738 1751 Cytoplasmic (Potential).
 FT TRANSMEM 1752 1772 S5 of repeat IV (Potential).
 FT DOMAIN 1773 1835 Extracellular (Potential).
 FT TRANSMEM 1836 1863 S6 of repeat IV (Potential).
 FT DOMAIN 1864 2353 Cytoplasmic (Potential).
 FT TRANSMEM 520 530 Poly-His.
 FT DOMAIN 1107 1110 Poly-Ser.
 FT TRANSMEM 1583 1586 Poly-Arg.
 FT SITE 378 Calcium ion selectivity and permeability
 FT SITE 974 (By similarity).
 FT SITE 1504 Calcium ion selectivity and permeability
 FT SITE 1808 Calcium ion selectivity and permeability
 FT CARBOHYD 192 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 271 N-linked (GlcNAc...) (Potential).
 Query Match 52.2%; Score 6210; DB 1; Length 2353;

Best Local Similarity 56.6%; Pred. No. 4.6e-274;
Matches 1364; Conservative 216; Mismatches 526; Indels 302; Gaps 59;

Qy	7	GAGAEAGQP-RSMRLNDLSGAGRPGCGSAEKDPSADSEAGLPPALAPVVFYLS	1016	EGQAE-----GDANRSDTDEKTSVHFEEDFKHLRELQTE	1052
Db	27	GASPEAGPAGREAGSEL-GVSPSESP-AAEAGAEAGDEQVRYPYALAAVVFCLG	1016	RKCLALVSGEHPKLSLLPLIIHTAATPMSLSTGLGEALGPARRTSSGSA	1075
Qy	66	QDSRPSKCLRTVCNPFERISMLVILLNCVTLGWPFCEDIACDSQCRILQAFDDFIP	1053	LKMCSLAVTPNGHLEGRGSLSPPLIMCTAATPMTKSSPFLDAAPSLDPSRRGSSSGD	1112
Db	85	QTTTPRSKCLVLCNPFHVSMLVIMVLCVTLGWPFCEDVEGSRCNLTLEAFDAFIP	1076	EPGAAHEMKPPSARSSPHSPWSAASWTSSRSNSIGRAPSLKRSRSPSGERSLSGSE	1135
Qy	126	APFAVEMVVMVAGLIGFKCYLGDWNRLDFFVIAGMLEYSLDQVSPSAVRTVRL	1113	PP--LGQOKPASPURSPCAPWPGSAWSSRRSSWSLGRAPSLKRRGQCGERSLSGSE	1170
Db	145	APFAVEMVVMVAGLIGFKCYLGDWNRLDFFVIAGMLEYSLDQVSPSAVRTVRL	1136	QBSQDEESSEBERASPA--GSDHRHRSGLEREAKSFDLPDTL-----QVPCGH---	1184
Qy	186	RPLRAINRPSMRILVTLDDTLPMGLNVLLCFVFFIFGIVGVQWAGLLNRCLPE	1171	GKGTDDDE--AEDGRAAPGPRATPLRAESLDPRPALPAALPTTKCRDRDQVVALPSDF	1228
Db	205	RPLRAINRPSMRILVTLDDTLPMGLNVLLCFVFFIFGIVGVQWAGLLNRCLPE	1185	--RTASGRGSAHQDCNGKSGASGRLARALRPDDPPLDGDODADDEGNLSKGERVRAMTRA	1242
Qy	246	NFSPLSDV-LERYVOTENEDESPICSPRENGMRCRSPV---TLRGDGGGPPCGLD	1229	FLRTDHSREDAEALDDSDSCCLRLHKVLEPKP-----QWCRS	1268
Db	265	AFVRNNLTFLRPIYQTEBGENPFICSSRRDNGMKCSHIPGRREL-----MPCTLG	1243	RLPACYLERDSWASAYIFPPQSRFRLLCHRIITHKMFHDHVLVIFILNCITIAMERP KIDP	1302
Qy	302	YEAYN-----SSNTTCVNNQYTNCSAGEHPKGAINFNIGYAMTAIFQVITL	1269	-----REAWDYLFPQNRFRVSCQKWITHKMFHDHVLVIFILNCITIALERP KIDP	1320
Db	319	WEATQPAEGVGARACINWQYVNCVSGSDSNPHNGAINFNIGYAMTAIFQVITL	1303	HSAEIRIFLTLSNIFTAVFLAEMTVKVVALGWCFCGEQAYLRSSWNVLDDLVLVLSVIDIL	1362
Qy	355	GWDMYFVMDAHFYNYFIFILLIIVGSPFMNLCVVIATQPSQKQESQMLREQRV	1321	GSTERVFLSVSNYIFTAIFVAEMVMKVVALGSLGSEHAYLQSSWNLLDGLLVLSVDIV	1380
Db	379	GWDMYFVMDAHFYNYFIFILLIIVGSPFMNLCVVIATQPSQKQESQMLREQRV	1363	VMVSSGTKILGMLRVLRLLRTPURVLSRAQGLKLVVETLMSLKSPTGNIVVICAP	1422
Qy	415	RFLSNASTLASFSFGCYBELLKVLVILKAAARLQAQVRAAGVRLGSSPAPLGGQ	1381	VAMASAGAKILGVLRLRTPURVLSRAQGLKLVVETLMSLKSPTGNIVVICAP	1440
Db	439	RFLSNASTLASFSFGCYBELLKVLVILKAAARLQAQVRAAGVRLGSSPAPLGGQ	1423	FIIFGILGVOLFPGKFFVCGEDTRNITKNSDCABASVYRVYRHKYKYNFDNLGOALMSFVL	1482
Qy	475	ETOPSSSCSSSHRR-LSVHLV-HHHHHHHHHLNGTLRAPRASPEIORDANGSRL	1441	FIIFGILGVOLFPGKFFVCGEDTRNITKNSDCABASVYRVYRHKYKYNFDNLGOALMSFVL	1500
Db	499	--GPHRRORAGRITASVHLVYVHHHHHHHHHYPHSGSPRPGPEACD-----TRLV	1483	ASKDGDWIDYDGLDVGVDQOQIMNHNPNMMLYFISFLITVAFVFLNMFVGVVVENPHK	1542
Qy	533	MLPPTSPALSGAPPGGAESVHSFYHADCHLE--PVRCAOPPPSPSEASGR-TVGSGKV	1501	SSKDGWNYDGLDVGVDQOQVQNHNPMMMLYFISFLITVAFVFLNMFVGVVVENPHK	1560
Db	552	RAGAPPSPGPGPPDAESVHSIYHADCHIEGPOEARVAHAATAAASLRLATGLTM	1543	CRQHEEEAARRREKRLREKKRR-----KQCKPYYSYDYSRFRLLVHLCTSHYLD	1596
Qy	590	-YPTV-----HTSP-----PPELTKALVEVAASSGPPTLTSLNIPGPY	1561	CRQHEEEAARRREKRLREKKRR-----KQCKPYYSYDYSRFRLLVHLCTSHYLD	1620
Db	612	NYPTILSPGVSGKSTPGPKWAGGPPGT-----CGHGPLSNS-----BDPY	1597	LFTGVGLNVMTVMMEHYOQPOLDEALAKCNVITFVFLVESVFLVAFGFRFRFQDR	1656
Qy	630	SSMHKLETOSTGACQS-----SKISSPCLKADGACGPDSCPYCARA-GAGEVELA	1621	LFTFIIICVNVITMSMEHYNQPSLDEALKCNVITFVFEAALKLVAFGFRFRFQDR	1680
Db	658	EKIPHVVGHEGLGQAPGHLGSLVPCPLPSP--PAGTLTCELKSCPYCTRALEDPEGELS	1657	WNQLDLAIVLLSIMGITLBEIEVNASLPINPITIRIMRVLRIARVLKLLKMAVGMRAILLD	1716
Qy	682	DREMPDSDEAVYBFTQDAQHSIDLDP-----HSRRQRSILGPDABESSV	1681	WNQLDLAIVLLSIMGITLBEIEVNASLPINPITIRIMRVLRIARVLKLLKMAVGMRAILLD	1740
Db	716	GSESGDSGRGVYEFTQDVRHGDWRDPTPRPRATDTPCGPGSPQRAAQRAAPGEPGMW	1717	TVNQALPQVGNLGLLMLFFIFAALGVLFGLDECDETHPCGELGRHATFRNFGMAFLT	1776
Qy	726	LAFWRLICDTPRKIVDSYKRGIMAILVNTLSMGIEYHQBPELTNALEISNIVTSL	1741	TVNQALPQVGNLGLLMLFFIFAALGVLFGLDECDETHPCGELGRHATFRNFGMAFLT	1800
Db	776	GRLVTFSGKLRLRIVDSKYSRGINMAILVNTLSMGIEYHQBPELTNALEISNIVTSM	1777	LFRVSTGDNWNGIMKTDIRDC---DQESTCYNVTISPFIYFVSFVLTAQFVLNVVAVLM	1833
Qy	786	FALEMLKLAVYGPFGYIKNPYNIFDGVIVVISVWEIVGQGGGLSVLRTFRLMRVLKV	1801	LFRVSTGDNWNGIMKTDIRDC---DQESTCYNVTISPFIYFVSFVLTAQFVLNVVAVLM	1860
Db	836	FALEMLKLAVYGPFGYIKNPYNIFDGVIVVISVWEIVGQGGGLSVLRTFRLMRVLKV	1834	KHLEESNKEAKEBAELEAELEMLKTLSPQSPGLSPFLWPGVGEPSDPS---DSPKPGA	1890
Qy	846	RFLPALQRLVLMKTMNDVATFCMLLMFLIFIFISILGMHLFGCKFASERD-GDTLPDRK	1861	KHLEESNKEAKEBAELEAELEMLKTLSPQSPGLSPFLWPGVGEPSDPS---DSPKPGA	1899
Db	896	RFLPALQRLVLMKTMNDVATFCMLLMFLIFIFISILGMHLFGCKFASERD-GDTLPDRK	1891	LHPAAHARSASHFSLEHTMQPHTELPG---PDLTVTRKSGVSRTHSLPNDSYMCRHG	1946
Qy	905	NFDSLLWAVTVFOILQEDWNKVLNGMASTSWAALYFIALMTFGNYVLFNLLVAIL	1900	-----PLPQESPGADAPNLV-ARKSVSRMLSLPLNDSYMFRPV	1937
Db	956	NFDSLLWAVTVFOILQEDWNKVLNGMASTSWAALYFIALMTFGNYVLFNLLVAIL	1947	STAEGP-----LGRHGWGLPKAGSGSVLSVHSOPADTSYIQLPKDAPHLLQPHSA	1997
Qy	965	EGFAEISKREDASGQLSCIQLPVDQGGDANKSESEPFPFSLDGD-----GD	1938	VPASAPHRPLQEVEMETYGAGTP---LGSVASVHSPAESCASLQIP-----LAVSSPA	1989
Db	1015	-----GD	1998	PTWGTTPKLPFGG--RSPLAQRPLRRQAAIRTSLSVQGLSGSREDLL--AEVSGPS--P	2051
Qy	1015	-----GD	1999	RSGEPLHALSPRGTAKEPSLSRLLCROEAVHTUSLEK-IDSPRDLTDPAPGPKTPVRP	2048

2052 LARAYSEWG--QSTOAOQHSRHSKISKHMTTPAPCPGPEPNWKGKPPETRSLSBLDTE 2109
 2049 VTGGSLQSPRPSPRPASVTRKHTFGQRCVSRPAAPGGE-----EAEASDPADSE 2100
 2110 LSWISGDLPL-----PGGQEEPP-----SPDLKKCYSEVAQSCORPTSMWLDQRHSIA 2160
 2101 VSHITSACQPWPTAEPHGPEASPVAGGERDLRLYSVDAQGFLDKP-GRADQWRPSAE 2159
 2161 VSCLDSSQPHLGTDPNSLGGQPLGGGSRPKKLSPPSITIDPP-ESQGPRTPPSP--- 2216
 2160 LGSGEPEAKAWGPE-----AEP--ALGARKKKMGPPCISVPPAEDEGSARPSAEGG 2212
 2217 GICLRRRAPS-----SDSKDPL-----ASGPPDSMA-----ASPPKKDVLSSLSGLSDPAD 2263
 2213 STTLRRTPSCATPHRDSLEPTEGSGAGGPAKGERWQASCRAEHLTVPSFAFEPLD 2272
 2264 L-----DP 2266
 2273 LGVPSGDP 2280

RESULT 9
 CCAH MOUSE
 ID CCAH_MOUSE STANDARD; PRT; 2365 AA.
 AC 088427; 09JKU5;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Voltage-dependent T-type calcium channel alpha-1H subunit (Voltage-
 gated calcium channel alpha subunit Cav3.2).
 DE Name=Cacnalh;
 GN Mus musculus (Mouse).
 OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OK NCBI_TaxID=10090;
 RN Mittman S.;
 RP STRAIN=BALB/c;
 RC Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 RA "Exon organization of mouse Cacnalh.";
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 RN SEQUENCE OF 1823-1952 FROM N.A.
 RP STRAIN=C57BL/6J;
 RC Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
 RL Cribbs L.L., Lee J.-H., Yang J., Daud A.N., Perez-Reyes E.;
 CC -!- FUNCTION: Voltage-sensitive calcium channels (VSCC) mediate the
 entry of calcium ions into excitable cells and are also involved
 in a variety of calcium-dependent processes, including muscle
 contraction, hormone or neurotransmitter release, gene expression,
 cell motility, cell division and cell death. The isoform alpha-1H
 gives rise to T-type calcium currents. T-type calcium channels
 belong to the "low-voltage activated (LVA)" group and are strongly
 blocked by nickel and mibefradil. A particularity of this type of
 channels is an opening at quite negative potentials, and a
 voltage-dependent inactivation. T-type channels serve pacemaking
 functions in both central neurons and cardiac nodal cells and
 support calcium signaling in secretory cells and vascular smooth
 muscle. They may also be involved in the modulation of firing
 patterns of neurons which is important for information processing
 as well as in cell growth processes.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- DOMAIN: Each of the four internal repeats contains five
 hydrophobic transmembrane segments (S1, S2, S3, S5, S6) and one
 positively charged transmembrane segment (S4). S4 segments
 probably represent the voltage-sensor and are characterized by a
 series of positively charged amino acids at every third position.
 CC -!- PTM: In response to raising of intracellular calcium, the T-type
 channels are activated by CaM-kinase II.
 CC -!- SIMILARITY: Belongs to the calcium channel alpha-1 subunits
 family.

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 between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
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 or send an email to license@isb-sib.ch).
 DR EMBL; AF226868; AAK21607.2; --
 DR EMBL; AY026385; AAK21607.2; JOINED.
 DR EMBL; AF051947; AAC67240.1; --
 DR MGI; 1328842; Cacnalh.
 DR InterPro; IPR001682; Ca/Na_pore.
 DR InterPro; IPR002111; Cat channel_TrpL.
 DR InterPro; IPR005821; Ion trans.
 DR InterPro; IPR005820; M+channel_nlg.
 DR InterPro; IPR005445; TVDCCALPHA1.
 DR Pfam; PF00520; Ion trans; 4.
 DR PRINTS; PR01629; TVDCCALPHA1.
 KW Calcium channel; Glycoprotein; Ion transport; Ionic channel;
 KW Multigene family; Phosphorylation; Repeat; Transmembrane;
 KW Voltage-gated channel.
 FT REPEAT 87 422 I.
 FT REPEAT 776 1015 II.
 FT REPEAT 1292 1569 III.
 FT REPEAT 1613 1874 IV.
 FT DOMAIN 1 100 Cytoplasmic (Potential).
 FT DOMAIN 101 119 S1 of repeat I (Potential).
 FT DOMAIN 120 139 Extracellular (Potential).
 FT TRANSMEM 140 160 S2 of repeat I (Potential).
 FT DOMAIN 161 189 Cytoplasmic (Potential).
 FT TRANSMEM 170 184 S3 of repeat I (Potential).
 FT DOMAIN 185 193 Extracellular (Potential).
 FT TRANSMEM 194 212 S4 of repeat I (Potential).
 FT DOMAIN 213 232 S5 of repeat I (Potential).
 FT TRANSMEM 233 253 Extracellular (Potential).
 FT DOMAIN 254 394 S6 of repeat I (Potential).
 FT TRANSMEM 395 419 Cytoplasmic (Potential).
 FT DOMAIN 420 790 S1 of repeat II (Potential).
 FT TRANSMEM 791 811 Extracellular (Potential).
 FT DOMAIN 812 824 S2 of repeat II (Potential).
 FT TRANSMEM 825 846 Extracellular (Potential).
 FT DOMAIN 847 852 S3 of repeat II (Potential).
 FT TRANSMEM 853 871 Extracellular (Potential).
 FT DOMAIN 872 879 S4 of repeat II (Potential).
 FT TRANSMEM 880 903 Cytoplasmic (Potential).
 FT DOMAIN 904 914 S5 of repeat II (Potential).
 FT TRANSMEM 915 935 Extracellular (Potential).
 FT DOMAIN 936 987 S6 of repeat II (Potential).
 FT TRANSMEM 988 1012 Cytoplasmic (Potential).
 FT DOMAIN 1013 1301 S1 of repeat III (Potential).
 FT TRANSMEM 1302 1324 Extracellular (Potential).
 FT DOMAIN 1325 1342 S2 of repeat III (Potential).
 FT TRANSMEM 1343 1363 Cytoplasmic (Potential).
 FT DOMAIN 1364 1373 S3 of repeat III (Potential).
 FT TRANSMEM 1374 1393 Extracellular (Potential).
 FT DOMAIN 1394 1407 S4 of repeat III (Potential).
 FT TRANSMEM 1408 1429 Cytoplasmic (Potential).
 FT DOMAIN 1430 1439 S5 of repeat III (Potential).
 FT TRANSMEM 1440 1463 Extracellular (Potential).
 FT DOMAIN 1464 1540 S6 of repeat III (Potential).
 FT TRANSMEM 1541 1566 Cytoplasmic (Potential).
 FT DOMAIN 1567 1627 S1 of repeat IV (Potential).
 FT TRANSMEM 1628 1648 Extracellular (Potential).
 FT DOMAIN 1649 1662 S2 of repeat IV (Potential).
 FT TRANSMEM 1663 1684 Cytoplasmic (Potential).
 FT DOMAIN 1685 1691 S3 of repeat IV (Potential).
 FT TRANSMEM 1692 1710 Extracellular (Potential).
 FT DOMAIN 1711 1724 S4 of repeat IV (Potential).
 FT TRANSMEM 1725 1748 Cytoplasmic (Potential).
 FT DOMAIN 1749 1762 S5 of repeat IV (Potential).
 FT TRANSMEM 1763 1783 Extracellular (Potential).
 FT DOMAIN 1784 1846 Extracellular (Potential).

FT	TRANSMEM	1847	1874	S6 of repeat IV (Potential).
FT	DOMAIN	1875	2365	Cytoplasmic (Potential).
FT	DOMAIN	521	531	Poly-His.
FT	DOMAIN	1594	1597	Poly-Arg.
FT	SITE	378	378	Calcium ion selectivity and permeability
FT	SITE	971	971	(By similarity).
FT	SITE	1515	1515	Calcium ion selectivity and permeability
FT	SITE	1819	1819	(By similarity).
FT	CARBOHYD	192	192	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	271	271	N-linked (GlcNAc. . .) (Potential).
FT	CONFLICT	1477	1477	GIM -> ARG (in Ref. 2).
FT	CONFLICT	1823	1825	D -> E (in Ref. 2).
FT	CONFLICT	1914	1914	APA -> LQ (in Ref. 2).
FT	CONFLICT	1945	1947	S -> A (in Ref. 2).
FT	CONFLICT	1952	1952	Missing (in Ref. 2).
FT	CONFLICT	1953	2351	Missing (in Ref. 2).
FT	SEQUENCE	2365	AA; 261944	MM; 9A9A17570C210596 CRC64;
Query Match				
Best Local Similarity 56.68; Score 6176.5; DB 1; Length 2365;				
Matches 1365; Conservative 235; Mismatches 528; Indels 285; Gaps 61;				
Qy	2	DEEDGAGAESGQPRFMRNDLS-GAGGRP----	GPFS----AEKDPGS---AD---SEA	48
Db	9	DEVVRPLGAPSA-PAAPVRASPASPGVPGREOQSGSGSLAPESPGTECGADLGADEE	67	
Qy	49	EGLPYPALAPVFPYLSQDSRPSWCLRTVCNPFERISMLVILNCVTGLGMRPCEA	108	
Db	68	QPVYPALAAATVPFCGLQGTTPRSWCLRLVCNPFERISMLVILNCVTGLGMRPCEA	127	
Qy	109	CDSORCILOAFDDFIFAPFAVENVMKVALGIPGKCYLGDWNRDFTFVLGMEYS	168	
Db	128	CRERCSCILAEAFDDFIFAPFAVENVMKVALGIPGKCYLGDWNRDFTFVLGMEYS	187	
Qy	169	LDLQNVFSASVTRVRLPRLAIRNPVSMRILVTLTLLDTPMLGNVLLLCFFVFFIFGIV	228	
Db	188	LDGHNVSLSAIRVRLPRLAIRNPVSMRILVTLTLLDTPMLGNVLLLCFFVFFIFGIV	247	
Qy	229	GVQLWAGLLNRCPLPENFSLPLSD-LERYOTENEDESPFICSQPRENGMSCRSVPT	287	
Db	248	GVQLWAGLLNRCPLPENFSLPLSD-LERYOTENEDESPFICSQPRENGMSCRSVPT	307	
Qy	288	---LRGDCGGGPPCGLDYEAY-----	NSSNTTCVNNQYNTNCSAGHNPPKGAINF	337
Db	308	RREL------VQCTLGWEAYGQPAEDGGAGRNACINNNQYNNVCSGFENPHNGAINF	361	
Qy	338	DNIGYAMIAIQVITLLEGWVDIMYVMDAHSFYNYFIYFILLIIVGSPFMINLCVVIATQ	397	
Db	362	DNIGYAMIAIQVITLLEGWVDIMYVMDAHSFYNYFIYFILLIIVGSPFMINLCVVIATQ	421	
Qy	398	FSETKQRESQIMRQVRVFLSNASTLASFPSPGSCYEELLYLYVILRKAARLAQVSR	457	
Db	422	FSETKQENQIMRQVRVFLSNASTLASFPSPGSCYEELLYLYVILRKAARLAQVSR	481	
Qy	458	AGVRVGLLSP-APLGQETQPSSSCSRRH-LSVHVLV-HHHHHHHVHLGNGTLRA	514	
Db	482	WQSRWRKVDPSSTLHQ--GPRRRPRAGRTASVHVLVYHHHHHHVHSHGSGPRR	539	
Qy	515	PRASPEIQDRDANGSRRLM--LPPTSTPALSGAPPGGAESVHSFYHADCHLEPVRCQAPP	572	
Db	540	P--SPE---PGAGDTRLVACVPPSPSGHGP--DSESVHSIYHADCHVEGQERARV	592	
Qy	573	PRSPSEASGRVTGG---KVPTV-----	HTSPPTLKEKALVEVAASSGPPTL	619
Db	593	AHTIATAASLKASGLGTMNYPTLPSCAVNSKGSTSRPKGLR-----SAGTFGA	643	
Qy	620	TS---LNI-PPGVSSMHKLETOSTGACQS-----	SKISSPCLKADSGAGCPDSCP	668
Db	644	TAHSPLSLGSPSPYEKIQHVVGEGGLGRASSHLSGLSVPCPLSP--QAGTLTCELKSCP	701	

Qy	669	YCARA-GAGEVELADREMPDSDSEAVYEFYTDQHQHSLDRP-----	HSSRRQ	714
Db	702	YCASALEDPFESGSGSDAHGVYEFYTDVHRGDCRDPVQQPHGGTPEGHNERWRP	761	
Qy	715	SLGPDAPSPVLAFWRLICDTRFKIVDSKYFGGIMIAILVNTLSMGIEVHEQPEELTNA	774	
Db	762	PLTASQPGGLRLMASFSSKLRRIVDSKYFNGGIMAAILVNTLSMGVHEQPEELTNA	821	
Qy	775	LEISNIVFTSLFALEMLLKVLYGPGYIKNPYIPDGVIVVSVWIEVGGQGLSVLR	834	
Db	822	LEISNIVFTSMFALEMLLKLACPLGYIRNPYIPDGVIVVSVWIEVGGQGLSVLR	881	
Qy	835	TFRLMRVILVRLPALORQLVLMKTMNDNVATFCMLLMFLIFIFSLGLHFLCKEASE	894	
Db	882	TFRLRLVILVRLPALORQLVLMKTMNDNVATFCMLLMFLIFIFSLGLHFLCKEASE	941	
Qy	895	RD-GDTLPDRKNFDSLLVAITVFOILTQSDMNKVLNGMASTSSWAAALFYALMTFGNY	953	
Db	942	TDSGDTVPDRKNFDSLLVAITVFOILTQSDMNKVLNGMASTSSWAAALFYALMTFGNY	1001	
Qy	954	VLFNLLVAILVEGFAEEISKREDASQQLSCIQLPVDSDGQDANKSSBSPFSPSLDGD	1013	
Db	1002	VLFNLLVAILVEGFAEEISKREDASQQLSCIQLPVDSDGQDANKSSBSPFSPSLDGD	1038	
Qy	1014	GDRLK-----CLALVSLGHEHPELRKSLPLLIHTAATPMSLPKSTSTGCGEALG	1063	
Db	1039	FDRLDRVATRMWYSLAVTPNG-HLEGRGSLPPLTHTAATPMPTPKS-SPHLDAHT	1096	
Qy	1064	PASRRYSSGASAPGAHEMKSPSPASPSHSPSAASSWTSRRSSRNSLRAPSLKRS	1123	
Db	1097	LLDSRSSGSDVDPQLG-DOKSLASLRSSPCAGPNASGSSRRSSWNSLRAPSLKRS	1155	
Qy	1124	PSGERSLLSGEGESQDEE-ESSEERASPGASHRHRGSLEREA-----KSSFDL---	1174	
Db	1156	QCGERESLLSGEGKSTDEAEDSRPNSTGTHPGASPGPRATPLRAESLGRSTMDLCP	1215	
Qy	1175	-PDLQVPLHRTASGRGSAEHQDCKGASGRLARALRPDPPLDGDADDGDNLSKG	1233	
Db	1216	RPATL-LP-----TKFRDCNQMVALLPSEFFLRIDSHKEDAAEFDDIEDSCC	1262	
Qy	1234	ERYAMIRARLPACYLERDSWSAYIPPPQSRFLCHRIITHKMFHVLVIIFLNCITI	1293	
Db	1263	FRUHKVLEPYAPQWCSRSSRWALYFPQNLRVSCQVIAHKMFHVLVIIFLNCITI	1322	
Qy	1294	AMERPDIHPSABRIFLTLSNYIFTAVFLAEMTVKVVVALGWCFGEOAYLRSSMNVLDGL	1353	
Db	1323	ALERPDIHPSABRIFLTLSNYIFTAVFLAEMTVKVVVALGWCFGEOAYLRSSMNVLDGL	1382	
Qy	1354	VLISVDILVMSVSDGSKTLGMLRVLRLLRPLRVISRAQGLKLVETLMSLXPIG	1413	
Db	1383	VLVSLVDIIVAVASAGAKILGLVLRLLRPLRVISRAQGLKLVETLMSLXPIG	1442	
Qy	1414	NIIVVICAPFIIFGILGVQLFGKFFVCCQGEDTRNITKSDCABASVYRVRHKNFNLG	1473	
Db	1443	NIIVVICAPFIIFGILGVQLFGKFFVCCQGEDTRNITKSDCABASVYRVRHKNFNLG	1502	
Qy	1474	QALMSFLVASKDGWVDIMYDGLDAGVQDQOPQVQNHNPMLLYFISFLIVAFVLMNFV	1533	
Db	1503	QALMSFLVASKDGWVDIMYDGLDAGVQDQOPQVQNHNPMLLYFISFLIVAFVLMNFV	1562	
Qy	1534	GVVVENPHKQHOEBEAREERREKRLRLLEKRR-----KAQCKYSDYSFRLLVH	1587	
Db	1563	GVVVENPHKQHOEBEAREERREKRLRLLEKRR-----KAQCKYSDYSFRLLVH	1622	
Qy	1588	HLCTSHVLDLFTGVIGLVNVTWMEHYQOPIILDEALKICNYIFTFVLESYFKLVAF	1647	
Db	1623	SLCTSHVLDLFTGVIGLVNVTWMEHYQOPIILDEALKICNYIFTFVLESYFKLVAF	1682	
Qy	1648	GFRFFQDRNQDLAIVLLSIMGITLIEEVNASLPINPTIIRIMVLRVLRVLLKLM	1707	
Db	1683	GFRFFQDRNQDLAIVLLSIMGITLIEEVNASLPINPTIIRIMVLRVLRVLLKLM	1742	

1708 AVGMRLDTVMQALPOVGNLGLFLLMFLFFIAALGVLFGLDCEDETHPCGELGRHATF 1767
1743 ATGKRLDITVVALPQVGNLGLFLLMFLFFIYALGVLEFGRLECSDEPNCEGLSRHATF 1802
1768 RNFMAFLTLFRVSTGDNWNGIMKOTLRDC---DOESTCVNTVISPFIYFVFLTAQFVL 1824
1803 TNFGMAFLTLFRVSTGDNWNGIMKOTLRDRECTEDKCLSYLPALSPVYFVFLTAQFVL 1862
1825 VNVVIAVIMKHLESKEAELEAELELEM-KTILSQPHPLSGPLFWPGVEGPDSP 1883
1863 VNVVAVIMKHLESKEAREDEADAEIELEIAQGSTAQPPSTAQES-----QGT-D-P 1915
1884 DSPKPGALHPAAHARSASHPSLEHPTMQPHTELPGLDITVRKSGVSRTHSLPNDSYMC 1943
1916 DT-----PMLLVKVSVMRLSLPNDSYMF 1941
1944 RHGSTAGPIGHRGWGLP-----KAQSGSVLHVHQPADTSYILQPKDAPHLLQPHSA 1997
1942 RPVAPAAAPHSH-----PLQEVEMETVGTPTSAAHSPSLPRTSFQVPSAASPAPA-SD 1995
1998 PTWGTIPKLPPEGSPPLAQRPLRQAIRTDLSLDVGLSGRDLLEAVSGSPPLARAYS 2057
1996 PLCALSPDPTP-RSLSLSILYRQEAHAELELEGQIDDDAGEDGIDPYTEPAENISMSQA 2053
2058 FWG-----QSSTQAQHSRSHSKISKHMTTPAPCPGPPNMGKGPETRSLSLELD 2107
2054 PLGTLRSPPCSPRPAVTRTKFTGQHCISSR-PPT-----LGDDDAEAADPAD 2101
2108 TELSWISGDLPL-----PGQREPP-----SPRLKKCYVEAQCORRPTSWLD 2152
2102 EEVSHITSSAHPWAPTEPHSPASPTASPAKGTGVGRDPHRCSDVAQSFDPK-GRPD 2160
2153 EQRHSTAVSCLDGSGQPHLGTDPNSLGGQPL-GPGSRPKKXLSPPSIIDPP-ESQGP 2210
2161 AQRSSVE-----LNG-DCHLESEVRARASELEPALKARRKKXKSPCISIDPTDEGS 2216
2211 RTTSPSP---GICLRRAPSSDSK-----DPLASGPPDSMAASPSPKQDV 2251
2217 SRPPAEGGNTLRRTPSCAALHRDCPSTEGPGTGGDPVAKGERWGA---SCRAEH 2273
2252 LSLSLSSDPA DL 2264
2274 LTVPNFAFEPLDM 2286
RESULT 10
CCAI_HUMAN
ID_CCAI_HUMAN STANDARD; PRT; 2223 AA.
AC Q9P0X4; Q95504; Q7Z6S9; Q8NFX6; Q9NZC8; Q9UH15; Q9UH30; Q9ULU9;
AC Q9UNE6;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUN-2004 (Rel. 44, Last annotation update)
DE Voltage-dependent T-type calcium channel alpha-1I subunit (Voltage-
DE gated calcium channel alpha subunit Cav3.3) (Ca(v)3.3).
GN Name=CACNAL1; Synonyms=KIAA1120;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC TISSUE=Brain;
RX MEDLINE=99381950; PubMed=10454147; DOI=10.1016/S0304-3940(99)00319-5;
RA Mitman S., Guo J., Emerick M.C., Agnew W.S.;
RT "Structure and alternative splicing of the gene encoding alpha1I, a
RL human brain T calcium channel alpha1 subunit.";
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 3).
RC TISSUE=Brain;
RX MEDLINE=20287513; PubMed=10749850; DOI=10.1074/jbc.C000090200;
RA Montell A., Chemin J., Leuranguer V., Altier C., Mennessier G.,

RA Bourinet E., Lory P., Nargeot J.;
RT "Specific properties of T-type calcium channels generated by the human
RT alpha1I subunit.";
RL J. Biol. Chem. 275:16530-16535 (2000).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 4), AND VARIANT VAL-1040.
RC TISSUE=Brain;
RX MEDLINE=12080115; PubMed=12080115;
RA Gomora J.C., Murbartian J., Arias J.M., Lee J.-H., Perez-Reyes E.;
RT "Cloning and expression of the human T-type channel Ca(v)3.3: insights
RT into prepulse facilitation.";
RL Biophys. J. 83:229-241 (2002).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=20057165; PubMed=10591208; DOI=10.1038/990031;
RA Dunham I., Hunt A.R., Collins J.E., Bruskewich R., Beare D.M.,
RA Clamp M., Smith L.J., Ainscough R., Almeida J.P., Babbage A.K.,
RA Bagguley C., Bailey J., Barlow K.F., Bates K.N., Bearnley O.P.,
RA Bird C.P., Blakey S.E., Bridgeman A.M., Buck D., Burgess J.,
RA Burrill W.D., Burton J., Carder C., Carter N.P., Chen Y., Clark G.,
RA Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R.,
RA Conroy D., Corby N.R., Coville G.J., Cox A.V., Davis J., Dawson E.,
RA Dhami P.D., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.G.,
RA Evans K.L., Fey J.M., Fleming K., French L., Garner A.A.,
RA Gilbert J.G.R., Goward M.E., Grafham D.V., Griffiths M.N.D., Hall C.,
RA Hall R.E., Hall-Tamlyn G., Heathcote R.W., Ho S., Holmes S.,
RA Hunt S.E., Jones M.C., Kershaw J., Kimberley A.M., King A.,
RA Laird G.K., Langford C.F., Leversha M.A., Lloyd C., Lloyd D.M.,
RA Martyn I.D., Mashregi-Wohammadi M., Matthews L.H., McCann O.T.,
RA McClay J., McLaren S., McMurray A.A., Milne S.A., Mortimore B.J.,
RA Odell C.N., Pavitt R., Pearce A.V., Pearson D., Phillimore B.J.C.T.,
RA Phillips S.H., Plumb R.W., Ramsay H., Ramsey Y., Rogers L., Ross M.T.,
RA Scott C.E., Sehra H.K., Skuce C.D., Smalley S., Smith M.L.,
RA Soderlund C., Spragon L., Steward C.A., Sulston J.E., Swann R.M.,
RA Vaudin M., Wall M., Wallis J.M., Whiteley M.N., Willey D.L.,
RA Williams L., Williams S.A., Williamson H., Wilmer T.E., Wilming L.,
RA Wright C.L., Hubbard T., Bentley D.R., Beck S., Rogers J., Shimizu N.,
RA Minoshima S., Kawasaki K., Sasaki T., Asakawa S., Kudon J.,
RA Shintani A., Shibuya K., Yoshizaki Y., Aoki N., Mitsuoyama S.,
RA Roe B.A., Chen F., Chu Y., Hu P., Hua A., Kenton S., Lai H., Lao H.I.,
RA Dorman A., Fang F., Fu Y., Hu P., Hua A., Kenton S., Lai H., Lao H.I.,
RA Lewis J., Lewis S., Lin S.-P., Loh P., Malaj E., Nguyen T., Pan H.,
RA Phan S., Qi S., Qian Y., Ray L., Ren Q., Shaull S., Sloan D., Song L.,
RA Wang Q., Wang Y., Wang Z., White J., Willingham D., Minx P.,
RA Zhan M., Zhang G., Chisoe S., Murray J., Miller N., Minx P.,
RA Fulton R., Johnson D., Bemis G., Bentley D., Bradshaw H., Bourne S.,
RA Cordes M., Du Z., Fulton L., Goela D., Graves T., Hawkins J.,
RA Hinds K., Kemp K., Latreille P., Layman D., Ozersky P., Rohlfing T.,
RA Scheet P., Walker C., Wansley A., Wohldmann P., Pepin K., Nelson J.,
RA Korf I., Bedell J.A., Hillier L.W., Mardis E., Waterston R.,
RA Wilson R., Emanuel B.S., Shaikh T., Kurahashi H., Saitta S.,
RA Budarf M.L., McDermid H.E., Johnson A., Wong A.C.C., Morrow B.E.,
RA Edelmann L., Kim U.J., Shizuya H., Simon M.I., Dumanski J.P.,
RA Payard M., Kedra D., Seroussi E., Fransson I., Tapia I., Bruder C.E.,
RA O'Brien K.P., Wilkinson P., Bodenteich A., Hartman K., Hu X.,
RA Khan A.S., Lane L., Tiliahun Y., Wright H.;
RT "The DNA sequence of human chromosome 22.";
RL Nature 402:489-495 (1999).
RN [5]
RP SEQUENCE OF 1200-2223 FROM N.A. (ISOFORM 1).
RC TISSUE=Brain;
RX MEDLINE=20039618; PubMed=10574461;
RA Hirosewa M., Nagase T., Ishikawa K.-I., Kikuno R., Nomura N.,
RA Ohara O.;
RT "Characterization of cDNA clones selected by the GeneMark analysis
RT from size-fractionated cDNA libraries from human brain.";
RL DNA Res. 6:329-336 (1999).
CC -I- FUNCTION: Voltage-sensitive calcium channels (VSCC) mediate the
CC entry of calcium ions into excitable cells and are also involved
CC in a variety of calcium-dependent processes, including muscle
CC contraction, hormone or neurotransmitter release, gene expression,
CC cell motility, cell division and cell death. Isoform alpha-1I
CC gives rise to T-type calcium currents. T-type calcium channels

CC belong to the "low-voltage activated (LVA)" group and are strongly
 CC blocked by nickel and mibefradil. A particularity of this type of
 CC channels is an opening at quite negative potentials, and a
 CC voltage-dependent inactivation. T-type channels serve pacemaking
 CC functions in both central neurons and cardiac nodal cells and
 CC support calcium signaling in secretory cells and vascular smooth
 CC muscle. They may also be involved in the modulation of firing
 CC patterns of neurons which is important for information processing
 CC as well as in cell growth processes. Gates in voltage ranges
 CC similar to, but higher than alpha 1g or alpha 1h (By similarity).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Name=1; Synonyms=Delta36b;
 CC IsoId=Q9POX4-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=Q9POX4-2; Sequence=VSP_000951;
 CC Name=3; Synonyms=Alpha1-a;
 CC IsoId=Q9POX4-3; Sequence=VSP_000950, VSP_000951;
 CC Name=4;
 CC IsoId=Q9POX4-4; Sequence=VSP_000950;
 CC -1- TISSUE SPECIFICITY: Brain specific.
 CC -1- DOMAIN: Each of the four internal repeats contains five
 CC hydrophobic transmembrane segments (S1, S2, S3, S5, S6) and one
 CC positively charged transmembrane segment (S4). S4 segments
 CC probably represent the voltage-sensor and are characterized by a
 CC series of positively charged amino acids at every third position.
 CC -1- PWM: In response to raising of intracellular calcium, the T-type
 CC channels are activated by CaM-kinase II (By similarity).
 CC -1- SIMILARITY: Belongs to the calcium channel alpha-1 subunits
 CC family.
 CC -1- CAUTION: Ref.4 (CAB62996) sequence differs from that shown due to
 CC erroneous gene model prediction.
 CC -----
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 CC or send an email to license@sib-sib.ch).
 CC -----
 CC DR EMBL; AF129133; AAD45251.1; -
 CC DR EMBL; AF142567; AAF25722.1; -
 CC DR EMBL; AF211189; AAF4626.1; -
 CC DR EMBL; AF393329; ANM67414.1; -
 CC DR EMBL; AL008716; CAA15494.1; -
 CC DR EMBL; AL022312; CAB62988.1; -
 CC DR EMBL; AL022319; CAB62996.1; ALT_SEQ.
 CC DR EMBL; AL022319; CAB29336.1; -
 CC DR EMBL; AB032946; BAA86434.1; -
 CC DR Genbank; HGNC:1396; CACNAL1.
 CC DR MIM; 608230; -
 CC DR GO; GO:0005891; C: voltage-gated calcium channel complex; NAS.
 CC DR GO; GO:0008332; P: low voltage-gated calcium channel activity; NAS.
 CC DR GO; GO:0006816; P: calcium ion transport; NAS.
 CC DR InterPro; IPR001682; Ca/Na pore.
 CC DR InterPro; IPR002111; Cat channel TrpL.
 CC DR InterPro; IPR002077; Ca channel_alpha.
 CC DR InterPro; IPR005821; Ion trans.
 CC DR InterPro; IPR005820; M-channel_nlg.
 CC DR InterPro; IPR005445; TVDCCAlphal.
 CC DR Pfam; PF00520; Ion trans; 4.
 CC DR PRINTS; PR01629; CACHANNEL.
 CC DR PRINTS; PR01629; TVDCCAlphal.
 CC KW Alternative splicing; Calcium channel; Calcium-binding; Glycoprotein;
 CC Ion transport; Ionic channel; Multigene family; Phosphorylation;
 CC Polymorphism; Repeat; Transmembrane; Voltage-gated channel.
 CC REPEAT 66 401
 CC I.
 CC FT REPEAT 626 865
 CC II.
 CC FT REPEAT 1157 1434
 CC III.
 CC FT REPEAT 1472 1733
 CC IV.
 CC DOMAIN 1 78
 CC Cytoplasmic (Potential).

FT	TRANSMEM	79	99	S1 of repeat I (Potential).
FT	DOMAIN	100	120	Extracellular (Potential).
FT	TRANSMEM	121	141	S2 of repeat I (Potential).
FT	DOMAIN	142	148	Cytoplasmic (Potential).
FT	TRANSMEM	149	168	S3 of repeat I (Potential).
FT	DOMAIN	169	173	Extracellular (Potential).
FT	TRANSMEM	174	191	S4 of repeat I (Potential).
FT	DOMAIN	192	211	Cytoplasmic (Potential).
FT	TRANSMEM	212	232	S5 of repeat I (Potential).
FT	DOMAIN	233	377	Extracellular (Potential).
FT	TRANSMEM	378	398	S6 of repeat I (Potential).
FT	DOMAIN	399	640	Cytoplasmic (Potential).
FT	TRANSMEM	641	661	S1 of repeat II (Potential).
FT	DOMAIN	662	676	Extracellular (Potential).
FT	TRANSMEM	677	697	S2 of repeat II (Potential).
FT	DOMAIN	698	702	Cytoplasmic (Potential).
FT	TRANSMEM	703	721	S3 of repeat II (Potential).
FT	DOMAIN	722	729	Extracellular (Potential).
FT	TRANSMEM	730	753	S4 of repeat II (Potential).
FT	DOMAIN	754	764	Cytoplasmic (Potential).
FT	TRANSMEM	765	785	S5 of repeat II (Potential).
FT	DOMAIN	786	841	Extracellular (Potential).
FT	TRANSMEM	842	862	S6 of repeat II (Potential).
FT	DOMAIN	863	1166	Cytoplasmic (Potential).
FT	TRANSMEM	1167	1187	S1 of repeat III (Potential).
FT	DOMAIN	1188	1209	Extracellular (Potential).
FT	TRANSMEM	1210	1230	S2 of repeat III (Potential).
FT	DOMAIN	1231	1244	Cytoplasmic (Potential).

Query Match 46.2%; Score 5496.5; DB 1; Length 2223;
 Best Local Similarity 51.3%; Pred. No. 1.2e-241;
 Matches 1241; Conservative 217; Mismatches 527; Indels 435; Gaps 60;

Qy	31	RPQSGAEKDPGSADSAEG----	LPYPALAPVVFYLSQDSRPSRCLRTVCNPFERI	86
Db	25	QPGSRSPSPGGLLEPLDGDGPHVPHPLDPIAFCLRTQTSRNNCKIKWCPWPCV	84	
Qy	87	SMVLILLNCVTILGNFRPCEDICQRCRIQAFDDFI	PAPFAVEMVMVVALGIFGKKC	146
Db	85	SMVLILLNCVTILGNFYQCDMDCLSDRCKILQVDFD	FIFFAMEMVLKVALGIFGKKC	144
Qy	147	YLGDTWNRLLDFFVIAGMLEYSLDLQNVFSAVRTV	RLPLRPLRINRVPNRIIVTLTLLD	206
Db	145	YLGDTWNRLLDFFVIAGMVEYSLDLQNLINSAINT	VLRLPLRPLRINRVPNRIIVNLILLD	204
Qy	207	TLPMGLNVLILCFVFFFIIGVIGVQWAGLNRNCR	LPENFSLPLSLDLERYQTEDE	266
Db	205	TLPMGLNVLILCFVFFFIIGVIGVQWAGLNRNCR	FLEENFTIQGDVALPPYQPEDDE	264
Qy	267	SPFICSQPRENGMRSCRSVETLRDGGGGPPCGI	-----DYEAYNSSNTT--CVWNQ	318
Db	265	MPTICSLSGDNGIMGCHEIPLKEQ-----	GRECCLSKDDVDYDFGAGRODLNAGSLCVNMR	321
Qy	319	YVYNTCSAGEHNPFGKAINFONIGVAMTAFQVIT	LEGWVDIMYVMDAHSFYNIYFILL	378
Db	322	YVNVCRGTSANPHKGAINFONIGVAMTAFQVIT	LEGWVEIMYVMDAHSFYNIYFILL	381
Qy	379	IIVGSFFMINCLVVIATQFSETKQESQLMRQEV	RFSLNASTLASFPGSGCYEBLLK	438
Db	382	IIVGSFFMINCLVVIATQFSETKQEHRLMLEQRQ	YLS-SSTVASYAEPGDCYEEIFQ	440
Qy	439	YLVYILKKAARLIAQVSRAGVRVGLLSSPAPICG	QGTQPSSSCSRSHRRLSVHVLVHH	498
Db	441	YVCHILKAKR-----RALGLYQALQSRQALG	PEAPAKP-----GPH	480
Qy	499	HHHHHHVH---LNGNLTLPRAPRASPEIODRDAN	-GSRRLM-LPPSPALSGAPPGAESV	553
Db	481	AKSPRHYHGTKGG-----DEGRHLGSRHCQT	LHGDPAS----GNDHSGR- --	523
Qy	554	HSFYHADCHLEPVRCQAPPRSPSEASGRVTGSG	SKVYFTVHTSPPTLKEALVEVAAS	613
Db	524	-----LC---POHSPLDATPHTL-----	VQPIPATL-----	546

QY 614 SGPTTLTSLNPPGPYSSMHKLETTOSTGACQSSCKISSPCLKADSGACGPDSCPCYCAR- 672
Db 547 -----AGAGEVELADREMPDSEAVVEFTODAQHSDLRDPHSRRQSRSLGPDAPSPSVL- 726
QY 673 -----AGAGEVELADREMPDSEAVVEFTODAQHSDLRDPHSRRQSRSLGPDAPSPSVL- 726
Db 560 DGRPPSGLGSTD-SGQEGSSGSAGGE--DEADGAGARSEDGASSELGKEEBEEOAD 616
QY 727 -----AFWRLICDTRFKIVDSKYFGRGIMTIALVNTLSMGIEYHQEPEELTNALEISN 779
Db 617 GAVMLCGDVWRETRAKLRGIVDSKYFNRIIMAILVNTVSMGIEHQEPEELTNALEICN 676
QY 780 IVTTSIPALEMLKLVYGPFGYKNPYNIFDGVIVISWEIVGQGGSLVLRFRML 839
Db 677 WFTSMFALEMLKLVAFGLFDYLRPNYIFDSIIWIEIVGQGGSLVLRFRML 736
QY 840 RVLKLVRLPALORQLVLMKTMNDVATFCMLLMFLIFISILGMHLFGCKFASERD-GD 898
Db 737 RVLKLVRLPALORQLVLMKTMNDVATFCMLLMFLIFISILGMHLFGCKFASERD-GD 796
QY 899 TLPDRKNFDSLLMAIVTVFOILLQEDWNKVLVYNGMASTSSWAALYFIATLMTFGNYVLENL 958
Db 797 TVPDRKNFDSLLMAIVTVFOILLQEDWNKVLVYNGMASTSSWAALYFIATLMTFGNYVLENL 856
QY 959 LVATLVGFOABEISKREDASGQSLCQLPVDQGGDANKSEGEPPFFS----- 1009
Db 857 LVATLVGFOABEISKREDASGQSLCQLPVDQGGDANKSEGEPPFFS----- 893
QY 1010 -LDGDRKCKKALVSLGHEPRLKSLPLLIHTAATPMSLPKSTSTGLGEALGPASRR 1068
Db 894 GLDSSGDPKLCPIPMTPNGH-----LDP-----SLPLGHLGPAGAAGPAPRL 936
QY 1069 T-----SSGSAPGAHEMKPPSARSSPHSPSWAASSWTSSRRSSSLGR 1115
Db 937 SLOQDPMVLVALGRKSSVMSLGRVSYDQSLSSRSSTYGPWGRSAWAWSRWSN----- 992
QY 1116 APSLKRSPSERSLSLGE--GQSSODEESSER--BRASPAGSDH----- 1158
Db 993 --SLKHKPPSAEHSLSLSAERGGAARVCEVAADGPPRAAPLHTPHAHHIIHGPHLAHRH 1050
QY 1159 -RHGSLREAKSFDPDPTLOVPLHRTASGR--GSASEHODONGKASGLARALRPD 1215
Db 1051 RHHRRTSLDNRDSVDLAELVPAVGAHPRAAWRAAGPAGHEDCNGRMPSTAKDVFTKMG 1110
QY 1216 DPPLDGDADDGKNSKGERVIRARLPACYLERSWSAYIIPPOSFRFLCHRIITH 1275
Db 1111 DRGDGED-EEEDITLCFRVRKMDVYKPDWCEVREDWSYLSFENRFRVLCQTIIAH 1169
QY 1276 KMFDRHVLVLIPLNCITIAMERPKIDPHSABRIFLTLSNYIFTAVFLAEMTVKVALGWC 1335
Db 1170 KLFVIVLAFIFLNCITIALERPOIEAGSTERIFLTVSNYIFTAIFVGEMLTKVYSLGLY 1229
QY 1336 FGEQYLRSSNNVLDGLVLVSDILVSMVSDSTKILGMRLVRLRLTLRLPLRVISRA 1395
Db 1230 FGEQYLRSSNNVLDGLVLFVSDIVVSLASAGAKILGVRLVRLRLTLRLPLRVISRA 1289
QY 1396 QGLKLVETLMSLPIGNIVVICCAFFIIFGILGVQLFKGFFVCQGEDTRNTNKSDC 1455
Db 1290 PGLKLVETLMSLPIGNIVVICCAFFIIFGILGVQLFKGFFVCQGEDTRNTNKSDC 1349
QY 1456 AFASRYVRHKKYFNONLQALMSLFLVASKOGVDVIMYDGLDGVDOQPIWHNPMWML 1515
Db 1350 MAANYRVHKKYFNONLQALMSLFLVASKOGVDVIMYDGLDGVDOQPIWHNPMWML 1409
QY 1516 YFISPLLIIVAFVLANFVGVVVENFKHQHQBEEAARRRERKRLRLEKKRKAQCKPY 1575
Db 1410 YFISPLLIIVAFVLANFVGVVVENFKHQHQBEEAARRRERKRLRLEKKRKAQCKPY 1469
QY 1576 YSDYRFRLLVHLCTSHYLDLFIITGVGLNVVTVMAHEYOQOILDEALKICNVIFTVI 1635
Db 1470 YATYCHTRLLIHSMTCTSHYLDLFIITGVGLNVVTVMAHEYOQOILDEALKICNVIFTVI 1529
QY 1636 FVLESFVKLVAFGRFFQDRNQLDLAIVLSIMGITLEEVNASLPINPTIIRMRV 1695

Db 1530 FVLEAVLKLVAFLGRFFQDRNQLDLAIVLSIMGITLEEVNASLPINPTIIRMRV 1589
QY 1696 LRIARVLKLVMAVGMALDVTMOALPOVGNLGLLPMLLFFIIPAAALGVLEFGLECDCT 1755
Db 1590 LRIARVLKLVMAVGMALDVTMOALPOVGNLGLLPMLLFFIIPAAALGVLEFGLECDCT 1649
QY 1756 HPCBGLGHATFRNFGMAFLTLFRVSTGDNWNGIMKDTLRDC-DOESTCVNTV--ISPIY 1812
Db 1650 NPCBGMSHATFRNFGMAFLTLFRVSTGDNWNGIMKDTLRDC-DOESTCVNTV--ISPIY 1709
QY 1813 FVSFVLTAQFVLVNVVIAVLMKHLBESNKEAEAELELEW-KTILSPQHSPLGSP 1871
Db 1710 FVSFVLTAQFVLVNVVIAVLMKHLBESNKEAEAELELEW-KTILSPQHSPLGSP 1769
QY 1872 FLMPGVEGPD-----SP-----DSKPKG 1889
Db 1770 GA-PG-RPGGAGGGDTEGGLCRRCYSIPAQENLWDSVSLI IKDSLEGEU TIIDNLSGS 1827
QY 1890 ALH-----PAA-----HARSAS-----HFSLEHPTWOP-----H 1913
Db 1828 IFHHYSSPAGCKCHHDKQEVQLAEATAEAFSLNSDRSSSILLGDDLSLEDDPTACPPGRKDS 1887
QY 1914 PTELPGDOLLTVRKSG-----VSRTHSLPN-DSVMCRHGSTAEGPLGHRGWLGPKAQSGS 1967
Db 1888 KGELDPPEPMRVGDLGECFFFLSSTAVSPDPENFLCEMBEIPFNIV--RSM--LKHDSQ 1943
QY 1968 VLSVHSQADTSYIQLPKDAPH-----LLQPHSAPTWTGTPKLPPLPG-----RSPLAQ 2016
Db 1944 APSPSPDASSPLLPMAEPFHPAVSASQKPEKGTGTGLPKIALQGSWASLSPRVN 2003
QY 2017 RPLRQAAIRTDLSVQGLSREDLLAEVSGPSPLARAYFWGQSSOQAQOHSRSHSKI 2076
Db 2004 CTLRQAQTGSDTSLD-----ASFSSAGSLQTTLEDLSLSDSPRRA----- 2045
QY 2077 SKHMTPPAPCPGPEPNWKGPPETRSSLSLELDTLWISGDLPLPGQEQEPSPRDLKCY 2136
Db 2046 ---LGPAPAPAPRAGLS---PAARRLSL-----RGRGLFSLR 2078
QY 2137 SVEAOSCRRPTSWLDEQRRHSIAVCLSDSGSQPHLGTDPN---LGQPLGGPSRPKK 2193
Db 2079 GLRA-----HQRSHSGGS-TSPGCTHDSMDPSDEGRGGAGGAGSEHSE 2125
QY 2194 KLSPPSIT---IDPPESQGPRTPPSGICLRERRAPSSDS---KQPLASGPPDSMAASPS 2246
Db 2126 TLSSLSLTLFCPPP-----PPAPGLTPARKFSTSSLAAPGRPHAAALHGLARSFS 2179
QY 2247 PKKDVLSLGLSDPADLDP 2266
Db 2180 WAAD-----RSKDPGGRAP 2193
RESULT 11
CCAI RAT STANDARD; PRT; 1835 AA.
AC Q20Y8; Q9EO59;
DT 30-MAY-2000 (Rel. 39, Created)
DT 10-OCT-2000 (Rel. 42, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Voltage-dependent T-type calcium channel alpha-II subunit (Voltage-gated calcium channel alpha subunit Cav3.3) (CaVt.3).
DE Name=Cacnall;
GN Rattus norvegicus (Rat).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RC SEQUENCE FROM N.A.
PC STEIN-Sprague-Dawley; TISSUE=Brain;
RX MEDLINE=99185796; PubMed=10066244;
RA Lee J.-H., Baud A.N., Cribbs L.L., Lacerda A.E., Pereverzev A.,
FA Kloeckner U., Schneider T., Perez-Reyes E.;
RT "Cloning and expression of a novel member of the low voltage-activated

RT	T-type calcium channel family.";	146	Cytoplasmic (Potential).	146	Cytoplasmic (Potential).
RN	J. Neurosci. 19:1912-1921(1999).	166	S3 of repeat I (Potential).	166	S3 of repeat I (Potential).
RL	[2]	171	Extracellular (Potential).	171	Extracellular (Potential).
RP	REVISIONS TO 345; 1656 AND 1737.	172	S4 of repeat I (Potential).	172	S4 of repeat I (Potential).
RA	Perez-Reyes B.;	189	Cytoplasmic (Potential).	189	Cytoplasmic (Potential).
RL	Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.	209	S5 of repeat I (Potential).	209	S5 of repeat I (Potential).
RN	[3]	210	Extracellular (Potential).	210	Extracellular (Potential).
RP	SEQUENCE FROM N.A.	231	S6 of repeat I (Potential).	231	S6 of repeat I (Potential).
RC	TISSUE=Brain;	372	Cytoplasmic (Potential).	372	Cytoplasmic (Potential).
RC	PubMed=11073957; DOI=10.1074/jbc.M008215200;	397	S1 of repeat II (Potential).	397	S1 of repeat II (Potential).
RX	McRory J.E., Santi C.M., Hamming K.S.C., Mezeyova J., Sutton K.G.,	599	Extracellular (Potential).	599	Extracellular (Potential).
RA	Baillie D.L., Seea A., Snutch T.P.;	632	Cytoplasmic (Potential).	632	Cytoplasmic (Potential).
RA	"Molecular and functional characterization of a family of rat brain T-	633	S2 of repeat II (Potential).	633	S2 of repeat II (Potential).
RT	type calcium channels.";	655	Cytoplasmic (Potential).	655	Cytoplasmic (Potential).
RT	J. Biol. Chem. 276:3999-4011(2001).	661	S3 of repeat II (Potential).	661	S3 of repeat II (Potential).
CC	-I- FUNCTION: Voltage-sensitive calcium channels (VSCC) mediate the	680	Extracellular (Potential).	680	Extracellular (Potential).
CC	entry of calcium ions into excitable cells and are also involved	688	S4 of repeat II (Potential).	688	S4 of repeat II (Potential).
CC	in a variety of calcium-dependent processes, including muscle	711	Cytoplasmic (Potential).	711	Cytoplasmic (Potential).
CC	contraction, hormone or neurotransmitter release, gene expression,	723	Extracellular (Potential).	723	Extracellular (Potential).
CC	cell motility, cell division and cell death. Isoform alpha-II	744	S5 of repeat II (Potential).	744	S5 of repeat II (Potential).
CC	gives rise to T-type calcium currents. T-type calcium channels	796	Extracellular (Potential).	796	Extracellular (Potential).
CC	belong to the "low-voltage activated (LVA)" group and are strongly	821	Cytoplasmic (Potential).	821	Cytoplasmic (Potential).
CC	blocked by nickel and mibefradil. A particularity of this type of	1126	Extracellular (Potential).	1126	Extracellular (Potential).
CC	channels is an opening at quite negative potentials, and a	1149	S1 of repeat III (Potential).	1149	S1 of repeat III (Potential).
CC	voltage-dependent inactivation. T-type channels serve pacemaking	1167	Extracellular (Potential).	1167	Extracellular (Potential).
CC	functions in both central neurons and cardiac nodal cells and	1188	Cytoplasmic (Potential).	1188	Cytoplasmic (Potential).
CC	support calcium signaling in secretory cells and vascular smooth	1198	Extracellular (Potential).	1198	Extracellular (Potential).
CC	muscle. They may also be involved in the modulation of firing	1218	S3 of repeat III (Potential).	1218	S3 of repeat III (Potential).
CC	patterns of neurons which is important for information processing	1232	Extracellular (Potential).	1232	Extracellular (Potential).
CC	as well as in cell growth processes. Gates in voltage ranges	1254	Cytoplasmic (Potential).	1254	Cytoplasmic (Potential).
CC	similar to, but higher than alpha 1G or alpha 1H.	1264	Extracellular (Potential).	1264	Extracellular (Potential).
CC	-I- SUBCELLULAR LOCATION: Integral membrane protein.	1288	S6 of repeat III (Potential).	1288	S6 of repeat III (Potential).
CC	-I- TISSUE SPECIFICITY: Brain.	1365	Cytoplasmic (Potential).	1365	Cytoplasmic (Potential).
CC	-I- DOMAIN: Each of the four internal repeats contains five	1391	Extracellular (Potential).	1391	Extracellular (Potential).
CC	hydrophobic transmembrane segments (S1, S2, S3, S5, S6) and one	1445	S1 of repeat IV (Potential).	1445	S1 of repeat IV (Potential).
CC	positively charged transmembrane segment (S4). S4 segments	1466	Extracellular (Potential).	1466	Extracellular (Potential).
CC	probably represent the voltage-sensor and are characterized by a	1480	Cytoplasmic (Potential).	1480	Cytoplasmic (Potential).
CC	series of positively charged amino acids at every third position.	1501	Extracellular (Potential).	1501	Extracellular (Potential).
CC	-I- PPM: In response to raising of intracellular calcium, the T-type	1509	S3 of repeat IV (Potential).	1509	S3 of repeat IV (Potential).
CC	channels are activated by CaM-kinase II (By similarity).	1528	Extracellular (Potential).	1528	Extracellular (Potential).
CC	-I- SIMILARITY: Belongs to the calcium channel alpha-1 subunits	1542	Cytoplasmic (Potential).	1542	Cytoplasmic (Potential).
CC	family.	1566	Extracellular (Potential).	1566	Extracellular (Potential).
CC		1580	Cytoplasmic (Potential).	1580	Cytoplasmic (Potential).
CC		1601	Extracellular (Potential).	1601	Extracellular (Potential).
CC		1624	S6 of repeat IV (Potential).	1624	S6 of repeat IV (Potential).
CC		1662	Cytoplasmic (Potential).	1662	Cytoplasmic (Potential).
CC		1693	Extracellular (Potential).	1693	Extracellular (Potential).
CC		355	Calcium ion selectivity and permeability	355	Calcium ion selectivity and permeability
CC		779	(By similarity).	779	(By similarity).
CC		1339	Calcium ion selectivity and permeability	1339	Calcium ion selectivity and permeability
CC		1637	(By similarity).	1637	(By similarity).
DR	EMBL; AF086827; AAD17796.2; --	171	Calcium ion selectivity and permeability	171	Calcium ion selectivity and permeability
DR	EMBL; AF290214; AAG35188.1; --	171	(By similarity).	171	(By similarity).
DR	InterPro; IPR001682; Ca/Na_pore.	242	N-linked (GlcNAc. . .)	242	N-linked (GlcNAc. . .)
DR	InterPro; IPR002111; Cat channel_Trlp.	309	N-linked (GlcNAc. . .)	309	N-linked (GlcNAc. . .)
DR	InterPro; IPR002077; Ca channel_alpha.	1301	N-linked (GlcNAc. . .)	1301	N-linked (GlcNAc. . .)
DR	InterPro; IPR005821; Ion_trans	1304	N-linked (GlcNAc. . .)	1304	N-linked (GlcNAc. . .)
DR	InterPro; IPR005820; M-channel_nlg.	193	M -> L (in Ref. 3).	193	M -> L (in Ref. 3).
DR	InterPro; IPR005445; TVDCCALphal.	291	C -> V (in Ref. 3).	291	C -> V (in Ref. 3).
DR	Pfam; PF00520; Ion_trans; 4.	394	V -> L (in Ref. 3).	394	V -> L (in Ref. 3).
DR	PRINTS; PR00167; CACHANNEL.	406	E -	406	E -
DR	PRINTS; PR01629; TVDCCALPHAL.	485	C -> N (in Ref. 3).	485	C -> N (in Ref. 3).
KW	Calcium channel; Multigene-binding; Glycoprotein; Ion transport;	512	D -> Y (in Ref. 3).	512	D -> Y (in Ref. 3).
KW	Ionic channel; Multigene family; Phosphorylation; Repeat;	558	S -> R (in Ref. 3).	558	S -> R (in Ref. 3).
KW	Transmembrane; Voltage-gated channel.	683	S -> S (in Ref. 3).	683	S -> S (in Ref. 3).
FT	REPEAT 64 399 I.	691	F -> S (in Ref. 3).	691	F -> S (in Ref. 3).
FT	REPEAT 584 823 II.	740	MH -> ID (in Ref. 3).	740	MH -> ID (in Ref. 3).
FT	REPEAT 1116 1393 III.	833	C -> Y (in Ref. 3).	833	C -> Y (in Ref. 3).
FT	REPEAT 1431 1692 IV.	846	F -> L (in Ref. 3).	846	F -> L (in Ref. 3).
FT	DOMAIN 1 76	856	S -> R (in Ref. 3).	856	S -> R (in Ref. 3).
FT	TRANSMEM 77 97	905	L -> R (in Ref. 3).	905	L -> R (in Ref. 3).
FT	DOMAIN 98 115	913	M -> YW (in Ref. 3).	913	M -> YW (in Ref. 3).
FT	TRANSMEM 116 137				
FT	TRANSMEM 116 137				

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EMBL; AF086827; AAD17796.2; -.

EMBL; AF290214; AAG35188.1; -.

InterPro; IPR001682; Ca/Na_pore.

Interpro: IPR02111; Cat_channel_TpL: Ca_channel_alpha

InterPro: IPR005821: Ion trans.
InterPro: IPR002077, Ca_channel_arppna.

InterPro; IPR005820; M+channel_nlg.

InterPro; IPR005445; TVDCCAlphal.

plam; PF00520; Ion_trans; 4.
PRINTS: PB00167: CACHANNET

PRINTS: PR01629: TVDCCAI.PHA1
FRINIS; FR00167; CACHANNEL.

Calcium channel; Calcium-binding; Glyc

Ionic channel; Multigene family; Phosph

Transmembrane; Voltage-gated channel.

REPEAT	64	399	1.
REPEAT	584	833	17

REPEAT	364	823	II.
REPEAT	1116	1393	III.

REPEAT	1431	1692	IV.
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DOMAIN	1	76	Cytoplasm

TRANSMEM	77	97	S1 of rep
CONV	88	115	CONV

DOMAIN	98	115	Extracell
TRANSMEM	116	137	S2 of ren

VOLUME CATEGORY

Db 1722 -----GPCPG-----PCPCPCPCGPRPLPTSSPG 1747

Qy 1926 ----RKSGVSRTHSLPNDSYMCRH 1945
||| : : : : :
Db 1748 APCRGGGAGAGG-DTSHLCRH 1769

RESULT 12

Q7Z6S8

ID Q7Z6S8 PRELIMINARY; PRT; 1994 AA.

AC Q7Z6S8;

DT 01-OCT-2003 (TrEMBLrel. 25, Created)

DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE DUL7B20.1 (Calcium channel, voltage-dependent, alpha 1I subunit)

DE (fragment).

GN Name=CACNAL1;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RA Phillips S.;

RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.

DR EMBL; AL022319; CAD92537.1; -.

DR GO; GO:0016021; C:integral to membrane; IEA.

DR GO; GO:0005261; P:cation channel activity; IEA.

DR GO; GO:0006812; P:cation transport; IEA.

DR InterPro; IPR001682; Ca/Na pore.

DR InterPro; IPR002111; Cat channel TrpL.

DR InterPro; IPR000345; CytC_heme_B5.

DR InterPro; IPR005821; Ion trans.

DR InterPro; IPR005820; M-channel_nlg.

DR Pfam; PF00520; Ion trans. 4.

DR PROSITE; PS00190; CYTOCHROME C; UNKNOWN 1.

DR Ion transport; Ionic channel; Transmembrane; Transport.

KW NON_TBR 1 1

FT SQ SEQUENCE 1994 AA; 220004 MW; A5EFA85FA32DCF76 CRC64;

Query Match 40.6%; Score 4836; DB 2; Length 1994;
Best Local Similarity 49.8%; Pred. No. 1.2e-211;
Matches 1117; Conservative 188; Mismatches 484; Indels 456; Gaps 55;

Qy 197 MRILVTLTLPMLGNVLLCPFPVFIIGVQVWAGLRNRCFLPENFSLPSVDLE 256
||| : : : : :
Db 1 MRILVNLDTLPMLGNVLLCPFPVFIIGVQVWAGLRNRCFLPENFTIQGDVALP 60

Qy 257 RYQTEDESPFCISQPRENGMRSCRSVPTLRGDDGGGPPCGI-----DYRAYNSSN 310
||| : : : : :
Db 61 PYYQPEDEMPFTCSLSDNGINGMGCEIPLKEQ---GRECCLSKDDVYDFGAGRODLN 117

Qy 311 TT--CVNNQYNTCSAGEHNPFGKAINPDNIGYAWIAITQVITLEGVDMIMYFVMDAHS 368
||| : : : : :
Db 118 ASGLCVNNRYNVCRTGSANPHKGAINDNIGAWIIVIQVITLEGVDMIMYFVMDAHS 177

Qy 369 FYNFIYFILLIIVGSFFMINLCLVVIATQFSETKQRESQMLREQRVFLSNASTLASFSE 428
||| : : : : :
Db 178 FYNFIYFILLIIVGSFFMINLCLVVIATQFSETKQREHRLMLEQRQVYLS--SSTVASYAE 236

Qy 429 PGSCYELLKYLVIILKAARLLAQVSRAGRVRLGLSSPAPLGGQGTQPSSCSRSHRR 488
||| : : : : :
Db 237 PGDCYEIFQVCHILRKAKR-----RALGLYQALQSRQALG----- 274

Qy 489 LSVHHLVHHHHHHHHYHGLNGTLRAPASPEIODRANGSRRLMLPPSTPALSAGPPG 548
||| : : : : :
Db 275 -----PEAPA--PAKPG 284

Qy 549 GAESVHSFYHADCHLEPVRQAPPPRSPSASGRTVGSKYPTVHTSPPETLKEKALV 608
||| : : : : :
Db 285 P-----HAK---EPRHVQLCPQHSFLDAPHTL-----VQPIPATL----- 317

Qy 609 EVAASSGPPTLTSLNIPPGPYSSMHKLETTQSTGACQSSCKISSPCLKADSGACGPDSCP 668

Db 318 -----ASDPASCP 325
||| : : : : :
Qy 669 YCAR-----AGAGEVELADREMPDSDSEAVYETQDAQHSDDLDRPHSRQRSGPDAEP 722
||| : : : : :
Db 326 CCQHEDGRRPSGLGSTD--SQEGSGSGSAGGE--DEADGDGARSSSDGASSELGKEEEE 382
||| : : : : :
Qy 723 SSVL-----AFWRLICDTFRKIVDSKYPGRGIMTALIVNTLSMGIEVHEQPEELTNA 774
||| : : : : :
Db 383 EQADGAVWLCGDVWRETRAKLRGIVDSKYFNGRIMAILVNTVSMGIEHHEQPEELTNI 442
||| : : : : :
Qy 775 LETSNIVFTSLFALEMLKLLVYGPFGYIKNPYNIPOGVIVVSWIWEIVGQGGSLVLR 834
||| : : : : :
Db 443 LEICNVVFTSMFALEMLKLAAPGLFDYLRNPYNIIFSIIIVISWIWGADGGLSVLR 502
||| : : : : :
Qy 835 TFLMRVYLKLVRFPLAQRLQVLMKTMNDNVATFCMLLMFLFIFISILGMHFLCKCFASE 894
||| : : : : :
Db 503 TFLLRVYLKLVRFMPALRRQLVLMKTMNDNVATFCMLLMFLFIFISILGMHFLCKCFSLR 562
||| : : : : :
Qy 895 RD--GDTLPDRKNFDSLWAIIVTFQILTOEDWKNVLYNGMASTSSWAAALFIALMTGNY 953
||| : : : : :
Db 563 TDTGDTVPDRKNFDSLWAIIVTFQILTOEDWNVLYNGMASTSPWASLYFVALMTFGNY 622
||| : : : : :
Qy 954 VLFNLLVAILVEGFOAEISKREDASGLSCIQLPVDSCGDANKSESDPDPFSPS--- 1009
||| : : : : :
Db 623 VLFNLLVAILVEGFOAE-----GDANRSYSDDEDQSSNTEEP 659
||| : : : : :
Qy 1010 -----LDGSDRKKCLALVSLGHEPRLKSLPLPLIHTAATPMSLPKSTSTGLGALG 1063
||| : : : : :
Db 660 DKLQEGLDSSGDPKLCIPMTNGH-----LDP-----SLPLGHLGPAGAAG 702
||| : : : : :
Qy 1064 PASRRT-----SSGSAEPGAHEMKSPPSARSSSPHSWASASSWTSRSSSR 1110
||| : : : : :
Db 703 PAPRLSLQDPMELVALGSRKSYMSLGRMSYDQRLSSRSRYYGPGRSAAWASRRSSW 762
||| : : : : :
Qy 1111 NSLGRAPSLARRSPGERRSLLSGE--QESQDSEESSE--ERASPAQSDH----- 1158
||| : : : : :
Db 763 N-----SLXKPPSAEHESLLSAERGGGARVCVAADGPPRAAPLHTPHAHHHGH 816
||| : : : : :
Qy 1159 -----RHRGSLEREAKSSFDLPOTLQVPGVGHRTASGR--GSASEHODCNKGSASGLAR 1210
||| : : : : :
Db 817 LAHRHRHRTLSLNDNRSDVLAELVPAGVCAHPRAAWRAAGPAGHEDCNGRMFSIAKDV 876
||| : : : : :
Qy 1211 ALRPDPPLDGDADDGNSLKGERRVAMTRARLPACYLDRDSWASVIFPPQSRFLCH 1270
||| : : : : :
Db 877 FTKMDGRDGRGD--EBEIDYTLCFVRVKMDIVKPDWCEVREDWSVLFSPENRFLVCQ 935
||| : : : : :
Qy 1271 RLITHKMFQHVHLVIIFLNCITITAMERPKIDPHSAERIFLTLSNYIETAVFLAEMTVKV 1330
||| : : : : :
Db 936 TIAHKLFDVYVLAFLPNCITIALERPQIEAGSTERIFLTVSNYIETAVFVGEWTKV 995
||| : : : : :
Qy 1331 ALGWCFCGEQAYLRSSWNVLDGLLVLSVIDILVSWVSDSGTKILGMLRVLRLTLRLPLR 1390
||| : : : : :
Db 996 SLGYFGEQAYLRSSWNVLDGLVFLVSIIDIVVSLASAGAKILGVRLVRLTLRLPLR 1055
||| : : : : :
Qy 1391 VISRAQGLKLVVTLMSLSKPIGNIVVICAFFIIFGILGVQLFKGKFFVCGQEDTNRIT 1450
||| : : : : :
Db 1056 VISRAPGLKLVETLISLKPIGNIVLICCAFFIIFGILGVQLFKGKFFHCLGVDTNRIT 1115
||| : : : : :
Qy 1451 NKSDCAEASRVWRHKYNFNLGNQALMSLFLVASKDGWDMIMYDGLDANGVDQOPIWNHN 1510
||| : : : : :
Db 1116 NRSDCAANRYWRVHKYNFNLGNQALMSLFLVASKDGWDMIMYDGLDANGVDQOPIWNHN 1175
||| : : : : :
Qy 1511 PMLLVPISELLIVAPFLNMFVGVVFNHFKRQHOEEERREKRRLRLEKKRKA 1570
||| : : : : :
Db 1176 PMLLVPISELLIVAPFLNMFVGVVFNHFKRQHOEEERREKRRLRLEKKRKA 1235
||| : : : : :
Qy 1571 QCKPYSDYGRFLLVHLCTSHYDLFITGVIGLVNVTWAMEHYQOQILDEALKI CNY 1630
||| : : : : :
Db 1236 QRLPYVATYCHTRLLIHSMTCTSHYDLFITFIIICLVNVTWMSLEHYNQTSLETALKY CNY 1295
||| : : : : :
Qy 1631 IFTVIVLESVFKLVAPFRFPDDRWNQDLALVLLSINGITLLEEEVNASLPINPTII 1690
||| : : : : :

Db 1296 MFTTVFVLEAVLKLAVGLRRFPKDRWNQDLDAVLVSVNGITLLEEIINAALPINPTII 1355
QY 1691 RIMRVLRIARVLKLLKAVGWRALLDTVMQALPOVGNLGLLMLFFIFPAALGVELFGDL 1750
Db 1356 RIMRVLRIARVLKLLKAVGWRALLDTVMQALPOVGNLGLLMLFFIFPAALGVELFGKL 1415
QY 1751 ECDTHPEGLRHATFRNFGMAFLTLFRVSTGDNWNGIMKDTLRDC-DQESTCYNTV-- 1807
Db 1416 VCNDEPNCEGWSRHATFENFGMAFLTLFQVSTGDNWNGIMKDTLRDCTHDSRCLSLQF 1475
QY 1808 ISPIYFVSFLTAQFVLVNVVIAVLMKHLBESNKEAEAEAELELELELELELELELELE 1866
Db 1476 VSLYFVSFLTAQFVLVNVVIAVLMKHLBESNKEAEAEAELELELELELELELELELE 1535
QY 1867 PLGSPFLWPGVEGD-----SP-----D 1884
Db 1536 PTGSPGA-PG-RPGGAGGGDTGGCLRCRCYSPAQENLWDSVLIKDSLGELTIID 1593
QY 1885 SPKPGALH-----PAA-----HARSAS-----HFSLEHPTMQP- 1912
Db 1594 NLGSGIFHYSSPAGCKCHDKQEVQAEAFSLNSDRSSSILLGDDLSLEDPTACPP 1653
QY 1913 -----HPTLPGPDLITVRKSG-----VSRTHSLPN-DSYNCRHGSAEGLPHRGWGLPK 1962
Db 1654 GRKDSKGELOPPBPMRVGDLGECFFPLSSTAVSPDPENFLCEMEEIPFNPV--RSM--LK 1709
QY 1963 AQSGSVLSVHSQPADTSYIQLPKDAPH-----LLQPHSAPTWTGTPKLPPLPPG-----R 2011
Db 1710 HDSQAPPSFPDASPLPMAEFPHPAVASQKPEKGTGTLPKIALOGSWASLR 1769
QY 2012 SPLAQRLRQAIRTDLSVOGLGSRDALLAEGVSGPSPLARAYSPWGSSTQAOQHSR 2071
Db 1770 SPRVNTLLRQATGSDTSLD-----ASPSSAGSLQTTLEDLSLSDSPRR 1815
QY 2072 SHSKISKHMTFPAPCPGPEPWGKGPETRSLSLELDTLSWISGDLPLPGQSEPSRPRD 2131
Db 1816 A-----LGPPAPAPGFRAGLS-----PAARRRSL-----RGRG 1844
QY 2132 LKRCYSVEAQSCORRPTSMWDEQRHSIAVSCLDGSGSQPHLGTDPN---LGGOPLGGPG 2188
Db 1845 LFSRLGLRA-----HQRSHSGGS-TSPGCTHDSWDPDEEGRGAGGGGAG 1891
QY 2189 SRPKKLSPPSIT---IDPPESOGPTPPSPGICLRRAPSSDS-----KDPASGPPDSM 2241
Db 1892 SEHSETLSLSLSTLFCPPP-----PPAPGLTPARKFSTSSLAAPGRPHAAALAHGL 1945
QY 2242 AASPSPKKDVLISGLSSDPAIDLDP 2266
Db 1946 ARSPSWAAD-----RSKOPPGRAP 1964

RESULT 13

Q7PQV4 PRELIMINARY; PRT; 1762 AA.
AC Q7PQV4
DT 01-MAR-2004 (TEMBLrel. 26, Created)
DT 01-MAR-2004 (TEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TEMBLrel. 26, Last annotation update)
DE ENSANGP0000003024 (Fragment).
GN Name=ENSANGG0000002480;
OS Anopheles gambiae str. PST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PEST;
RA Anopheles Genome Sequencing Consortium;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAB01008859; EAA08229.2; -.

DR GO:0016021; C:integral to membrane; IEA.
DR GO:0005261; F:voltage-gated calcium channel activity; IEA.
DR GO:0005245; F:voltage-gated calcium channel activity; IEA.
DR GO:0006816; P:calcium ion transport; IEA.
DR GO:0006812; P:calcium ion transport; IEA.
DR InterPro: IPR001682; Ca/Na_pore.
DR InterPro: IPR002111; Cat channel_TpPL.
DR InterPro: IPR005821; Ion trans.
DR InterPro: IPR005820; M4channel_nlg.
DR Pfam: PF00520; Ion trans. 4.
DR PRINTS: PR01629; TVDCCALPHA1.
KW Ion transport; Ionic channel; Transmembrane; Transport.
FT NON_TER 1
FT TER 1762 1762
SQ SEQUENCE 1762 AA; 19928 MW; AF70F5349068E2 CRC64;

Query Match 35.3%; Score 4200.5; DB 2; Length 1762;
Best Local Similarity 48.6%; Pred. No. 8.9e-183;
Matches 923; Conservative 268; Mismatches 48; Indels 261; Gaps 48;
QY 82 WFERISMLVILLNCVTLGMFRPCEDTACDSQRCRILOAFDDTFAFFAVEMVVMVALGI 141
Db 2 WFERISMLVILLNCVTLGMFRPCEDTACDSQRCRILOAFDDTFAFFAVEMVVMVALGI 61
QY 142 FGKCYLGTWNRDLFFVIAGMLEYSLDLQNVFSAVRTVRVLRPLRAINRVPSMRILV 201
Db 62 WKGKTYLADSWNRDLFFVIAGMLEYSLDLQNVFSAVRTVRVLRPLRAINRVPSMRILV 121
QY 202 TLLDTPMLGNVLLCFVFFIFGIVGVLWAGLNRCF--LPENFSLPLSVDLERY 259
Db 122 MLLDTPMLGNVLLCFVFFIFGIVGVLWAGLNRCF--LPENFSLPLSVDLERY 180
QY 260 OTENEDESPICSOPRENGMRSCRSVPTLRDGGGPP-----PCGLDVEANSSNTTCVN 315
Db 181 ERSKEQD--YICSPEDSGWHLCONLPYR-----IGPLCNDLSALPY-SENEFTATACVN 233
QY 316 WNOYTCNSAGEHNPFGAINFDNIGYAWIAIQVITLEGWVDIMYFVMDAHSFYNIYP 375
Db 234 WNOYTCNSAGEHNPFGAINFDNIGYAWIAIQVITLEGWVDIMYFVMDAHSFYNIYP 293
QY 376 ILLIIVGSFMINCLVIAIATQSETKORESOLMRQVRFLSNASTLAF---SEPGSC 432
Db 294 VLLIIVGSFMINCLVIAIATQSETKORESOLMRQVRFLSNASTLAF---SEPGSC 352
QY 433 YEBLLKYLVLKKAARLAAQVSRAGVRV-----GLLSSPAPLGGQETQPSSSCSRSHR 487
Db 353 YAEIVKVIYGHLYRRFKERLILKLLRYKYMOKKESGLI-----PCTPETI 397
QY 488 RLVSVHLVHHHHHHHHYHLNGTGLRAPASPIQDRDANGSR----- 530
Db 398 TLSPNKIKAHHP-----KCPRMGALLQQQHASITNLQQQXKXKHDQLQSSLSIN 444
QY 531 -----RLMLPPSTPALSG---APPGGAESV-----HSFYHADCHLEVRQCA---PPP 573
Db 445 RTGVTLNHPEPGTIVPSADNQVSSPEVSEIVSLKNNLNNTTYLNEEDROKULLKI 504
QY 574 RSPSEASGRITVSGKYVYVHTSPPEITLKEALVEVAASGSPPTL---TSLNIPPGPYS 630
Db 505 NNEDQNSGQVRGWLGMVW-----EGRSTFEGSSLSLAQDHH 545
QY 631 SMHKLLETSTGACQSSC-----KISSP-----CL-KADSGACQPS---C 667
Db 546 CMPSLLSPSSAGRRSSVMFNVVHLTPPTITEPPQDKNVYCLEKMTQAAANPATSRRA 605
QY 668 PYCARAGAEVELADREMPDSSEAVYETQDAQHSDDLDPHRRORSRGLPDAEPSSVLA 727
Db 606 PASTRCRPASTTSTWRSLSAATST-----TKTRAWRRSRDS-APSRGSSWR 653
QY 728 FWRLICDTFR-----KIVDSKYFGRGIMIAILVNTLSMGIEYHEQPELTNALISNIVFT 783
Db 654 CFPRTCHLTRVLVKLVHDHKYFQOQIGILLAILINTLSMGIEYHDPQPAELTAIVETSNI 713

RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J., Svirskas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celnikier S.E.,
RT "the transposable elements of the Drosophila melanogaster euchromatin:
a genomics perspective.";
RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
RN (4)
RP SEQUENCE FROM N.A.
RX MEDLINE=22426069; PubMed=12537572;
RA Miara S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celnikier S.E., de Grey A.D., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.,
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review.";
RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
RN (5)
RP SEQUENCE FROM N.A.
RX FlyBase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RN (6)
RP SEQUENCE FROM N.A.
RX FlyBase;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE003436; AAP46127.2; -
DR FlyBase; FBgn0029846; Ca-alpha-1T.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0005261; F: cation channel activity; IEA.
DR GO; GO:0005245; F: voltage-gated calcium channel activity; IEA.
DR GO; GO:0006816; P: calcium ion transport; IEA.
DR GO; GO:0006812; P: cation transport; IEA.
DR InterPro; IPR001682; Ca/Na_pore.
DR InterPro; IPR002111; Cat_channel_TripL.
DR InterPro; IPR005479; Cphp synth_L_D2.
DR InterPro; IPR001073; GAP_dhdrogenase.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR005820; M-channel_nlg.
DR InterPro; IPR005445; TVDCCALPHAL.
DR Pfam; PF00520; Ion_trans; 4.
DR PRINTS; PR01629; TVDCCALPHAL.
DR PROSITE; PS00867; CPSASE 2; UNKNOWN 1.
DR PROSITE; PS00071; GAPDH; UNKNOWN 1.
KW Ion transport; Ionic channel; Transmembrane; Transport.
SQ SEQUENCE 2893 AA; 321264 MW; 551BDC88D79A8DB2 CRC64;
Query Match 35.1%; Score 4180; DB 2; Length 2893;
Best Local Similarity 36.7%; Pred. No. 1.3e-181;
Matches 1060; Conservative 313; Mismatches 613; Indels 900; Gaps 81;
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QY 258 YYQTEDESPFICQPRENGMRCRSVPTLRGCGGGPGCGLDYEA--YNSSTNTTCVN 315
DB 183 YYFESKQD--YICSTNDSNMLCGNPPYR---IGSLVNEAKLFDENPTNTECVN 237
QY 316 WNQYITNCAGEHPNPFKGAINFQWIAIFQVITLEGVMDIMYFVMDAHSFYNIYF 375
DB 238 WNQYITTCQSGENPFQGTISFDNIGMAWVAIFLVISLEGWTDIMYVQDAHSFMDWIF 297

QY 376 ILLIIVGSPFMNLCIVVIATQFSETKORESOLMREQVRFLSNASTLASF---SPGSC 432
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QY 433 YBELLKYLVIILKARRLAQVSR----- 456
DB 357 YABIVKYIAHLWRRFKRRMLKKYLYQYQORKEGLLPNADNLTFSPRIKCHHPKCPK 416
QY 457 -----AAGVRVGLLSPAPL-----GG-----QET 476
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QY 477 QPSSSC-----SRSHRRLSVHLVHHHHHHHHYHLG----- 508
DB 477 NNAASCTTVALVNGINGSAASTVMSAHHQHQHLLQHQHQHQQOQQOQQOQQOQSSDNT 536
QY 509 -----NGLRAPASPEIQ-DRDANGSRRLMLPPP-----S 538
DB 537 EQLAPDGLPRSSSLKSTAHQKPEGSAABQKTLILKFPQOMIDSEQLILQNLGKS 596
QY 539 TPALSG--APPGGAEVSHFYHADCHLEPVRCAQPPRSPSEASGRT----- 593
DB 597 HPCSTGFLSPPTSASRRPSVMFN---EYVLLHTPALNADPATAGTTTVAPTVATVAG 652
QY 584 -----VGSKVY----- 590
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QY 623 -----NIPPGPYSSMHKLETTQST-GACQSSCKISSPCLKADSCAGCPDSCP--- 668
DB 773 EALRAHKKRPSVPTG-----QNQTPGAEGATVMVAS-----TAGDTGTLQSTV 818
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DB 992 PFYRIANGFNVFDGIIVILSAIEICQTFMNGTGGGGGLSVLRTFLRLILKLVRFMPN 1051
QY 851 LQRLVVLMTDMNVATFCMLMLFIFISILGMHLFGCKFASERDGTLPDRKNFDSLL 910
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QY 971 ETSKREDAAGQL----- 982
DB 1172 RNREREREORELVKRLREBTLAENYSDGMVDSRSEADSTTNDSYEVNRRWSAEDVR 1231
QY 983 ---SCITQLPVDSSOGG-----DANKSESEPDFSPSLDG-----DGRD----- 1016
DB 1232 KLODSVELIIEAKSNMHRQLLPQTHDYQINELPASSAAPSASGTSGASAPGDRDRDR 1291
QY 1017 -----KKCLALVS-LGEHPELEKSL--- 1036
DB 1292 DR 1351
QY 1037 PPLIHTAATPMSLPKST----- 1054

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 16, 2005, 00:03:00 ; Search time 20628 Seconds
(without alignments)
5322.839 Million cell updates/sec

Title: US-09-611-257a-37

Perfect score: 11904

Sequence: 1 MDEEDGAGAEESQPRFSFM.....PKDVLSLGLSDPADLDP 2266

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Zgapop 6.0 , Zgapext 7.0
Delep 6.0 , Delext 7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODE=frame+ p2n.model -DEV=xlh
-Q=/cgn2 1/USPTO.spool/US09611257/runat 13042005 170152 155/app_query.fasta_1.2439
-DB=GenEmbl -OPMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-LOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09611257 @CGN 1 1 13214 @runat 13042005 170152 155 -NCPU=6 -ICPU=3
-NO MMAP -LARGEBUFFER -NEG_SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl.*

1: gb.ba.*

2: gb.htg.*

3: gb.in.*

4: gb.om.*

5: gb.ov.*

6: gb.pat.*

7: gb.ph.*

8: gb.pl.*

9: gb.pr.*

10: gb.ro.*

11: gb.sts.*

12: gb.sy.*

13: gb.un.*

14: gb.vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	ID	Description
1	11895	99.9	6801 9 AF227751	AF227751 Homo sapi
2	11877.5	99.8	6822 6 AR201014	AR201014 Sequence
3	11877.5	99.8	6822 9 AF227744	AF227744 Homo sapi
4	11877.5	99.8	7741 6 AR201015	AR201015 Sequence

5	11872	99.7	6855	9	AF227749	Homo sapi
6	11843.5	99.5	6966	9	AF227745	Homo sapi
7	11838	99.4	6999	9	AF227750	Homo sapi
8	11815.5	99.3	7648	9	AF134986	Homo sapi
9	11758.5	98.8	7253	9	AF126965	Homo sapi
10	11741	98.6	7274	9	AF126966	Homo sapi
11	11741	98.6	7349	9	AF190860	Homo sapi
12	11735.5	98.6	6786	9	AF227747	Homo sapi
13	11707	98.3	6897	9	AF227746	Homo sapi
14	11703	98.3	6921	9	AF227748	Homo sapi
15	11251.5	94.5	7030	9	AF134985	Homo sapi
16	11246.5	94.5	7030	6	CQ724231	Sequence
17	11133.5	93.5	7625	10	MMU012569	Mus muscu
18	11111	93.3	7129	6	BD224078	T-type ca
19	11111	93.3	7285	6	BD224079	T-type ca
20	11111	93.3	7286	10	AF125161	Rattus no
21	10945	91.9	6942	10	AF290212	Rattus no
22	10945	91.9	7542	10	RNCA1G	Rattus no
23	10913	91.7	7527	10	BC057399	Mus muscu
24	10890.5	91.5	7540	6	AX068898	Sequence
25	8977	75.4	5475	9	AB032949	Homo sapi
26	7705	64.7	4903	9	AB012043	Homo sapi
27	6573	55.2	4944	10	AK129294	Mus muscu
28	6315.5	53.1	3993	9	AF124351	Homo sapi
29	6224.5	52.3	7044	9	HS420779	Homo sapi
30	6223	52.3	8447	6	AX068900	Sequence
31	6222.5	52.3	7868	10	AF290213	Rattus no
32	6215.5	52.2	7898	6	BD087035	Calcium c
33	6215.5	52.2	7898	9	AF073931	Homo sapi
34	6214.5	52.2	7898	6	BD087032	Calcium c
35	6211.5	52.2	7762	9	AF051946	Homo sapi
36	5713	48.0	6941	6	BD087036	Calcium c
37	5637.5	47.4	6924	6	CQ730788	Sequence
38	5496.5	46.2	6990	9	AF142567	Homo sapi
39	5493	46.1	6911	10	AF086827	Rattus no
40	5492.5	46.1	6816	6	AR175747	Sequence
41	5492.5	46.1	6816	6	AR352550	Sequence
42	5484	46.1	6855	6	AR175748	Sequence
43	5484	46.1	6855	6	AR352551	Sequence
44	5484	46.1	9896	9	AF393329	Homo sapi
45	5432.5	45.6	6740	9	AF129133	Homo sapi

ALIGNMENTS

RESULT 1	AF227751	6801 bp	mRNA	linear	PRI 06-MAR-2000
LOCUS	AF227751	Homo sapiens	voltage-dependent calcium channel alpha 1G subunit		
DEFINITION	isoform bc (CACNA1G) mRNA, complete cds.				
ACCESSION	AF227751				
VERSION	AF227751.1	GI:7159274			
KEYWORDS					
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	1 (bases 1 to 6801)				
AUTHORS	Monteil,A., Chemin,J., Bourinet,E., Mennessier,G., Lory,P. and Nargeot,J.				
TITLE	Molecular and functional properties of the human alpha(1G) subunit that forms T-type calcium channels				
JOURNAL	J. Biol. Chem. 275 (9), 6090-6100 (2000)				
MEDLINE	20158909				
PUBMED	10692398				
REFERENCE	2 (bases 1 to 6801)				
AUTHORS	Monteil,A., Mennessier,G., Bourinet,E., Lory,P. and Nargeot,J.				
TITLE	Direct Submission				
JOURNAL	Submitted (21-JAN-2000) C.N.R.S., Human Genetics Institute (I.G.H.)				
FEATURES	U.P.R. 1142, 141 rue de la Cardonille, Montpellier 34396, France				
source	Location/Qualifiers				
	1..6801				
	/organism="Homo sapiens"				

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1321 GTGTACATCTTCTGTAAGCAGCCGCGAGGCTGCTCAGGTCTCTCGGCGACGAGGTGTG 1380
Dy
Qy ArgValGlyLeuLeuSerSerProAlaProLeuGlyGlyGlnGluThrGlnProSerSer 480
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Dy 1501 CATCACCACTACCACTGGGCAATGGGACGCTCAGGGCCCCCGGGCGAGCCCGGAG 1560
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Dy 1681 TGCCACTTAGAGCCAGTCCGCTGCGCAGCGCCCCCTCCAGTCCCTCCATCTGAGGCATCC 1740
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Dy 1741 GGCAGGACTGTGGGACGCGGAGGTGTATCCACCGGTGTACACAGCCCTCCACCGGAG 1800
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Dy 1801 ACGCTGAAGCAGAGGACCTAGTAGAGTGGTGCAGCTCTCGGCCCCCCCAACCTCACC 1860
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Dy 1921 ACAGTGCTGCCAAGCTCTTGCAGATCTCCAGCCCTTGTCTTGAAGCAGACAGTGGGA 1980
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ACCESSION AR201014
VERSION AR201014.1 GI:20251902
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 6822)
AUTHORS Dubin,A.E., Galindo,J.E., Pyati,J., Zhu,J.Y. and Erlander,M.G.
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Best Local Similarity: 99.60% Mismatches: 1
Query Match: 99.78% Indels: 7
DB: 6 Gaps: 1

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RESULT 3
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DEFINITION Homo sapiens voltage-dependent calcium channel alpha 1G subunit
isoform ae (CACNALG) mRNA, complete cds.
ACCESSION AF227744
VERSION AF227744.1 GI:7159260
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 6822)
AUTHORS Montell,A., Chemin,J., Bourinet,E., Mennessier,G., Lory,P. and Nargeot,J.

TITLE Molecular and functional properties of the human alpha (1G) subunit that forms T-type calcium channels

J. Biol. Chem. 275 (9), 6090-6100 (2000)

20158909

10692398

REFERENCE 2 (bases 1 to 6822)

AUTHORS Montell, A., Mennessier, G., Bourinet, E., Lory, P. and Nargeot, J.

TITLE Direct Submission

JOURNAL Submitted (21-JAN-2000) C.N.R.S., Human Genetics Institute (I.G.H.) U.P.R. 1142, 141 rue de la Cardonille, Montpellier 34396, France

FEATURES

Location/Qualifiers

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ORIGIN

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Percent Similarity: 99.65% Conservative: 1

Best Local Similarity: 99.60% Mismatches: 1

Query Match: 99.78% Indels: 7

DB: 9 Gaps: 1

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DB 2641 ATCCTGGGATGATGATCTTTCGGCTGCAAGTTTGCTCTGAGGGGATGGGACACCTGTG 2700
QY 901 ProAspArgLysAsnPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIleLeu 920
DB 2701 CCAGACCGGAGAAATTTGACTCTTGTCTTGGGCCATCGTCACTGTCTTTCAGATCCTG 2760
QY 921 ThrGlnGluAspTrpAsnLysValLeuTyrAsnGlyMetAlaSerThrSerSerTrpAla 940
DB 2761 ACCCAGGAGGACTGGAAACAAAGTCTCTCAATGGTATGGCTTCCACGTCGCTCGGCG 2820
QY 941 AlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuVal 960
DB 2821 GCCTTTATTTTCATTTGCCCTCATGACTTCCGCACTACGTGCTCTTCAATTTGCTGGTC 2880
QY 961 AlaIleLeuValGluGlyPheGlnAlaGluGluIleSerLysArgGluAspAlaSerGly 980
DB 2881 GCCATCTGTGTGGAGGCTTCCAGCGGAGGAAATCAGCAAAACGGGAAGATGCGAGTGA 2940
QY 981 GlnLeuSerCysIleGlnLeuProValAspSerGlnGlyValAspAlaAsnLysSerGlu 1000
DB 2941 CAGTTAAGCTGTATTTCAGCTGCTGCACTCCAGGGGGAGATGCCAACACAGTCCGAA 3000
QY 1001 SerGluProAspPhePheSerProSerLeuAspGlyAspGlyAspArgLysLysCysLeu 1020
DB 3001 TCAGAGCCCATTTTCTTCTCACCCAGCTGATGGTGTGATGGGACAGGAAGAAGTGTGTG 3060
QY 1021 AlaLeuValSerIleuGlyGluHisProGluLeuArgLysSerLeuProLeuIle 1040
DB 3061 GCCTTGTGTCCCTGGGAGAGCACCCGAGCTCGGAAGAGCTGTGTGCTGCCCTCTCTATC 3120
QY 1041 IleHisThrAlaAlaThrProMetSerLeuProLysSerThrSerThrGlyLeuGlyGlu 1060
DB 3121 ATCCACAGCGCGGCCACCCCATGTGCTGCCCAAGACACACGACGAGCGGCGTGGCGAG 3180
QY 1061 AlaLeuGlyProAlaSerArgArgThrSerSerSerGlySerAlaGluProGlyAlaAla 1080

Db 3181 GCGCTGGGCGCTCGCTCGCGCGCACACAGCAGCGGTCGGCAGAGCCCTGGGGCGGCC 3240
Qy 1081 HisGluMetLysSerProProSerAlaArgSerSerProHisSerProTrpSerAlaAla 1100
Db 3241 CACGAGATGAAGTCAACCGCCAGCGCCCGCAGCTCTCGGCACAGCCCTGGAGCGCTGCA 3300
Qy 1101 SerSerTrpThrSerArgSerSerArgSerLeuGlyArgAlaProSerLeuLys 1120
Db 3301 AGCAGCTGGACACAGCAGCGCTCCAGCCGGAACACCTCGGCGGTGACCCAGCCCTGAAG 3360
Qy 1121 ArgArgSerProSerGlyArgArgSerLeuSerGlyGluGlyGlnGluSerGln 1140
Db 3361 CGGAGAAGCCCAAGTGGAGAGCGCGCTCCCTGTGTGGAGAGAGCCAGGAGCCAG 3420
Qy 1141 AspGluGluSerSerGluGluArgAlaSerProAlaGlySerAspHisArgHis 1160
Db 3421 GATGAAGAGGAGAGCTCAGAAGAGAGCGCGGCGCAGCCCTGGCGGCGAGTGCACATCGCCAC 3480
Qy 1161 ArgGlySerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeuGlnVal 1180
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Qy 1181 ProGlyLeuHisArgThrAlaSerGlyArgGlySerAlaSerGluHisGlnAspCysAsn 1200
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Qy 1201 GlyLysSerAlaSerGlyArgLeuAlaArgAlaLeuArgProAspAspProLeuAsp 1220
Db 3601 GCGAAGTCGGCTTCAGGCGCGCTCGCGCGGCGCTCGCGCTGCATGACCCCGCCACTGGAT 3660
Qy 1221 GlyAspAlaAspAspGluGlyAsnLeuSerLysGlyArgValArgValArgAlaTrpIle 1240
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Qy 1241 ArgAlaArgLeuProAlaCysTrpLeuGluArgAspSerTrpSerAlaTrpIlePhePro 1260
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Qy 1261 ProGlnSerArgPheArgLeuLeuCysHisArgIleIleThrHisLysMetPheAspHis 1280
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Qy 1281 ValValLeuValIleIlePheLeuAsnCysIleThrIleAlaMetGluArgProLysIle 1300
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Qy 1301 AspProHisSerAlaGluArgIlePheLeuThrLeuSerAsnTrpIlePheThrAlaVal 1320
Db 3901 GACCCCAACAGCGCTGAACGATCTCTTGACCCCTCTCCATTCATCTTCACGCGAGTC 3960
Qy 1321 PheLeuAlaGluMetThrValLysValValAlaLeuGlyTrpCysPheGlyGluGlnAla 1340
Db 3961 TTTCTGGCTGAATGACAGTGAAGGTGGTGCACTGGGCTGGTCTCGGGGAGCAGCGC 4020
Qy 1341 TyrLeuArgSerSerTrpAsnValLeuAspGlyLeuLeuValLeuIleSerValIleAsp 1360
Db 4021 TACTCGCGAGCAGTGGAACTGCTGACCGGCTGTGGTGTCTCATCTCCGTTCATCGAC 4080
Qy 1361 IleLeuValSerMetValSerAspSerGlyThrLysIleLeuGlyMetLeuArgValLeu 1380
Db 4081 ATTCTGGTGTCTATGCTCTCTGACAGCGGACCAAGATCTCTGGGCATGCTGAGGGTGTG 4140
Qy 1381 ArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeuLysLeu 1400
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Qy 1401 ValValGluThrLeuMetSerSerLeuLysProIleGlyAsnIleValIleCysCys 1420
Db 4201 GTGGTGGAGAGCGCTGATCTCTCATCTGAACCCCATCGCAACATTTGATGATCTGCTGT 4260
Qy 1421 AlaPhePheIleIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPhePheVal 1440
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Qy 1441 CysGlnGlyGluAspThrArgAsnIleThrAsnLysSerAspCysAlaGluAlaSerTyr 1460
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Qy 1461 ArgTrpValArgHisLysTrpAsnPheAspAsnLeuGlyGlnAlaLeuMetSerLeuPhe 1480
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Qy 1481 ValLeuAlaSerLysAspGlyTrpValAspIleMetTyrAspGlyLeuAspAlaValGly 1500
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Qy 1501 ValAspGlnGlnProIleMetAsnHisAsnProTrpMetLeuLeuTyrPheIleSerPhe 1520
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Qy 1521 LeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValValIleGluAsnPhe 1540
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Qy 1541 HisLysCysArgGlnHisGlnGluGluAlaArgArgArgGluGluLysArgLeu 1560
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Qy 1561 ArgArgLeuGluLysLysArgArg-----LysAlaGlnCysLys 1573
Db 4681 CGAAGACTGGAGAAAAAG 4740
Qy 1574 ProTyrTrpSerAspTyrSerArgPheArgLeuLeuValHisHisLeuCysThrSerHis 1593
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Qy 1594 TyrLeuAspLeuPheIleThrGlyValIleGlyLeuAsnValValThrMetAlaMetGlu 1613
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Db 4861 CACTACCAGCAGCGCCAGATTCTGGATGAGGCTCTGAAGATCTGCAACTATCTTCACT 4920
Qy 1634 ValIlePheValLeuGluSerValPheLysLeuValAlaPheGlyPheArgArgPhePhe 1653
Db 4921 GTCATCTTGTCTTGGAGTCAGTTTTCAAACTTGGGCTTGTGTTTCCGTCGGTCTTTC 4980
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Db 4981 CAGGACAGGTGGAACCAAGCTGGACCTGGCCATTGCTGCTGTCCATCATCGGCATCAG 5040
Qy 1674 LeuGluIleGluValAsnAlaSerLeuProIleAsnProThrIleIleArgIleMet 1693
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Qy 1694 ArgValLeuArgIleAlaArgValLeuLysLeuLysMetAlaValGlyMetArgAla 1713
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Qy 1714 LeuLeuAspThrValMetGlnAlaLeuProGlnValGlyAsnLeuGlyLeuLeuPheMet 1733
Db 5161 CTGCTGGACACGGTGTATGACGGCCCTGCCCCAGGTGGGAACTTGGGACTTCTCTTCATG 5220
Qy 1734 LeuLeuPhePheIlePheAlaLeuGlyValGluLeuPheGlyAspLeuGluCysAsp 1753
Db 5221 TTGTTGTTTTTTCATCTTTGCAGCTCTCGGCTGGAGCTCTTTGGAGACCTGGAGTGCAC 5280
Qy 1754 GluThrHisProCysGluGlyLeuGlyArgHisAlaThrPheArgAsnPheGlyMetAla 1773
Db 5281 GAGACACACCCCTGTGAGGCGCTGGCGGTGCATGCCACCTTTCGGAACCTTTGGCATGGCC 5340
Qy 1774 PheLeuThrLeuPheArgValSerThrGlyAspAsnTrpAsnGlyIleMetLysAspThr 1793
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Qy 101 PheArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPhe 120
Db 823 TTCGGCCATCGAGGACATCGCTGTGACATCCACGCGTCCGCGATCCTGCGAGCCCTTT 882
Qy 121 AspAspPheIlePheAlaPheAlaValGluMetValValLysMetValAlaLeuGly 140
Db 883 GATGACTTCATCTTTGCTCTTTGCGCGTGAGATGGTGGAGATGGTGGCCCTTGGGC 942
Qy 141 IlePheGlyLysLysCysTyrluGlyAspThrTrpAsnArgLeuAspPheIleVal 160
Db 943 ATCTTTGGGAAAAAGTGTACCTGGGAGACACTTGGAAACCGGCTTGACTTTTCATCGTC 1002
Qy 161 IleAlaGlyMetLeuGluTyrluSerLeuAspLeuGlnAsnValSerPheSerAlaValArg 180
Db 1003 ATCGAGGGATGCTGGAGTACTCGCTGGACCTGCAGAAACGTCAGCTTCTCAGCTGTGAGG 1062
Qy 181 ThrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeu 200
Db 1063 ACAGTCCGTGTCTGCGACCGCTCAGGGCCATTAAACCGGGTGCCAGCATGGGCATCTT 1122
Qy 201 ValThrLeuLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePhe 220
Db 1123 GTACAGTGTGCTGATACGCTGCCATGCTGGGCAACGTCCTGCTGCTGCTGCTCTTC 1182
Qy 221 ValPhePheIlePheGlyIleValGlyValGlnIleuTrpAlaGlyLeuLeuArgAsnArg 240
Db 1183 GTCCTTCATCTTCGGCATCGTGGCGTCAGCTGTGGGAGGGCTGCTTCGGAACCGA 1242
Qy 241 CysPheLeuProGluAsnPheSerLeuProLeuSerValAspLeuGluArgTyrluGln 260
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Qy 261 ThrGluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArg 280
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Qy 281 SerCysArgSerValProThrLeuArgGlyAspGlyGlyGlyProProCysGlyLeu 300
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Qy 301 AspTyrluAlaTyrluAsnSerSerAsnThrThrCysValAsnTrpAsnGlnTyrlu 320
Db 1423 GACTATGAGGCTTACACAGCTCCAGCAACACACCTGTGTCAACTGGAACCACTACTAC 1482
Qy 321 ThrAsnCysSerAlaGlyGluHiAsnProPheLysGlyAlaIleAsnPheAspAsnIle 340
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Qy 341 GlyTyrluAlaTrpIleAlaIlePheGlnValIleThrLeuGluGlyTrpValAspIleMet 360
Db 1543 GGCTATGCTGGATCGCCATCTTCAGGTCTATCAGCTGCAGGGGCTGGGTGCGATCATG 1602
Qy 361 TyrPheValMetAspAlaHisSerPheTyrluAsnPheIleTyrluPheIleLeuLeuIle 380
Db 1603 TACTTTGTGATGGATGCTCATCTTCTACAAATTCATCTACTTCACTCTCTCATCATC 1662
Qy 381 ValGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGlu 400
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Qy 401 ThrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAla 420
Db 1723 ACCAAGCAGCGGAAAGCAGCTGATGCGGAGCAGCGGTGTGGCGTTCCTGTCGAACGCC 1782
Qy 421 SerThrLeuAlaSerPheSerGluProGlySerCysTyrluGluGluLeuLysTyrluLeu 440
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Qy 441 ValTyrluLeuArgLysAlaAlaArgArgLeuAlaGlnValSerArgAlaAlaGlyVal 460
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Qy 461 ArgValGlyLeuLeuSerSerProAlaProLeuGlyGlyGlnGluThrGlnProSerSer 480

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Qy 481 SerCysSerArgSerHisArgArgLeuSerValHisHisLeuValHisHisHisHis 500
Db 1963 AGCTGCTCTGCTCCACCCGCGCTATCGCTCCACACCTGGTGTCACCCACCCACCCAC 2022
Qy 501 HisHisHisHisTyrluHisLeuGlyAsnGlyThrLeuArgAlaProArgAlaSerProGlu 520
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Qy 521 IleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProSerThrPro 540
Db 2083 ATCCAGACAGGATGCAATGGGTCCGCGAGGCTCATGTCGCCACCACTCTCAGCGCT 2142
Qy 541 AlaLeuSerGlyAlaProProGlyGlyAlaGluSerValHisSerPheTyrluHisAlaAsp 560
Db 2143 GCCCTCTCCGGGGCCCCCTGGTGGCGCAGAGTCTGTGCACAGCTTCTACCATGCGCAG 2202
Qy 561 CysHisLeuGluProValArgCysGlnAlaProProProArgSerProSerGluAlaSer 580
Db 2203 TGCCACTTAGAGCCAGTCCGCTGCAGCGCCCCCTCCAGGTCCCATCTCTGAGGCACTC 2262
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Qy 601 ThrLeuLysGlyLysAlaLeuValGluValAlaAlaSerSerGlyProProThrLeuThr 620
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Qy 621 SerLeuAsnIleProProGlyProTyrluSerSerMetHisLysLeuLeuGluThrGlnSer 640
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Qy 701 GlnHisSerAspLeuArgAspProHisSerArgArgGlnArgSerLeuGlyProAspAla 720
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Qy 761 GlyIleGluTyrluHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnIle 780
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DEFINITION Homo sapiens voltage-dependent calcium channel alpha 1G subunit
isoform bce (CACNA1G) mRNA, complete cds.
ACCESSION AF227749
VERSION AF227749.1 GI:7159270
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 6855)
AUTHORS Montell,A., Chemen,J., Bourinet,E., Mennessier,G., Lory,P. and Nargeot,J.
TITLE Molecular and functional properties of the human alpha (1G) subunit that forms T-type calcium channels
J. Biol. Chem. 275 (9), 6090-6100 (2000)
MEDLINE 20158909
PubMed 10492398
REFERENCE 2 (bases 1 to 6855)
AUTHORS Montell,A., Mennessier,G., Bourinet,E., Lory,P. and Nargeot,J.
TITLE Direct Submission
JOURNAL Submitted (21-JAN-2000) C.N.R.S., Human Genetics Institute (I.G.H.)
U.P.R. 1142, 141 rue de la Cardonille, Montpellier 34396, France
FEATURES
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ORIGIN
Alignment Scores:
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Score: 11872.00 Matches: 2264
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Best Local Similarity: 99.12% Mismatches: 1
Query Match: 99.73% Indels: 18
Gaps: 1
DB: 9
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AF227745 6966 bp mRNA linear PRI 06-MAR-2000
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DEFINITION isoform aef (CACNA1G) mRNA, complete cds.
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VERSION AF227745.1 GI:7159262
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
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AUTHORS Montell, A., Chemin, J., Bourin, E., Mennessier, G., Lory, P. and Nargeot, J.
TITLE Molecular and functional properties of the human alpha (1G) subunit that forms T-type calcium channels
JOURNAL J. Biol. Chem. 275 (9), 6090-6100 (2000)
MEDLINE 20158909
PUBMED 10692398
REFERENCE 2 (bases 1 to 6966)
AUTHORS Montell, A., Mennessier, G., Bourin, E., Lory, P. and Nargeot, J.
TITLE Direct Submission
JOURNAL Submitted (21-JAN-2000) C.N.R.S., Human Genetics Institute (I.G.H.)
U.P.R. 1142, 141 rue de la Cardonille, Montpellier 34396, France

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CDS

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ORIGIN

Alignment Scores:

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Db 2041 GCCGACCGTGAATGCCTGACTCAGACAGCGAGGCAGTTTATGAGTTTCAACAGGATGCC 2100
Qy GlnHisSerAspLeuArgAspProHisSerArgArgGlnArgSerLeuGlyProAspAla 720
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Qy GluProSerSerValLeuAlaPheTrpArgLeuIleCysAspThrPheArgLysIleVal 740
Db 2161 GAGCCCACTCTGTGCTGGCTTCTGGAGGCTAATCTGTGACACCTTCCGAAAGATTGTG 2220
Qy AspSerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerMet 760
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Qy GlyIleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnIle 780
Db 2281 GGCATCGAATACACAGCAGCGCCCGGAGGCTTACCAACCGCCCTAGAAATCAGCAACATC 2340
Qy ValPheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuLeuValTyrGlyProPhe 800

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Qy GlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleValIleValIleSerValTrp 820
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Qy GluIleValGlyGlnGlnGlyGlyLeuSerValLeuArgThrPheArgLeuMetArg 840
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Qy ProAspArgLysAsnPheAspSerLeuLeuTrpAlaIleValIleThrValPheGlnIleLeu 920
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Qy ArgArgSerProSerGlyGluArgArgSerLeuLeuSerGlyGluGlnGluSerGln 1140
Db 3361 CGGAGAGCCCAAGTGGAGAGCGCGGTCTTGTGTGGGAGAGGCGCAGAGAGCCAG 3420
Qy AspGluGluGluSerSerGluGluGluAlaSerProAlaGlySerAspHisArgHis 1160
Db 3421 GATGAGAGGAGAGCTCAGAGAGAGCGGCGCCAGCCCTTGGGGCAGTGCACATCGCCAC 3480

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Qy	1181	ProGlyLeuHisArgThrAlaSerGlyArgGlySerAlaSerGluHisGlnAspCysAsn	1200
Db	3541	CCAGGGCTGCATCGCACTGCCAGTGGCCGAGGGTCTGCTTCTGACACCAGGACTGCAAT	3600
Qy	1201	GlyIysSerAlaSerGlyArgLeuAlaArgAlaLeuArgProAspAspProIleuAsp	1220
Db	3601	GGCAAGTCGGCTTCAGGGCGCTTGGCGCGGGCCCTGCGCCCTGATGATGCCCCCACTGGAT	3660
Qy	1221	GlyAspAlaAspAspGluGlyAsnLeuSerLysGlyGluArgValArgAlaTrpIle	1240
Db	3661	GGGGATGACCCCGATGACAGGGCAACCTGAGCAAGGGAGACGGGTCCGCGCTGGATC	3720
Qy	1241	ArgAlaArgLeuProAlaCysIylsLeuGluArgAspSerTrpSerAlaTrpIlePhePro	1260
Db	3721	CGAGCCCGACTCCCTGCTCTGCTCGAGCGAGACTCCTGTGTGACCTTACATCTTTCCT	3780
Qy	1261	ProGlnSerArgPheArgIleuLeuCysHisArgIleIleThrHisIylsMetPheAspHis	1280
Db	3781	CCTCAGTCCAGGTTCCGCCCTCTGTGTACCGGATCATCACCAAGAATGTTCCGCCAC	3840
Qy	1281	ValValLeuValIleIlePheLeuAsnCysIleThrIleAlaMetGluArgProIylsIle	1300
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Db	4081	ATTCTGTGTCTCATGGTCTCTGACAGCGGCACCAAGATCCTGGGCATGCTGAGGGTGTCTG	4140
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Qy	1401	ValValGluThrLeuMetSerSerLeuLysProIleGlyAsnIleValValIleCysCys	1420
Db	4201	GTGGTGGAGACGCTGATGTCTCTCTGAAACCCATCGGCAACATGTGTAGTCATCTGCTGT	4260
Qy	1421	AlaPhePheIleIlePheGlyIleLeuGlyValGlnLeuPheIylsGlyLysPhePheVal	1440
Db	4261	GCCTTCTTTCATCATTTTCGGCATCTTGGGGGTGCAGCTCTTTCAAGAGGAAGTTTTTCGTG	4320
Qy	1441	CysGlnGlyGluAspThrArgAsnIleThrAsnLysSerAspCysAlaGluAlaSerTyr	1460
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Qy	1521	LeuLeuIleValAlaPhePheValLeuAenMetPheValGlyValValValGluIleAsn	Phe	1540
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Qy	1541	HisIysCysArgGlnHisGlnGluGluGluAlaAaArgArgGluGluIlylsArgLeu		1560
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Qy	1794	LeuArgAspCysAspGlnGluSerThrCysTyrAsnThrValIleSerProIleTyrPhe		1813
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LOCUS Homo sapiens voltage-dependent calcium channel alpha 1G subunit
DEFINITION isoform bcef (CACNA1G) mRNA, complete cds.
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VERSION AF227750.1 GI:7159272
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 6999)
AUTHORS Montell,A., Chamin,J., Bourinet,E., Mennessier,G., Lory,P. and Nargeot,J.
TITLE Molecular and functional properties of the human alpha (1G) subunit that forms T-type calcium channels
J. Biol. Chem. 275 (9), 6090-6100 (2000)
JOURNAL 20158909
MEDLINE 10692398
REFERENCE 2 (bases 1 to 6999)
AUTHORS Montell,A., Mennessier,G., Bourinet,E., Lory,P. and Nargeot,J.
TITLE Direct Submission
JOURNAL Submitted (21-JAN-2000) C.N.R.S., Human Genetics Institute (I.G.H.)
U.P.R. 1142, 141 rue de la Cardonille, Montpeillier 34396, France
FEATURES
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ORIGIN

Alignment Scores:

Pred. No.:	0	Length:	6999
Assignment Score:	11938.00	Matches:	2364
Score:	97.13%	Conservative:	1
Percent Similarity:	97.13%	Mismatches:	1
Best Local Similarity:	97.08%	Indels:	66
Best Global Similarity:	99.45%	Gaps:	2
Query Match:	9		
DB:	9		

UUS-09-611-257A-37 (1-2266) x AF227750 (1-6999)

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Db	361	GAT	GACT	TTCA	CTTT	TG	CCCT	TTT	TTC	CGC	TG	GAG	AT	TGG	TGT	GTAA	GAT	TGG	TGG	CCCT	420
Qy	141	Ile	Phe	Gly	Iys	Val	Cys	Cys	Tyr	Leu	Gly	Asp	Thr	Trp	Asn	Arg	Leu	Asp	Phe	Ile	160
Db	421	ATC	TTT	TGG	AAAA	AGT	GT	TCT	CGG	AGAC	ACT	TGG	AAAC	CCG	CGT	TGAC	TTTTT	TTC	TGC	T	480
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DEFINITION

complete cds.

AF134986
VERSION AF134986.1 GI:6625658

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 7648)

AUTHORS

Mittman, S., Guo, J. and Agnew, W.S.

TITLE

Structure and alternative splicing of the gene encoding alpha1g, a

JOURNAL

Neurosci. Lett. 274 (3), 143-146 (1999)

MEDLINE

20014446

PUBMED

10548410

REFERENCE

2 (bases 1 to 7648)

AUTHORS

Mittman, S., Guo, J. and Agnew, W.S.

TITLE

Direct Submission

JOURNAL

Submitted (15-MAR-1999) Anesthesiology/Critical Care Medicine, The

FEATURES

Location/Qualifiers

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QSPAPAPSLGGSDPOIPLAEMEARSLTSEIYSEPSCSIALATDDSLPDDMDHTLLISA
LESNMOPHTPELGPDLITVRKSCVSRTHSLPNDSYMCRHGSTAEGPLGRWGMLPKA
QSGSVLSVHQPADTSLIOLPKDAPHLLOPHSNAPTWGTTPKLPGRSPSLAQRPLER
QAIIRDSLDVQNGSREDLAEVSPSPELARAYSFWGSSSTQAQHSKRSKISKH
MTTPAPCPPEFNMGPPTBTRSLSDLETSWISGDLPLPPGQOESPSPRDLKKCY
VEAQSCORRTSWLDEGRHSIAVCLDSGSOPLHGTDPNGLGQPLGPGSPKKKL
SPSITIDPPESQGRTPPSFGICLRRRAPSSDSKDPPLASGPPPDSMAASPSPKKDVLS
LSGLSSDPADLDP"

ORIGIN

Alignment Scores:

Pred. No.: 0 Length: 7648
Score: 11815.50 Matches: 2264
Percent Similarity: 95.29% Conservative: 1
Best Local Similarity: 95.25% Mismatches: 1
Query Match: 95.26% Indels: 111
DB: 9 Gaps: 2

US-09-611-257A-37 (1-2266) x AFI34986 (1-7648)

Qy	1	MetAspGluGluAspGlyAlaGlyAlaGluSerGlyGlnProArgSerPheMet	20
Db	1	ATGGACGAGGAGGAGATGGAGCGGCGCGGAGGATCGGACAGCCCGGAGCTTCATG	60
Qy	21	ArgLeuAsnAspLeuSerGlyAlaGlyAlaGlyArgProGlyProGlySerAlaGluLysAsp	40
Db	61	CGGCTCAACGACCTGTCCGGGGCGCGGGCGCGGGCGGGGTGAGCAGAGAAAGGAC	120
Qy	41	ProGlySerAlaAspSerGluAlaGluGlyLeuProTyrProAlaLeuAlaProValVal	60
Db	121	CCGGCGCAGCGGACTCCGAGCGGAGGGGTGCGCTACCGCGGCTGGCCCGCGTGGTT	180
Qy	61	PhePheTyrLeuSerGlnAspSerArgProArgSerTyrCysLeuArgThrValCysAsn	80
Db	181	TTCCTTCTACTTGACCGAGGACAGCGCGCGGAGCTGGTGTCTCCGACAGCTCTGTAAC	240
Qy	81	ProTyrPheGluArgIleSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMet	100
Db	241	CCCTGGTTTGAGCGCATCAGCATGTGTCTCATCTCTCAACTCGGTGACCTGGGCATG	300
Qy	101	PheArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPhe	120
Db	301	TTCGGCGCATCGAGGACATCGCTGTGACTCCAGAGCGTCCGCGATCCTGCAGCGCTTT	360
Qy	121	AspAspPheIlePheAlaPhePheAlaValGluMetValValLysMetValAlaLeuGly	140
Db	361	GATGACTTCATCTTGGCTTTTCCCTGGAGATGGTGGTGAAGATGGTGGCTTGGGC	420
Qy	141	IlePheGlyLysLysCysTyrLeuGlyAspThrTrpAsnArgLeuAspPhePheIleVal	160
Db	421	ATCTTTGGAAAAAGTGTACCTGGGAGACACTTGGAAACCGCTTGACTTTTTCATCGTC	480
Qy	161	IleAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArg	180
Db	481	ATCCGAGGATGCTGGAGTACTCGCTGGACCTGCAGAACGTCAGCTTCTCAGCTGTGAGG	540
Qy	181	ThrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeu	200
Db	541	ACAGTCCGTGTGTGGACCGCTCAGGGCCATTAAACGGGTGCCAGCATCGCATCTT	600
Qy	201	ValThrLeuLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePhe	220
Db	601	GTCAGTGTCTGTGATACGTGCCATGTGCGCAACGTCCTGCTGCTGTCTGCTTCTTC	660
Qy	221	ValPhePheIlePheGlyValGlyValGlnLeuTrpAlaGlyLeuLeuLeuArgAsnArg	240
Db	661	GTCCTTCTTCATCTTCGGCATCGTGGCGTCCAGCTGTGGGAGGGCTGCTTCGGAACCGA	720
Qy	241	CysPheLeuProGluAsnPheSerLeuProLeuSerValAspLeuGluArgTyrTyrGln	260
Db	721	TGCTTCTTACCTGAGAAATTCAGCTCTCCCTGAGCGTGGACCTGGAGCGCTATTACGAG	780

Qy	261	ThrGluAsnGluAspGluSerPropheIleCysSerGlnProArgGluAsnGlyMetArg	280
Db	781	ACAGAGAACGAGGATGAGAGCCCTTCACTGTCTCCAGCACCGCAGAACGCGATCGCG	840
Qy	281	SerCysArgSerValProThrLeuArgGlyAspGlyGlyGlyProProCysGlyLeu	300
Db	841	TCTCTCAGAGAGCGTGCACCGCTGCGCGGGAGCGGGGGTGGCCACCTTCGCGGTCTG	900
Qy	301	AspTyrGluAlaTyrAsnSerSerAsnThrThrCysValAsnTrpAsnGlnTyrTyr	320
Db	901	GACTATGAGGCCTTACACAGCTCCAGCAACACCACTGTGTCACTGGAAACAGTACTAC	960
Qy	321	ThrAsnCysSerAlaGlyGluHisAsnProPheLysGlyAlaIleAsnPheAspAsnIle	340
Db	961	ACCAACTGTCTCAGCGGGAGCACAACCCCTTCAAGGGGCCATCAACTTTTGACACATT	1020
Qy	341	GlyTyrAlaTrpIleAlaIlePheGlnValIleThrLeuGluGlyTrpValAspIleMet	360
Db	1021	GGCTATGCTTGGATCGCCATCTTCCAGGTCATCACGCTGGAGGGCTGGGTGCAATCATG	1080
Qy	361	TyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleIle	380
Db	1081	TACTTTGTGATGATGCTCATCTTCTACAAATTTCTACTTCTCATCTCTCATCATC	1140
Qy	381	ValGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGlu	400
Db	1141	GTGGGCTCTCTTCTTATGATCAACCTGTGCTGTGTGTATGCCACGCGAGTTCTCAGAG	1200
Qy	401	ThrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAla	420
Db	1201	ACCAAGCAGCGGGAAGACCACTGATGCGGAGCAGCGTGTGCGGTCTCTGTCTCAACGCC	1260
Qy	421	SerThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLysTyrLeu	440
Db	1261	AGCACCTTGGCTAGCTTCTCTGAGCCGCGCAGCTGTCTATGAGGAGTGTCTCAAGTACTG	1320
Qy	441	ValTyrIleLeuArgLysAlaAlaArgArgLeuAlaGlnValSerArgAlaAlaGlyVal	460
Db	1321	GTGTATCATCTTCTGTAAGCAGCCCGCAGGCTGGCTCAGGTCTCTCGGGCAGCGGTGTG	1380
Qy	461	ArgValGlyLeuLeuSerSerProAlaProLeuGlyGlyGlnGluThrGlnProSerSer	480
Db	1381	CGGTTTGGGCTGTCTAGCAGCCCGACCCCTCGGGGGCCAGGAGACCCAGCCAGCAGC	1440
Qy	481	SerCysSerArgSerHisArgArgLeuSerValHisHisLeuValHisHisHisHis	500
Db	1441	AGCTGTCTCGCTCCCAACCGCCCTATCCGTCACCACTGGTGACACCAACCAACCCAC	1500
Qy	501	HisHisHisHisTyrHisLeuGlyAsnGlyThrLeuArgAlaProArgAlaSerProGlu	520
Db	1501	CATCACCAACCATACCACTGGGCAATGGGACGCTCAGGGCCCCCGGGCCAGCCCGGAG	1560
Qy	521	IleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProSerThrPro	540
Db	1561	ATCAGGACAGGATGCCAATGGGTCCGCGAGCTCATGTGCGCACCACTCCAGCCCT	1620
Qy	541	AlaLeuSerGlyAlaProProGlyGlyAlaGluSerValHisSerPheTyrHisAlaAsp	560
Db	1621	GCCTCTCCGGGGCCCCCTGTGTGGCGCAGAGTCTGTGCACAGCTTCTACCATGCCGAC	1680
Qy	561	CysHisLeuGluProValArgCysGlnAlaProProArgSerProSerGluAlaSer	580
Db	1681	TGCCACTTAGAGCAGTCCGCTGCCAGCGCCCCCTCCAGGTCCTCCATCTGAGGCATCC	1740
Qy	581	GlyArgThrValGlySerGlyLysValTyrProThrValHisThrSerProProGlu	600
Db	1741	GGCAGGACTGTGGGACGCGGAGGTGTATCCACCGTGCACACCAAGCCCTCCACCGGAG	1800
Qy	601	ThrLeuLysGluLysAlaLeuValGluValAlaAlaSerSerGlyProProThrLeuThr	620
Db	1801	ACGTGAAGGAGAGGACCTAGTAGAGGTGGTCCAGCTCTGGGCCCCCAACCCCTCACC	1860
Qy	621	SerLeuAsnIleProProGlyProTyrSerSerMetHisLysLeuLeuGluThrGlnSer	640

1861 AGCCTCAACATCCACCGCGGCTTACAGCTCCATGCAAGCTCTCTGGAGACAGAGT 1920
641 ThrGlyAlaCysGlnSerSerCysLysIleSerSerProCysLeuLysAlaAspSerGly 660
1921 ACAGGTGCTGCAAAAGCTCTTGCAAGATCTCCAGCCCTTGCTTGAAGAGACAGAGTGA 1980
661 AlaCysGlyProAspSerCysProTyrCysAlaArgAlaGlyAlaGlyGluValGluLeu 680
1981 GCCTGTGTGCAGACAGCTGCCCCCTACTGTGCCCCGCGCGGAGGAGGTGGAGCTC 2040
681 AlaAspArgGluMetProAspSerAspSerGluAlaValTyrGluPheThrGluAspAla 700
2041 GCCGACCTGAAATGCCCTGACTCAGACAGCGAGGAGGATTAAGTTTACACAGAGATGCC 2100
701 GlnHisSerAspLeuArgAspProHisSerArgArgGlnArgSerLeuGlyProAspAla 720
2101 CAGCACAGCAGCTCCGGGACCCCCACAGCGCGGGCAACGAGCCTGGGCCAGATGCA 2160
721 GluProSerSerValLeuAlaPheThrArgLeuLysCysAspThrPheArgLysIleVal 740
2161 GAGCCCACTGTGCTGCGCTTCTGGAGGCTAATCTGTGACACCTTCCGAAAGATTGTG 2220
741 AspSerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerMet 760
2221 GACAGCAGTACTTGGCGGGGAATCATGATCGCCATCTCTGGTCAACACACTCAGCATG 2280
761 GlyIleGluTyrHisGluGlnProGluLeuThrAsnAlaLeuGluLysSerAsnIle 780
2281 GGCAATCGAATACACGAGCAGCGCGAGGAGCTTACCAAGCGCCCTAGAAATCAGCAACATC 2340
781 ValPheThrSerLeuPheAlaLeuGluMetLeuLysLeuLeuValTyrGlyProPhe 800
2341 GTCTTACCAAGCTCTTTGCCCTGGAGATGCTGCTGAAGCTGTGTGTATGGTCCCTTT 2400
801 GlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleValIleValIleSerValTyr 820
2401 GGCTACATCAAGATCCCTACACATCTTCATGTGTGTCATGTGTGTCATCAGCGTGTGG 2460
821 GluIleValGlyGlnGlnGlyGlyLeuSerValLeuArgThrPheArgLeuMetArg 840
2461 GAGATCGTGGCCAGCAGCGGGCGGCTGCTGCTGCTGCGGACCTTCCGCTCATGCGT 2520
841 ValLeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetLys 860
2521 GTGCTGAAGCTGGTGGCTTCTGCGCGCTGCGAGCGGAGCTGGTGGTCTCATGAAG 2580
861 ThrMetAspAsnValAlaThrPheCysMetLeuMetLeuPheIlePheIlePheSer 880
2581 ACCATGGCAACGTGGCCACCTTCTGCATGCTGCTTATGCTTTCATCTTCATCTTCAGC 2640
881 IleLeuGlyMetHisLeuPheGlyCysLysPheAlaSerGluArgAspGlyAspThrLeu 900
2641 ATCTGGGATGCATCTCTTCGGTGCAGATTGGCTCTGAGCGGATGGGGACACCTGT 2700
901 ProAspArgLysAsnPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIleLeu 920
2701 CCAGACCGGAAGAAATTTGACTCTGCTGGGCCATCGTCACTGTCTTTTCAGATCCTG 2760
921 ThrGlnGluAspTrpAsnLysValLeuTyrAsnGlyMetAlaSerThrSerSerTrpAla 940
2761 ACCCAGGAGGACTGGAAAGTCTCTACAAATGGTATGGCTCCACGCTGCTCGGGCG 2820
941 AlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuVal 960
2821 GCCCTTATTTCAATGGCCCTCATGACCTTCGGCACTACGTGCTCTTCAATTCCTGCTC 2880
961 AlaIleLeuValGluGlyPheGlnAlaGluLysSerLysArgGluAspAlaSerGly 980
2881 GCCATTCGTGGAGGGCTTCAGCGCGAGGAAATCAGCAACCGGAAGATGCGAGTGA 2940
981 GlnLeuSerCysIleGlnLeuProValAspSerGlnGlyAspAlaAsnLysSerGlu 1000

2941 CAGTTAAGCTGTATTACGCTGCTGTGACTCCCGAGGGGGAGATGCCAACAGTCCGAA 3000
1001 SerGluProAspPhePheSerProSerLeuAspGlyAspGlyAspArgLysCysLeu 1020
3001 TCAGAGCCGATTTCTTCTCACCCAGCTGATGATGATGGGACAGGAAGAAGTGTCTG 3060
1021 AlaLeuValSerLeuGlyGluHisProGluLeuArgLysSerLeuLeuProLeuLeu 1040
3061 GCCTTGTGTCTCTGGGAGAGACCCGAGCTGGGAAAGAGCCTGCTGCCGCTCTCATC 3120
1041 IleHisThrAlaAlaThrProMetSerLeuProLysSerThrSerThrGlyLeuGlyGlu 1060
3121 ATCCACACGGCGCCGACACCCATGTGCTGCCCAAGAGACACAGACGGGCTTGGGCCAG 3180
1061 AlaLeuGlyProAlaSerArgThrSerSerSerGlySerAlaGluProGlyAlaAla 1080
3181 GCGCTGGGCCCTGCTGCGCGCCGACACAGCAGCAGCGGCTCGGAGAGCCTGGGGCGCC 3240
1081 HisGluMetLysSerProProSerAlaArgSerSerProHisSerProTrpSerAlaAla 1100
3241 CACGAGATGAAGTCAACGCCCGCCGAGCTCTCCGCAACAGCCCTGGAGCGCTGCA 3300
1101 SerSerTrpThrSerArgArgSerSerArgAsnSerLeuGlyArgAlaProSerLeuLys 1120
3301 AGCAGCTGGACACAGCGGCTCCAGCGGAAAGCTTCCGCGCTGCAACCGCTGAG 3360
1121 ArgArgSerProSerGlyGluArgSerSerLeuLeuSerGlyGlyGlnGluSerGln 1140
3361 CGGAGAAGCCCAAGTGGAGAGCGCGCTCTCTGTTGTCGGGAGAGGCCAGAGAGCCAG 3420
1141 AspGluGluSerSerGluGluArgAlaSerProAlaGlySerAspHisArgHis 1160
3421 GATGAAGAGGAGAGCTCAGAAGAGAGCGGCCAGCCCTGCGGCGAGTGCACCATGCCAC 3480
1161 ArgGlySerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeuGlnVal 1180
3481 AGGGGCTCCCTGGAGCGGAGGCCAGAGTTCTTTTACCTGCCAGACACACTGCGGTG 3540
1181 ProGlyLeuHisArgThrAlaSerGlyArgGlySerAlaSerGluHisGlnAspCysAsn 1200
3541 CCAGGGCTGCATCGCATCGCATCGCGCGGCGGCTGCTTCTGAGCACCAGGACTGCAAT 3600
1201 GlyLysSerAlaSerGlyArgLeuAlaArgAlaLeuArgProAspAspProProLeuAsp 1220
3601 GGCAAGTCCGCTTCCAGCGCGCTGCGCGCGGCTGCTGAGTGCATGCCCTCCAT 3660
1221 GlyAspAspAlaAspAspGluGlyAsnLeuSerLysGlyGluArgValArgAlaTrpIle 1240
3661 GGGATGACCCCGATGACGAGGGGCACTGAGCAAGGGGAAACGGGTCGCGCGGTGGATC 3720
1241 ArgAlaArgLeuProAlaCysTyrLeuGluArgAspSerTrpSerAlaTyrIlePhePro 1260
3721 CGAGCCGACTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3780
1261 ProGlnSerArgPheArgLeuLeuCysHisArgIleIleThrHisLysMetPheAspHis 1280
3781 CCTCAGTCCAGTTCGCTCTCTGTGTACCGGATCATCACCACAAAGATGTTCCAGCCAC 3840
1281 ValValLeuValIleIlePheLeuAsnCysIleThrIleAlaMetGluArgProLysIle 1300
3841 GTGTCCTTGTCTATCTCTCTTAACTGATCATCACCATCGCATGGAGCGGCCCAAAAT 3900
1301 AspProHisSerAlaGluArgIlePheLeuThrLeuSerAsnTyrIlePheThrAlaVal 1320
3901 GACCCCAACAGCGCTGAACGCATCTTCTGACCCCTCTCCAAATTAATATTCACCGCAGTC 3960
1321 PheLeuAlaGluMetThrValLysValValAlaLeuGlyTrpCysPheGlyGluGlnAla 1340
3961 TTTCTGCTGAAATGACAGTGAAGTGGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4020
1341 TyrLeuArgSerSerTrpAsnValLeuAspGlyLeuLeuValLeuIleSerValIleAsp 1360
4021 TACTGCGGAGCAGTTGGAACGTGCTGGACGGGCTGTTGGTGTCTCATCTCCGTATCGAC 4080

DB: 9 Gaps: 1
US-09-611-257A-37 (1-2266) x AF126965 (1-7253)

Qy 1 MetAspGluGluAspGlyAlaGlyAlaGluSerGlyGlnProArgSerPheMet 20
Db 176 ATGACGAGGAGGAGATGGAGCGGGCGCGAGAGTCCGGACACCGCCCGAGCTTCATG 235

Qy 21 ArgLeuAsnAspLeuSerGlyAlaGlyClyArgProGlySerAlaGluLysAsp 40
Db 236 CGGCTCAACACCTTGTCCGGGGCGCGGGCGCGGGCGCGGGTCCAGCAGAAAGAC 295

Qy 41 ProGlySerAlaAspSerGluAlaGluGlyLeuProTyrProAlaLeuAlaProValVal 60
Db 296 CCGGGCAGCGGACTCCGAGCGGAGGGCTGCGGTACCGCGCTGGCCCGCGTGGTT 355

Qy 61 PhePheTyrLeuSerGlnAspSerArgProArgSerTyrCysLeuArgThrValCysAsn 80
Db 356 TTCTTCTACTTGAAGCAGGACAGCGCGCGCGAGCTGGTGTCTCCGACGGTCTGTAAC 415

Qy 81 ProTyrPheGluArgIleSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMet 100
Db 416 CCCTGGTTTGAAGCGCATCAGCATGTGTATCTTCTCACTCGCTGACCCCTGGGATG 475

Qy 101 PheArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPhe 120
Db 476 TTCGGCCATCGAGGACATCGCTGTGACTCCCGAGCGCTGCGGATCCTCGACGGCCTTT 535

Qy 121 AspAspPheIlePheAlaPhePheAlaValGluMetValValLysMetValAlaLeuGly 140
Db 536 GATGACTTCATCTTGCCTTCTTTCGCGTGAGATGGTGTGAAGATGGTGGCCCTGGGC 595

Qy 141 IlePheGlyLysCysTyrLeuGlyAspThrTrpAsnArgLeuAspPhePheIleVal 160
Db 596 ATCTTTGGAAAAAGTGTACTCTGGAGACACTTGGAAACCGGCTTGACTTTTCATCGTC 655

Qy 161 IleAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArg 180
Db 656 ATCGCAGGATGCTGGAGTACTCGCTGGACCTGCAGAACGTCAGCTTCTCAGCTGTCCAG 715

Qy 181 ThrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeu 200
Db 716 ACAGTCCGTGTGTCGACCGCTCAGGGCCATTAAACCGGGTGCACGATCGCATCCTT 775

Qy 201 ValThrLeuLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePhe 220
Db 776 GTACGTGTCTGTGGATACGCTGCCATGCTGGCAACGTCCTGCTGCTCTCTTC 835

Qy 221 ValPhePheIlePheGlyIleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArg 240
Db 836 GTCTTCTTCACTTCGGCATCGTCGGCTCCAGCTGTGGCGAGGGCTGCTTCGGAAACCGA 895

Qy 241 CysPheLeuProGluAsnPheSerLeuProLeuSerValAspLeuGluArgTyrTrpGln 260
Db 896 TGCTTCTTACCTGAGAAATTCAGCTCCCTGAGCGTGGACCTGGAGCGCTATTACCA 955

Qy 261 ThrGluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArg 280
Db 956 ACAGAGAACGAGGATGAGAGCCCTTCATCTGCTCCAGCCACCGGAGAACGGATCGGG 1015

Qy 281 SerCysArgSerValProThrLeuArgGlyAspGlyGlyProProCysGlyLeu 300
Db 1016 TCCTGCAAGAGCGTGCACCGCTGCGGGGACGGGGCGGTGGCCACCTTGGCGGTCTG 1075

Qy 301 AspTyrGluAlaTyrAsnSerSerSerAsnThrThrCysValAsnTrpAsnGluTyrTyr 320
Db 1076 GACTATGAGGCTTACAAAGCTTCCAGCAACACCTGTGTCACTGGAAACGATCTAC 1135

Qy 321 ThrAsnCysSerAlaGlyGluIleAsnProPheLysGlyAlaIleAsnPheAsnIle 340
Db 1136 ACCAACTGCTCAGCGGGGAGCACAAACCTTCAAGGGCGGCATCACTTTGACAACTT 1195

Qy 341 GlyTyrAlaTrpIleAlaIlePheGlnValIleThrLeuGluGlyTrpValAspIleMet 360

Db 1196 GGCTATGCGCTGGATCGCCATCTTCCAGGTCATCACCTGGAGGGCTGGGTGCGACATCATG 1255

Qy 361 TyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIle 380
Db 1256 TACTTTGTGATGATGCTCATCTCTTCTACAAATTCATCTACTTCTCTCTCATCATC 1315

Qy 381 ValGlySerPhePheMetIleAsnLeuCysLeuValIleAlaThrGlnPheSerGlu 400
Db 1316 GTGGGCTCCTTCTTCATGATCAACCTGTGCTGGTGGTATTGCCACGCGAGTTCTCAGAG 1375

Qy 401 ThrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAla 420
Db 1376 ACCAAGCAGCGGAAAGCCAGCTGATCGGGAGCAGCGTGTGGGTTCCTGTCAACGCC 1435

Qy 421 SerThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLeuLysTyrLeu 440
Db 1436 AGCACCTTGCTAGCTTCTCTGAGCCCGCAGCAGTGTATGAGGAGTGTCTCAAGTACTG 1495

Qy 441 ValTyrIleLeuArgLysAlaAlaArgArgLeuAlaGlnValSerArgAlaAlaGlyVal 460
Db 1496 GTGTACATCCTTCTGAAGCGAGCCCGCAGGCTGGCTCAGGTCTCTCGGGCAGCAGGTGTG 1555

Qy 461 ArgValGlyLeuLeuSerSerProAlaProLeuGlyGlyGlnGluThrGlnProSerSer 480
Db 1556 CGGGTTGGGCTGTCTCAGCAGCCCGCAGCACCTCTCGGGGGCCAGAGACCCAGCCAGCAGC 1615

Qy 481 SerCysSerArgSerHisArgArgLeuSerValHisHisLeuValHisHisHis 500
Db 1616 AGTGTCTCTCGCTCCACCGCCCTTATCGCTCCACCATCTGTGTGCACACACCCACCAC 1675

Qy 501 HisHisHisTyrHisLeuGlyAsnGlyThrLeuArgAlaProArgAlaSerProGlu 520
Db 1676 CATCACCACTTACCACTGGGCAATGGAGCGCTCAGGGCCCGCCGGGCGAGCCGCGAG 1735

Qy 521 IleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProSerThrPro 540
Db 1736 ATCCAGACAGGATGCCAATGGTCCCGCGCTCATGTGCCACCATCCCTCGACGCT 1795

Qy 541 AlaLeuSerGlyAlaProProGlyGlyValAlaGluSerValHisSerPheTyrHisAlaAsp 560
Db 1796 GCCTCTCCGGGGCCCCCTTGTGGCGCAGAGTCTGTGCACAGTCTTACCATGCCGAC 1855

Qy 561 CysHisLeuGluProValArgCysGlnAlaProProProArgSerProSerGluAlaSer 580
Db 1856 TGCACCTTAGAGCCAGTCCGCTGCCAGCGCCCTCCAGGTCCCATCTCGAGGCATCC 1915

Qy 581 GlyArgThrValGlySerGlyLysValTyrProThrValHisThrSerProProGlu 600
Db 1916 GGCAGGACTGTGGCGAGCGGAAGGTGTATCCACCGTGCACACCGCTTCCACCGGAG 1975

Qy 601 ThrLeuLysGluLysAlaLeuValGluValAlaAlaSerSerGlyProProThrLeuThr 620
Db 1976 ACCTGAGAGGAGGACACTAGTAGAGTGTGCTGCCAGTCTGGGCCCCCCAACCTCCACC 2035

Qy 621 SerLeuAsnIleProProGlyProTyrSerSerMetHisLysLeuLeuGluThrGlnSer 640
Db 2036 AGCCTCAACTCCACCCGGGCGCTACAGCTCCATGCACAAAGCTGTGTGGAGACACAGAT 2095

Qy 641 ThrGlyAlaCysGlnSerSerCysLeuIleSerSerProCysLeuLysAlaAspSerGly 660
Db 2096 ACAGGTGCTGCCAAAGCTTGTCAAGATCTTCCAGCCCTTGTGTGAAGCAGCAGTGGGA 2155

Qy 661 AlaCysGlyProAspSerCysProTyrCysAlaArgAlaGlyAlaGlyGluValGluLeu 680
Db 2156 GCCTGTGTCAGACAGCTGCCCTACTGTGTCCCGGGCCGGGCGAGGGAGGTGGAGCTC 2215

Qy 681 AlaAspArgGluMetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAla 700
Db 2216 GCGCAGCGTGAATGCTGACTCAGACGCGGAGCAGTGTATGAGTTTACACAGATGCTC 2275

Qy 701 GlnHisSerAspLeuArgAspProHisSerArgGlnArgSerLeuGlyProAspAla 720

Db 2276 CAGCACAGCGACCTCCGGGACCCACACAGCGCGGCAACGAGGCTGGGCCCCAGATGCA 2335
Qy 721 GluProSerSerValLeuAlaPheTrpArgLeuIleCysAspThrPheArgIleVal 740
Db 2336 GAGCCACAGCTGTGTGCTGGCCCTCTCGAGGCTAATCTGTGACACCTCCGAAAGATTGTG 2395
Qy 741 AspSerIleValPheGlyArgGlyIleMetIleAlaIleValAsnThrLeuSerMet 760
Db 2396 GACAGCAAGTACTTTGGCGGGGAATCATGATCGCCATCTTGGTCAACACACTCAGCATG 2455
Qy 761 GlyIleGluIleHisGluGlnProGluLeuThrAsnAlaLeuGluIleSerAsnIle 780
Db 2456 GGCATCGAATACACAGCAGCGCCGAGGAGCTTACCAACGCCCTAGAAATCAGCAACATC 2515
Qy 781 ValPheThrSerLeuPheAlaLeuGluMetLeuIleValValValValValValValVal 800
Db 2516 GTCTTACAGCCCTCTTTGGCCCTGAGATGCTGTGTAAGCTGCTGTGTATGCTCCCTTT 2575
Qy 801 GlyIleIleValAsnProTyrAsnIlePheAspGlyValIleValValIleValIleVal 820
Db 2576 GGCTACATCAAGAATCCCTACAAACATCTTCGATGTGTGTCATGTGTGTCATCAGCGTGTG 2635
Qy 821 GluIleValGlyGlnGlnGlyGlyLeuSerValLeuArgThrPheArgLeuMetArg 840
Db 2636 GAGATCGTGGCGCAGCAGCGGGCGGCTGTGCGTGTGCGGACCTTCGCGCTGATGCGT 2695
Qy 841 ValLeuIleValValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetIle 860
Db 2696 GTGCTGAAGCTGTGTGCTGCTGCGCGCTGCGAGCGAGCTGTGTGTGCTCATGAAG 2755
Qy 861 ThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePheIlePheSer 880
Db 2756 ACCATGGACAACGTGGCCACCTTCGATGCTGTGCTTATGCTTTCATCTTCAGC 2815
Qy 881 IleLeuGlyMetHisLeuPheGlyCysIlePheAlaSerGluArgAspGlyAspThrLeu 900
Db 2816 ATCTTGGGATGCACTCTCTCGGCTGCAAGTTTGCCTCTGAGCGGATGGGAGCACCTG 2875
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DEFINITION Homo sapiens voltage-dependent calcium channel alpha 1G subunit a
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ACCESSION AF126966
VERSION   AF126966.1 GI:4761540
KEYWORDS .
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 7274)
AUTHORS  Montell,A., Chemin,J., Bourinet,E., Mennessier,G., Lory,P. and
          Nargeot,J.
TITLE    Molecular and functional properties of the human alpha(1G) subunit
          that forms T-type calcium channels
JOURNAL  J. Biol. Chem. 275 (9), 6090-6100 (2000)
MEDLINE  20158909
PUBMED   10692398
REFERENCE 2 (bases 1 to 7274)
AUTHORS  Montell,A., Mennessier,G., Bourinet,E., Lory,P. and Nargeot,J.
TITLE    Direct Submission
JOURNAL  Submitted (09-FEB-1999) Human Genetics Institute (I.G.H.) U.P.R.
          1142, C.N.R.S., 141 rue de la Cardonille, Montpellier 34396, France
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ORIGIN

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521 IleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProSerThrPro 540

1736 ATCCAGCAGCAGGATGCCAATGGTCCCGCGGCTCATGTGCACACCCACCTCGACGCT 1795
541 AlaLeuSerClyAlaProProGlyGlyAlaGluSerValHisSerPheTyrHisAlaAsp 560
542 AlaLeuSerClyAlaProProGlyGlyAlaGluSerValHisSerPheTyrHisAlaAsp 560
1796 GCCTCTTCCGGGCCCCCTTGTGGCGAGAGTCTGTGCACAGCTTCTACCATGCCGAC 1855
561 CysHisLeuGluProValArgCysGlnAlaProProArgSerProSerGluAlaSer 580
562 CysHisLeuGluProValArgCysGlnAlaProProArgSerProSerGluAlaSer 580
1856 TGCCACTTAGAGCCAGTCCGCTGCCAGGCGCCCCCTCCAGGTCCTCCATCTGAGGCATCC 1915
581 GlyArgThrValGlySerGlyLysValTyrProThrValHisThrSerProProGlu 600
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1916 GGCAGGACTGTGGCGCAGCGGAAAGTGTATCCACCGTGCACACCGCCCTCCACCGGAG 1975
601 ThrLeuLysGlyLysAlaLeuValGluValAlaAlaSerSerGlyProProThrLeuThr 620
602 ThrLeuLysGlyLysAlaLeuValGluValAlaAlaSerSerGlyProProThrLeuThr 620
1976 ACCTTGAAGAGAGGACCTAGTAGAGTGGTCCAGCTCTGGGCCCCCAACCTCACC 2035
621 SerLeuAsnIleProProGlyProTyrSerSerMetHisLysLeuLeuGluThrGlnSer 640
622 SerLeuAsnIleProProGlyProTyrSerSerMetHisLysLeuLeuGluThrGlnSer 640
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641 ThrGlyAlaCysGlnSerSerCysLysIleSerSerProCysLysLysAlaAspSerGly 660
642 ThrGlyAlaCysGlnSerSerCysLysIleSerSerProCysLysLysAlaAspSerGly 660
2096 ACAGGTGCTTCCCAAGCTCTTGCAGAGATCTCCAGGCTTGTGTAAGCAGACAGTGA 2155
661 AlaCysGlyProAspSerCysProTyrCysAlaArgAlaGlyAlaGlyGluValGluLeu 680
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2156 GCCTGTGGTCCAGACAGCTGCCCTACTGTGCCCGGCGGCGAGGAGGTGGAGCTC 2215
681 AlaAspArgGluMetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAla 700
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2216 GCCGACCGTGAATGCTGACTCAGACAGCGAGGAGTATGAGTTTACACAGGATGCC 2275
701 GlnHisSerAspLeuArgAspProHisSerArgArgGlnArgSerLeuGlyProAspAla 720
702 GlnHisSerAspLeuArgAspProHisSerArgArgGlnArgSerLeuGlyProAspAla 720
2276 CAGCAGACGACCTCCGGGACCCCAACAGCGCGGCAACGAGAGCTTGGGCGCAGATGCA 2335
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RESULT 11

AF190860 7349 bp mRNA linear PRI 23-FEB-2000
LOCUS Homo sapiens low voltage-activated T-type calcium channel alpha 1G
DEFINITION splice variant Cavt.1a (CACNA1G) mRNA, complete cds.
ACCESSION AF190860
VERSION AF190860.1 GI:7021332
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 7349)
AUTHORS Cribbs,L.L., Gomora,J.C., Daud,A.N., Lee,J.H. and Perez-Reyes,E.

|||||
3268 ATCCACGGCGCCACACCCATGTCGTGCCCAAGACACAGCCGGCTCGGGCAG 3327
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Db CGCTGGGCGCTCGCTCGCGCGCACACAGCAGCAGCGGTCCGAGAGCCTGGGGCGGCC 3387
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DEFINITION isoform bc (CACNA1G) mRNA, complete cds.
ACCESSION AF227747
VERSION AF227747.1 GI:7159266
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 6786)
AUTHORS Montell,A., Chemin,J., Bourinet,E., Mennessier,G., Lory,P. and Nargeot,J.
TITLE Molecular and functional properties of the human alpha (1G) subunit that forms T-type calcium channels
JOURNAL J. Biol. Chem. 275 (9), 6090-6100 (2000)
MEDLINE 20158909
FUBMED 10692398
REFERENCE 2 (bases 1 to 6786)
AUTHORS Montell,A., Mennessier,G., Bourinet,E., Lory,P. and Nargeot,J.
TITLE Direct Submission
JOURNAL Submitted (21-JAN-2000) C.N.R.S., Human Genetics Institute (I.G.H.)
U.P.R. 1142, 141 rue de la Cardonille, Montpellier 34396, France
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ORIGIN

Alignment Scores:

Pred. No.: 0 Length: 6786
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 Percent Similarity: 98.16% Conservative: 1
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 DB: 9 Gaps: 2

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Qy 1081 HisGluMetLysSerProProSerAlaArgSerSerProHisSerProTyrSerAlaAla 1100
Db 3172 CACGAGATGAAGTCAACGCCCGCCAGCGCTCTCCGACAGCCCTTGAGCGCTGCA 3231
Qy 1101 SerSerTyrThrSerArgArgSerSerArgAsnSerLeuGlyArgAlaProSerLeuLys 1120
Db 3232 AGCAGCTGGACAGCAGCGCTCCAGCGGAAACAGCCCTCGGCGCTGCACCCAGCTGAAG 3291
Qy 1121 ArgArgSerProSerGlyGluArgArgSerLeuLeuSerGlyGlyGlnGlnSerGln 1140
Db 3292 CGGAGAAGCCCAAGTGGAGAGCGCGCTCTGTGTGGGAGAGGAGGAGAGAGCAG 3351
Qy 1141 AspGluGluGluSerSerGluGluArgAlaSerProAlaGlySerAspHisArgHis 1160
Db 3352 GATGAAGAGGAGAGCTCAGAAAGAGGAGCGGCGCCAGCCCTGCGGCGAGTGCATCGCCAC 3411
Qy 1161 ArgGlySerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeuGlnVal 1180
Db 3412 AGGGGTCTCTGGAGCGGAGGCGCAAGATTCTCTTTCCTGCTGCCAGACACACTCGAGGTG 3471
Qy 1181 ProGlyLeuHisArgThrAlaSerGlyArgGlySerAlaSerGluHisGlnAspCysAsn 1200
Db 3472 CCAGGCTGTGATCCACTGCACTGCGGCGGAGGGTCTCTTCTGAGCACACGAGTGCAT 3531
Qy 1201 GlyLysSerAlaSerGlyArgLeuAlaArgAlaLeuArgProAspAspProProLeuAsp 1220
Db 3532 GGCAAGTCGGCTTCAGGGCGCTTGGCCCGGCGCTGCGGCTGTGATGATGATGATGATGAT 3591

5752	CTGACTGTGCGGAAGTCTGGGGTTCAGCCGACGCACTCTCTGCCCCAATGACGCTACATG	5811
1943	CysArgHisGlySerThrAlaGluGlyProLeuGlyHisArgGlyTyrGlyLeuProLys	1962
5812	TGTTCGGCATGGGAGCACTGCCGAGGGGCCCTTCGGACACAGGGGCTGGGGCTCCCCAAA	5871
1963	AlaGlnSerGlySerValLeuSerValHisSerGlnProAlaAspThrSerTyrIleLeu	1982
5872	GCTCAGTCAGGCTCCGCTTGTTCGTTCATCCCGACGACAGATACCACTACATCCTG	5931
1983	GlnLeuProLysAspAlaProHisLeuGlnProHisSerAlaProThrTyrGlyThr	2002
5932	CAGCTTCCCAAGATGACCTCATCTGCTCCAGCCCAACAGCCGCCCACTGGGCGACC	5991
2003	IleProLysLeuProProGlyArgSerProLeuAlaGlnArgProLeuArgGln	2022
5992	ATCCCCAACTGCCCCACCAGGAGGCTCCCTTTGGCTCAGAGGCACTCAGCGCCACG	6051
2023	AlaAlaIleArgThrAspSerLeuAspValGlnGlyLeuGlySerArgGluAspLeuLeu	2042
6052	GCAGCAATAAGGACTGACTCTTGGACGTTTCAGGGTCTGGGCAAGCCGGGAAGACCTT	6111
2043	AlaGluValSerGlyProSerProProLeuAlaArgAlaTyrSerPheTyrGlyGlnSer	2062
6112	GCAGAGTGTAGTGGGCCCTCCCGCCCTTCGCGCGGCTTACTCTTCTGGGCGCCAGTCA	6171
2063	SerThrGlnAlaGlnGlnHisSerArgSerHisSerLysIleSerLysHisMetThrPro	2082
6172	AGTACCCAGGCACAGCAGCACTCCCGCAGCCACAGCAAGATCTTCCAAGCACATGACCCCG	6231
2083	ProAlaProCysProGlyProGluProAsnTyrGlyLysGlyProGluThrArgSer	2102
6232	CCAGCCCTTGCCTCAGGCCCCAGAACCCAACTGGGGCAAGGGCCCTCCAGAGACCAGAGC	6291
2103	SerLeuGluLeuAspThrGluLeuSerTyrIleSerGlyAspIleLeuProProGlyGly	2122
6292	AGCTTAGATTGGACACGGAGCTGAGCTGGATTTCAGGAGACCTCTCTGCCCTCGCGGC	6351
2123	GlnGluGluProProSerProArgAspLeuLysCysTyrSerValGluAlaGlnSer	2142
6352	CAGAGAGAGCCCCCATCCCCACGGGACTGAGAGAGTGTACAGCGTGGAGGCCAGAGC	6411
2143	CysGlnArgArgProThrSerTyrLeuAspGluGlnArgHisSerIleAlaValSer	2162
6412	TGCCAGCGCCGCCCACTGCTGGCTGGATGAGCAGAGGAGACACTCTATCGCCGTCAGC	6471
2163	CysLeuAspSerGlySerGlnProHisIleGlyThrAspProSerAsnLeuGlyGln	2182
6472	TGCCTTGACAGCGGCTCCCAACCCCACTGGGCAACAGCCCTCTAACCTTGGGGCCAG	6531
2183	ProLeuGlyGlyProGlySerArgProLysLysLysLeuSerProProSerIleThrIle	2202
6532	CCTCTTGGGGGCTCGGAGCCGCCCAAGAAAAAAGCTCAGCCCGCTAGTATCACCATA	6591
2203	AspProProGluSerGlnGlyProArgThrProProSerProGlyIleCysLeuArgArg	2222
6592	GACCCCCCGAGAGCAAGTCTTCGACCCCGCCAGCCCTGTGTATCTGCCTCCGAGG	6651
2223	ArgAlaProSerSerAspSerLysAspProLeuAlaSerGlyProProAspSerMetAla	2242
6652	AGGCTCCGTCAGGGACTCCAAGATCCCTTGGGCTCTGGCCCCCTTGACAGCATGGCT	6711
2243	AlaSerProSerProLysLysAspValLeuSerLeuSerGlyLeuSerSerAspProAla	2262
6712	GCCTCGCCCTCCCCAAAGAAAGATGTGTGAGTCTCTCCGGTTTATCTCTGACCCAGCA	6771
2263	AspLeuAspPro	2266
6772	GACCTGGACCCC	6783
RESULT 13		
AF227746		
LOCUS	AF227746	PRI 06-MAR-2000
	6897 bp	mRNA linear

DEFINITION	ACCESSION VERSION KEYWORDS SOURCE ORGANISM	REFERENCE AUTHORS	TITLE	JOURNAL MEDLINE PUBMED REFERENCE AUTHORS TITLE JOURNAL	FEATURES SOURCE
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AF227746
AF227746.1 GI:7159264

AF227746.1 GI:7159264

AF227746.1 GI:7159264

- Homo sapiens (human)

PKDAPHLIOPHSAPTWTGTPKLPPLPPRSPLAORPLRQAAIRTDLSLDVQGLSREDLL
 AEVSGPSPLARAFWQCSQSTQAOHRSRSHKSKXMTWPPAPCPGPRPNWKGPPET
 RSSLELDTELNSIGDLLPPGQEEFPPDLKCYISVEAQCORRPPSWLDEQRHHS
 IAVSLDSGSPHLGTDSNLGGPLGPGFSRPPKRLSPSPSITIDPPESQGPRTPPSP
 GICLRRAPSSDSKDLASGPPDSMAASPSPKDVLISLGLSSDPADLDP"

ORIGIN

Alignment Scores:

Pred. No.: 0 Length: 6897
 Score: 11707.00 Matches: 2241
 Percent Similarity: 96.60% Conservativity: 1
 Best Local Similarity: 96.55% Mismatches: 1
 Query Match: 98.35% Indels: 78
 DB: 9 Gaps: 3

US-09-611-257A-37 (1-2266) x AF227746 (1-6897)

Qy 1 MetAspGluGluGluAspGlyAlaGluGluSerGlyGlnProArgSerPheMet 20
 Db 1 ATGGACGAGGAGGAGTGGAGCGGCGCCGAGGAGTGGACACCCCGGAGCTTCATG 60
 Qy 21 ArgLeuAsnAspLeuSerGlyAlaGlyArgProGlyProGlySerAlaGlyAsp 40
 Db 61 CGGCTCAACGACCTGTCGGGGCGCGGGCGCGGGCGGGGTCAGCAGAAAAGGAC 120
 Qy 41 ProGlySerAlaAspSerGluAlaGluGlyLeuProTyrProAlaLeuAlaProVal 60
 Db 121 CCGGGCAGCGCGGACTCCGAGCGGAGGAGGCTGCCGTACCGGGCGCTGGCCCGGTT 180
 Qy 61 PhePheTyrLeuSerGlnAspSerArgProArgSerTrpCysLeuArgThrValCysAsn 80
 Db 181 TTCTTCTACTTGACGACGACAGCGCGCGGAGCTGGTGTCTCCGACACGGTCTGTAAAC 240
 Qy 81 ProTrpPheGluArgIleSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMet 100
 Db 241 CCCTGGTTGAGCGCATCAGCATGTTGGTTCATCTTCTCAACTGCGTGACCTGGGCATG 300
 Qy 101 PheArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPhe 120
 Db 301 TTCGGCGCATCGGAGGACATCGCTGTGACTCCAGCGCGCTCCGAGATCTCGAGCGCTTT 360
 Qy 121 AspAspPheIlePheAlaPhePheAlaValGluMetValValIysMetValAlaLeuGly 140
 Db 361 GATCACTTCATCTTGGCTCTTTGCCGTGAGATGGTGGTGAAGATGGTGGCTTGGGC 420
 Qy 141 IlePheGlyIysCysTyrLeuGlyAspThrTrpAsnArgLeuAspPheIleVal 160
 Db 421 ATCTTTGGGAAAAAGTGTACCTGGGAGACACTTGGAAACCGGCTTGACTTTTTCATGTC 480
 Qy 161 IleAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArg 180
 Db 481 ATCGACGGATGCTGGAGTACTCGCTGGACCTGCAGAACGTCAGCTTCTCAGCTGTGAGG 540
 Qy 181 ThrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeu 200
 Db 541 ACAGTCCGTGTCTGGACCGCTCAGGCGCAATTAAACGGGGTCCGAGCATCGCATCTTT 600
 Qy 201 ValThrLeuLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePhe 220
 Db 601 GTCAGTTGCTGTGATACGCTGCCATGCTGGGCAACGTCCTGCTGCTGCTTCTTTC 660
 Qy 221 ValPhePheIlePheGlyIleValGlyValGlnIleuTrpAlaGlyLeuLeuArgAsnArg 240
 Db 661 GTCTTCTTCACTTTCGGCATCGTCGGGCTCAGCTGTGGGCGAGGCTGCTTCGGAACCGA 720
 Qy 241 CysPheLeuProGluAsnPheSerLeuProLeuSerValAspLeuGluArgTyrTrpGln 260
 Db 721 TGTCTTCTTACCTGAGAAATTTTTCAGCTTCCCTGAGCGTGGACCTGGAGCGCTATTACAG 780
 Qy 261 ThrGluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArg 280
 Db 781 ACAGAGAACGAGGATGAGAGGCCCTTTCATCTGCTCCAGGCCACCGGAGACGGCATGGCG 840

Qy 281 SerCysArgSerValProThrLeuArgGlyAspGlyGlyGlyProProCysGlyLeu 300
 Db 841 TCTGCGAAGACGCGCCACGCTCGCGGGGACCGGGGGCGGTGGCCCACTTGGCGGTCTG 900
 Qy 301 AspTyrGluAlaTyrAsnSerSerAsnThrThrCysValAsnTrpAsnGlnTyrTyr 320
 Db 901 GACTATGAGGCTACACAGCTCCAGCNACACCACTGTGTCTCACTGGAACCACTACTAC 960
 Qy 321 ThrAsnCysSerAlaGlyGluHisAsnProPheIysGlyAlaIleAsnPheAspAsnIle 340
 Db 961 ACCAACTGCTCAGCGGGGAGCACAACCCCTTCAAGGGCGGCATCAACTTTGACAACATT 1020
 Qy 341 GlyTyrAlaTrpIleAlaIlePheGlnValIleThrLeuGluGlyTrpValAspIleMet 360
 Db 1021 GGCTATGCTGATCGCCATCTTCAGGTCAACGCTGAGGGGTGGGTGGACATCATG 1080
 Qy 361 TyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIle 380
 Db 1081 TACTTTGTGATGGATGCTCATCTCTTACAAATTTCTACTTCTCATCTCTCTCATCATC 1140
 Qy 381 ValGlySerPhePheMetIleAsnLeuCysLeuValIleAlaThrGlnPheSerGlu 400
 Db 1141 GTGGGCTCTTCTTTCATGATCAACCTGTGCTGGTGGTGAATTGCCACGACGTCTCAGAG 1200
 Qy 401 ThrIysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAla 420
 Db 1201 ACCAAGCAGCGGGAAGCCAGCTGATCGGAGCAGCGTGTGCGGTTCTCTGTCACACGCC 1260
 Qy 421 SerThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLeuLysTyrLeu 440
 Db 1261 AGCACTTGGTAGTCTCTGAGCCCGGAGCTGCTATGAGGAGCTGCTCAAGTACCTG 1320
 Qy 441 ValTyrIleLeuArgIysAlaAlaArgArgLeuAlaGlnValSerArgAlaAlaGlyVal 460
 Db 1321 GTGTACATCTTCTGAAGGAGCAGCCCGCAGGCTGGCTCAGGTCTCTCGGGCAGCAGGTGTG 1380
 Qy 461 ArgValGlyLeuLeuSerSerProAlaProLeuGlyGlyGlnGluThrGlnProSerSer 480
 Db 1381 CGGGTTGGGTGCTCAGCAGCCAGCAGCCCTCGGGGGCCAGGAGATCCAGCCAGCAGC 1440
 Qy 481 SerCysSerArgSerHisArgArgLeuSerValHisLeuValHisHisHisHis 500
 Db 1441 AGCTGCTCTGGTCCCAACCGCGCTATCGGTCCACCACTGGTGGACACCAACCAAC 1500
 Qy 501 HisHisHisTyrHisLeuGlyAsnGlyThrLeuArgAlaProArgAlaSerProGlu 520
 Db 1501 CATCACCACTACCACTGGGCAATGGGAGCTCAGGGCCCCCGGGCCAGCCCGGAG 1560
 Qy 521 IleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProSerThrPro 540
 Db 1561 ATCCAGGACAGGGATGCCAATGGGTCCCGCGGCTCATGTGCCACCACTCCGACGCT 1620
 Qy 541 AlaLeuSerGlyAlaProGlyGlyAlaGluSerValHisSerPheTyrHisAlaAsp 560
 Db 1621 GCCCTCTCCGGGGCCCCCTTGTGGGCGAGAGTCTGTGCACAGCTTCTACCATGCCGAC 1680
 Qy 561 CysHisLeuGluProValArgCysGlnAlaProProProArgSerProSerGluAlaSer 580
 Db 1681 TGCCACTTAGAGCCAGTCCGCTGCCAGCGCCCCCTCCAGGTCCCCCATCTGAGGCGATCC 1740
 Qy 581 GlyArgThrValGlySerGlyIysValTyrProThrValHisThrSerProProGlu 600
 Db 1741 GGCAGGACTGTGGGCGAGGAGGTGTATCCCACTCCGTCACACAGCCCTCCACCGGAG 1800
 Qy 601 ThrLeuLysGluLysAlaLeuValGluValAlaAlaSerSerGlyProProThrLeuThr 620
 Db 1801 AGCTTGAAGAGAGGACCTAGTAGAGTGGTCCAGCTCTGGGGCCCCAACCCCTCACC 1860
 Qy 621 SerLeuAsnIleProProGlyProTyrSerSerMetHisIysLeuLeuGluThrGlnSer 640
 Db 1861 AGCTTCAACATCCACCCCGGGCCCTACAGCTCCATGCACAAAGCTGTGGAGACACAGGT 1920
 Qy 641 ThrGlyAlaCysGlnSerSerCysLysIleSerSerProCysLeuLysAlaAspSerGly 660

Db 1921 ACAGGTGCTGCCAAAGCTCTTGAAGATCTCCAGCCCTTGGTTGAAAGCAGACAGTGA 1980
Qy 661 AlaCysGlyProAspSerCysProTyrCysAlaArgAlaGlyGluValGluLeu 680
Db 1981 GCCTGTGGTCCAGACAGCTGCCCTACTGTGCCGGGCCGGGAGGGAGGTGGAGCTC 2040
Qy 681 AlaAspArgGluMetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAla 700
Db 2041 GCCGACCGTGAATGCTGACTCAGACGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2100
Qy 701 GlnHisSerAspLeuArgAspProHisSerArgArgGlnArgSerLeuGlyProAspAla 720
Db 2101 CAGCACAGCAGCTCCGGGACCCCAAGCGCGGCAACGAGGAGGAGGAGGAGGAGGAGGAGG 2160
Qy 721 GluProSerSerValLeuAlaPheTyrArgLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 740
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Qy 741 AspSerLysTyrPheGlyArgGlyLeuMetLeuAlaLeuValLeuValLeuValLeuVal 760
Db 2221 GACAGCAAGTACTTTGGCGGGGAAATCATGATGCCATCTCTGGTCAACACACTCAGCATG 2280
Qy 761 GlyLeuGlyTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGluLeuLeuSerAsnIle 780
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Qy 781 ValPheThrSerLeuPheAlaLeuGluMetLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 800
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Db 2521 GTGTGAAGCTGT 2580
Qy 861 ThrMetAspAenValAlaThrPheCysMetLeuLeuMetLeuPheIlePheIlePheSer 880
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Qy 881 IleLeuGlyMetHisLeuPheGlyCysLysPheAlaSerGluArgAspGlyAspThrIleu 900
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Qy 921 ThrGlnGluAspTrpAsnLysValLeuTyrAsnGlyMetAlaSerThrSerSerTrpAla 940
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Db 4012 ATTCTGTGTCTGT 4071

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VERSION	AF227748.1	GI:7159268		
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AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
TITLE	Montell, A., Chemin, J., Bourinet, E., Mennessier, G., Lory, P. and Nargeot, J.			
JOURNAL	Molecular and functional properties of the human alpha(1G) subunit that forms T-type calcium channels			
MEDLINE	J. Biol. Chem. 275 (9), 6090-6100 (2000)			
PUBMED	20158909			
REFERENCE	2 (bases 1 to 6921)			
AUTHORS	Montell, A., Mennessier, G., Bourinet, E., Lory, P. and Nargeot, J.			
TITLE	Direct Submission			
JOURNAL	Submitted (21-JAN-2000) C.N.R.S., Human Genetics Institute (I.G.H.)			
FEATURES	U.P.R. 1142, 141 rue de la Cardonille, Montpellier 34396, France			

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 REFERENCE 1 (bases 1 to 7030)
 AUTHORS Mittman,S., Guo,J. and Agnew,W.S.
 TITLE Structure and alternative splicing of the gene encoding alpha1G, a human brain T calcium channel alpha1 subunit
 JOURNAL Neurosci. Lett. 274 (3), 143-146 (1999)
 MEDLINE 20014446
 PUBMED 10548410
 REFERENCE 2 (bases 1 to 7030)
 AUTHORS Mittman,S., Guo,J. and Agnew,W.S.
 TITLE Direct Submission
 JOURNAL Submitted (15-MAR-1999) Anesthesiology/Critical Care Medicine, The Johns Hopkins University School of Medicine, 600 N. Wolfe Street, Meyer 297, Baltimore, MD 21287-7294, USA

FEATURES

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ORIGIN

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Qy 901 ProAspArgIysAsnPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIleLeu 920
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Db 2992 GCCTTGTGTCTCTGGGAGACACCCGAGCTGGAGAGCCTGCTGCCCTCTCATC 3051
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Db 4432 GTGGACGAGCAGCCCATCATGAACCAACACCCCTGGATGCTGTGTATCTTCATCTCGTTC 4491
Qy 1521 LeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValValValGluAsnPhe 1540
Db 4492 CTGCTCATTTGGGCTTCTTGTCTGAACATGTTTGTGGGTGGTGGTGGAGAACTTC 4551
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Qy 1954 GlyHisArgGlyTrpGlyLeuProLysAlaGlnSerGlySerValLeuSerValHisSer 1973
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Qy 1974 GlnProAlaAspThrSerTyrIleLeuGlnLeuProLysAspAlaProHisLeuLeuGln 1993
Db 5872 CAGCAGCAGATACAGCTACATCTCGAGGTTCCCAAGATGACCTCATCTGTCTCAG 5931
Qy 1994 ProHisSerAlaProThrTrpGlyThrIleProLysLeuProProGlyArgSerPro 2013
Db 5932 CCCACACGCGCCCAACCTGGGGCACCATCCCCAACTGCCCCACACGAGCGCTCCCT 5991
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Search completed: April 16, 2005, 09:17:42
Job time : 21178 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 15, 2005, 23:55:55 ; Search time 2319 Seconds
(without alignments)
5784.448 Million cell updates/sec

Title: US-09-611-257A-37

Perfect score: 11904
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Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Deiop 6.0 , Delext 7.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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Database :

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13: Geneseqn2004bs: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	11877.5	99.8	7741	4	AAD04756
2	11874	99.7	6892	5	Aaf31684 Human T-t
3	11815.5	99.3	7648	13	Adg89063 Human alp
4	11815.5	99.3	7648	13	Adg89063 Human uro
5	11756.5	98.8	6729	2	AdS16298 Human vol
					Aax83484 Human T-t

6	11741	98.6	6750	2	AAX83481	Aax83481 Human T-t
7	11735.5	98.6	6783	2	AAX83482	Aax83482 Human T-t
8	11727	98.5	6804	2	AAX83483	Aax83483 Human T-t
9	11627.5	97.7	8002	4	AAH98402	Aah98402 Human EST
10	11111	93.3	7286	3	AAZ52309	Aaz52309 Rat pancr
11	10962.5	92.1	6741	2	AAX83488	Aax83488 Rat T-typ
12	10945	91.9	6762	2	AAX83485	Aax83485 Rat T-typ
13	10945	91.9	6942	13	ADS16295	AdS16295 Rat volta
14	10939.5	91.9	6795	2	AAX83486	Aax83486 Rat T-typ
15	10925	91.8	6816	2	AAX83487	Aax83487 Rat T-typ
16	10890.5	91.5	7540	5	AAF31677	Aaf31677 Rat alpha
17	6315.5	53.1	3993	4	AAS01624	Aas01624 Human T-t
18	6223	52.3	8447	5	AAF31678	Aaf31678 Rat alpha
19	6216.5	52.2	7898	2	AAX59081	Aax59081 Human act
20	6215.5	52.2	7898	8	ABZ58365	Abz58365 Human T-t
21	6214.5	52.2	7898	2	AAX59080	Aax59080 Human act
22	5902.5	49.6	6114	2	AAX83490	Aax83490 Human T-t
23	5892.5	49.5	6132	2	AAX83489	Aax83489 Human T-t
24	5713	48.0	6941	2	AAX59082	Aax59082 Human act
25	5496.5	46.2	6990	13	ADS16296	AdS16296 Human vol
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28	5492.5	46.1	6816	12	ADH69264	Adh69264 Human TCC
29	5484	46.1	6855	6	AAS16827	Aas16827 Human T-t
30	5484	46.1	6855	8	ABX93561	Abx93561 Human cDN
31	5484	46.1	6855	12	ADH69266	Adh69266 Human TCC
32	5418.5	45.5	6503	12	ADH69275	Adh69275 Rat TCVC
33	5366	45.1	5505	2	AAX83492	Aax83492 Rat T-typ
34	5361.5	45.0	5469	2	AAX83491	Aax83491 Human T-t
35	5209	43.8	5735	5	AAF31679	Aaf31679 Rat brain
36	4013.5	33.7	7969	4	ABL07263	AbL07263 Drosophil
37	3959.5	33.3	5562	2	AAS7542	Aas7542 Human cal
38	3959.5	33.3	5562	5	AAF31674	Aaf31674 Human alp
39	3867	32.5	6073	13	ADS16299	AdS16299 C. elegan
40	3451.5	29.1	6933	5	AAS75141	Aas75141 DNA encod
41	3427	28.8	2212	5	AAF31681	Aaf31681 Human alp
42	2140	18.0	3464	4	AAK94358	Aak94358 Human ful
43	2140	18.0	3464	12	ADL31040	AdL31040 Full leng
44	1971.5	16.6	1669	2	AAX59083	Aax59083 Human act
45	1788.5	15.0	7362	2	AAQ37817	Aaq37817 Sequence

ALIGNMENTS

RESULT 1

AAD04756

ID AAD04756 standard; cDNA; 7741 BP.

AC AAD04756;

XX 17-JUL-2001 (first entry)

DT Human T-type low voltage activated calcium channel alpha1G-c cDNA.

XX Human T-type low voltage activated calcium channel alpha1G-c; stress;

KW epilepsy; schizophrenia; depression; sleep disorder; Cushing's disease;

KW endocrine disorder; respiratory disorder; peripheral muscle disorder;

KW muscle excitability; fertilization; contraception; hypertension;

KW neuronal firing regulation; cardiovascular disorder; Gene therapy;

KW forensic analysis; epidemiological study; neuroleptic; ss.

XX Homo sapiens.

OS Key

PH 5'UTR

FT Location/Qualifiers

FT 1..522

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FT 523..7344

FT /*tag= b

FT /product= "Human T-type low voltage activated calcium

FT channel alpha1G-c protein"

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FT /transl_except= (pos:5560..5562, aa:Pro)

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FT /note= "The CDS is specifically claimed in claim 2 as SEQ
FT ID NO:3"
FT 3'UTR 7345..7741
FT /*tag= C
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FN WO200130844-A1.
XX
XX 03-MAY-2001.
XX
XX 06-OCT-2000; 2000WO-US027761.
XX
XX 26-OCT-1999; 99US-00426998.
XX
XX (ORTH ) ORTHO-MCNEIL PHARM INC.
XX
XX Dubin AE, Galindo JE, Pyati J, Zhu JY, Erlander MG;
XX
XX WPI; 2001-300486/31.
XX
XX P-PSDB; RAE01019.
XX
XX New nucleic acid encoding human calcium channel protein, useful for
XX identifying specific modulators and potential pharmaceuticals for
XX treating e.g. epilepsy.
XX
XX Claim 2; Page 76-81; 115pp; English.
XX
XX The invention relates to isoform of human T-type low voltage activated
XX calcium channel (alpha1G-c) cDNA and protein. Cells transformed with
XX calcium channel DNA to express calcium alpha1G-c channel protein are used
XX to identify specific modulators (antagonists or agonists). These
XX modulators are useful as therapeutic agents and are used for treating
XX wide range of calcium alpha1G-c channel-mediated disorders, e.g. stress
XX epilepsy, schizophrenia, depression, sleep disorders, Cushing's disease,
XX endocrine disorders, respiratory disorder, peripheral muscle disorder,
XX muscle excitability, fertilisation, contraception, disorders involving
XX hypertension, neuronal firing regulation, potentiation of synaptic
XX signals and cardiovascular disorders (e.g. atherosclerosis, cardiac
XX hypertrophy, angina pectoris). Calcium alpha1G-c channel DNA is useful
XX for isolating and identifying related molecule mutations. It is also
XX optionally used as antisense sequences, in gene therapy. Calcium channel
XX alpha1G-c DNA, protein and antibodies are useful for forensic analysis,
XX diagnosis and epidemiological studies, by standard hybridisation or
XX immunological assays. The present sequence is T-type low voltage
XX activated calcium channel alpha1G-c cDNA. This sequence is isolated from
XX human thalamus cDNA library
XX
XX Sequence 7741 BP; 1469 A; 2496 C; 2287 G; 1489 T; 0 U; 0 Other;
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XX Alignment Scores:
XX Pred. No.: 0 Length: 7741.
XX Score: 11877.50 Matches: 2264
XX Percent Similarity: 99.65% Conservative: 1
XX Best Local Similarity: 99.60% Mismatches: 1
XX Query Match: 99.78% Indels: 7
XX DB: 4 Gaps: 1
XX
XX US-09-611-257A-37 (1-2266) x AAD04756 (1-7741)
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XX 523 ATGGACGAGGAGGAGGATGGAGCGGGCCGCGGAGGATCGGAGACGCCCGGAGCTTCATG 582
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XX 21 ArgLeuAsnAspLeuSerGlyAlaGlyGlyArgProGlyProGlySerAlaGluLysAsp 40
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XX 583 CGGCTCAACGACCTGTGGGGGCCCGGGCCGCGGGCCGGGGTTCAGCAGAAAGGAC 642
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XX 41 ProGlySerAlaAspSerGluAlaGluGlyLeuProTyrProAlaLeuAlaProValVal 60
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XX 643 CCGGGCAGCGCGGACTCCGAGCGGAGGGGTGCGGTACCGCGCTGGCCCGCGTGGT 702
XX
XX 61 PhePheTyrLeuSerGlnAspSerArgProArgSerTyrCysLeuArgThrValCysAsn 80
XX
XX
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Db 703 TTCTTCTACTGTAGCCAGGACAGCCGCCCGGAGCTGGTGTCTCCGACAGGTCTGTAAAC 762
Qy 81 ProTyrPheGluArgIleSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMet 100
Db 763 CCCTGGTTTTCAGCGCATCAGCATGTTGGTTCATCTTCTCACTGGGTGACCTTGGGCATG 822
Qy 101 PheArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPhe 120
Db 823 TTCGGCCATCGCAGGACATCGCTGTGACTCCGAGCGCTGCCGGATCTTCGAGGCCCTTT 882
Qy 121 AspAspPheIlePheAlaPhePheAlaValIleGluMetValValLysMetValAlaLeuGly 140
Db 883 GATGACTTTCATCTTTGCCCTTCTTTGCCGTGGAGATGGTGGTGAAGATGGTGGCCCTTGGGC 942
Qy 141 IlePheGlyLysLysCysTyrLeuGlyAspThrTyrAsnArgLeuAspPheIleVal 160
Db 943 ATCTTTGGGAAAAAGTGTACTCTGGGAGACACTTGGAAACCGGCTTGACTTTTTCATCGTC 1002
Qy 161 IleAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArg 180
Db 1003 ATCGCAGGGATGCTGGAGTACTCGCTGGACCTGCAGAACGTCAGCTTCTCAGCTGTGAGG 1062
Qy 181 ThrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeu 200
Db 1063 ACAGTCGTGTGTGCGACCGCTCAGGGCCATTAAACGGGTGCCACGATCGGCATCTT 1122
Qy 201 ValThrLeuLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePhe 220
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Qy 321 ThrAsnCysSerAlaGlyGluHisAsnProPheLysGlyAlaIleAsnPheAspAsnIle 340
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Qy 341 GlyTyrAlaTrpIleAlaIlePheGlnValIleThrLeuGluGlyTrpValAspIleMet 360
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Qy 361 TyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleIle 380
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Qy 381 ValGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGlu 400
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Db 1723 ACCAAGCAGCGGAAAGCCAGCTGATGCGGAGCAGCGTGTGGGTTCCTGTCCAAACGCC 1782
Qy 421 SerThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLeuLysTyrLeu 440
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441 ValTyrIleLeuArgLysAlaAlaArgLeuAlaGlnValSerArgAlaAlaGlyVal 460
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461 ArgValGlyLeuLeuSerSerProAlaProLeuGlyGlyGlnGluThrGlnProSerSer 480
1903 CGGGTGGGCTGCTCAGCAGCCAGCACCCTCGGGGGCCAGGAGACCAGCCAGCAGC 1962
481 SerCysSerArgSerHisArgArgLeuSerValHisHisHisHisHisHisHis 500
1963 AGCTGCTCTCCGCTCCACCGCGCTATCCGTCCACCACTCTGGTGGTGCACCAACCAC 2022
501 HisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHis 520
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521 IleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProProSerThrPro 540
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541 AlaLeuSerGlyAlaProProGlyGlyAlaGluSerValHisHisHisHisHisHis 560
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561 CysHisLeuGluProValArgCysGlnAlaProProProArgSerProSerGluAlaSer 580
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581 GlyArgThrValGlySerGlyLysValTyrProThrValHisThrSerProProProGlu 600
2263 GGCAGGACTGTGGGACGGGAGGTATCCCACTGGGCACACAGCCCTCCACCGGAG 2322
601 ThrLeuLysGluLysAlaLeuValGluValAlaAlaSerSerGlyProProThrLeuThr 620
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621 SerLeuAsnIleProProGlyProTyrSerSerMetHisLysLeuLeuGluThrGlnSer 640
2383 AGCCTCAACTCCACCGCGGCCCTTACAGCTTCCATGCACAAGCTGTGGAGACACAGAGT 2442
641 ThrGlyAlaCysGlnSerSerCysLysIleSerSerProCysLeuLysAlaAspSerGly 660
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681 AlaAspArgGluMetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAla 700
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701 GlnHisSerAspLeuArgAspProHisSerArgArgGlnArgSerLeuGlyProAspAla 720
2623 CAGCACAGCAGCTCCGGGACCCCCACAGCGGGGCAACGGAGCCTGGGGCCAGATGCA 2682
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741 AspSerLysTyrPheGlyArgGlyIleMetIleAlaLeuValAsnThrLeuSerMet 760
2743 GACAGCAAGTACTTTGGCGGGGAATCATGATCGCCATCTCTGGTCAACACACTCAGCATG 2802
761 GlyIleGluTyrHisGluGlnProGluLeuThrAsnAlaLeuGluIleSerAsnIle 780
2803 GGCATCGAATACCAAGCAGCAGCCGAGAGCTTACCAACCGCCCTAGAAATCAGCAACATC 2862
781 ValPheThrSerLeuPheAlaLeuGluMetLeuLysLeuLeuValTyrGlyProPhe 800
2863 GTCTTCACCACTCTTTGGCTGGAGATGCTGTGAGCTGTGTGTGTGTGTGTGTGTGT 2922

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2923 GGCATACATCAAGAATCCCTACAACATCTTCATGGTGTTCATGTGGTTCATCAGCGGTGG 2982
821 GluIleValGlyGlnGlnGlyGlyLeuSerValLeuArgThrPheArgLeuMetArg 840
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3043 GTGCTGAAGCTGTGTGGCTTCTCTCGCGCGCTGACGCGGACGTGGTGTGTCTCATGAAG 3102
861 ThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePheIlePheSer 880
3103 ACCATGACAAACGTGGCCACCTTCTGCATGCTGTCTATGCTCTTCATCTTTCATCTTACG 3162
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3163 ATCTTGGGATGATCTCTTCCGGTGCAGATTTGCCCTCTGAGCGGATGGGACACCTGTG 3222
901 ProAspArgLysAsnPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIleLeu 920
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3283 ACCCAGGAGGACTCGAAACAAAGTCTCTACAAATGGTATGGCTCCACGCTGTCTGGGCG 3342
941 AlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuVal 960
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961 AlaIleLeuValGluGlyPheGlnAlaGluIleSerLysArgGluAspAlaSerGly 980
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981 GlnLeuSerCysIleGlnLeuProValAspSerGlnGlyAspAlaAsnLysSerGlu 1000
3463 CAGTTAAGCTGTATTTAGCTGCTTCCAGTCCCGGGGGAGATGCCAAACAGTCCGAA 3522
1001 SerGluProAspPhePheSerProSerLeuAspGlyAspGlyAspArgLysLysCysLeu 1020
3523 TCAGAGCCGATTTCTTCTCACCCAGCTGTGATGGTGTGGGGCAGAGAAAGTGTCTT 3582
1021 AlaLeuValSerLeuGlyGluHisProGluLeuArgLysSerLeuLeuProProLeuIle 1040
3583 GCCTTGTGTCTCTGGGAGAGCACCCGAGCTGCGGAAGAGCCTGTCTCCGCTCTCATC 3642
1041 IleHisThrAlaAlaThrProMetSerLeuProLysSerThrSerThrGlyLeuGlyGlu 1060
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1061 AlaLeuGlyProAlaSerArgArgThrSerSerGlySerAlaGluProGlyAlaAla 1080
3703 GCGTGTGGGCTGTGCTCGGCCGACCCAGCAGCAGCGGCTCGGACAGCTTGGGGCGGCC 3762
1081 HisGluMetLysSerProProSerAlaArgSerSerProHisSerProTrpSerAlaAla 1100
3763 CACGAGATGAAGTCAACCGCCAGCGCCCGAGCTCTCCGCACAGCCCCCTGGAGCGCTGCA 3822
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3883 CGGAGAGCCCAATGGAGAGCGCGGTCTCTTGTTCGGGAGAGGCGCAGAGAGCCAG 3942
1141 AspGluGluGluSerSerGluGluArgAlaSerProAlaGlySerAspHisArgHis 1160
3943 GATCAAGAGGAGACTCAGAAAGAGAGCGGCCAGCCCTGCGGGCAGTGCACCATCGCCAC 4002
1161 ArgGlySerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeuGlnVal 1180

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6223 GCGGCCCCAGCGAGATCAGCCCTCCACCTTTTCCCTGGAGCACCACCGATGACGCCCCAC 6282
1914 ProThrGluLeuProGlyProAspLeuThrValArgLysSerGlyValSerArgThr 1933
6283 CCCAGGAGCTGCCAGACAGACTTACTGACTGTGGGAAGTCTGGGGTCAGCGGACG 6342
1934 HisSerLeuProAsnAspSerTyrMetCysArgHisGlySerThrAlaGluGlyProLeu 1953
6343 CACTCTCTGCCCAATGACAGCTACATGTGTGGCATGGAGCACTGGCGAGGGGCCCTG 6402
1954 GlyHisArgGlyTTrpGlyLeuProLysAlaGlnSerGlySerValLeuSerValHisSer 1973
6403 GGACACAGGGGCTGGGGCTCCCAAGCTCAGTCAGGCTCCGCTTGTTCGGTTCACCTCC 6462
1974 GlnProAlaAspThrSerTyrIleLeuGlnLeuProLysAspAlaProHisLeuGln 1993
6463 CAGCCAGCAGATACAGCTACATCTCGAGCTTCCCAAGATGACCTCATCTGCTCCAG 6522
1994 ProHisSerAlaProThrTTrpGlyThrIleProLysLeuProProGlyArgSerPro 2013
6523 CCCACAGCGGCCCAACCTGGGGCACCATCCCAAACTGCCCCACAGGAGCTCCCT 6582
2014 LeuAlaGlnArgProLeuArgArgGlnAlaAlaIleArgThrAspSerLeuAspValGln 2033
6583 TTGGCTCAGAGGCCACTCAGCGCCAGCGCAACAATAAGGACTGACTCCTTGGAGCTTCAG 6642
2034 GlyLeuGlySerArgGluAspLeuAlaGluValSerGlyProSerProProLeuAla 2053
6643 GGTCTGGGCACCGGGAAGACTCTGTGGCAGAGTGAGTGGGCCCTCCCGCCCTGGCC 6702
2054 ArgAlaTyrSerPheTTrpGlyGlnSerSerThrGlnAlaGlnGlnHisSerArgSerHis 2073
6703 CGGGCCTACTCTTCTGGGGCAGTCAAGTAGTACCAGGCACAGCAGCACTCCCGCAGCCAC 6762
2074 SerLysIleSerLysHisMetThrProProAlaProCysProGlyProGluProAsnTrp 2093
6763 AGCAAGATCTCCAAGCAGATACCCCGCCAGCCCTTGGCCAGGCGCCAGAACCCCACTGG 6822
2094 GlyLysGlyProProGluThrArgSerSerLeuGluLeuAspThrGluLeuSerTrpIle 2113
6823 GGCAGGGCCCTCCAGAGACCAAGCAGAGCTTAGAGTTGGACGAGCTGAGCTGGATT 6882
2114 SerGlyAspLeuLeuProProGlyGlyGlnGluProProSerProArgAspLys 2133
6883 TCAGGAGACCTCTCTGCCCCCTGGCGCCAGAGGAGCCCATCCACAGCGGACCTGAAG 6942
2134 LysCysTyrSerValGluAlaGlnSerCysGlnArgArgProThrSerTrpIleAspGlu 2153
6943 AAGTGCTACAGCTGGAGGCCAGAGCTGCCAGGCGCGGCTAGCTCTGCTGGCTGGATGAG 7002
2154 GlnArgArgHisSerIleAlaValSerCysLeuAspSerGlySerGlnProHisLeuGly 2173
7003 CAGAGGAGCACTCTATCGCCGTGAGCTGCTGGACAGCGGCTCCCAACCCACCTGGGC 7062
2174 ThrAspProSerAsnLeuGlyGlyGlnProLeuGlyProGlySerArgProLysLys 2193
7063 ACAGACCCCTCTAACCTTGGGGCCAGGCTCTTGGGGGGCCCGGAGCGGCCCAAGAA 7122
2194 LysLeuSerProProSerIleThrIleAspProProGluSerGlnGlyProArgThrPro 2213
7123 AAACCTCAGCCCGCTAGTATCACCATAGACCCCGCCAGAGCAAGGTCTCTCGGACCCCG 7182
2214 ProSerProGlyIleCysLeuArgArgAlaProSerSerAspSerLysAspProLeu 2233
7183 CCCAGCCCTGTGTATCTGCTCCCGAGGAGGGCTCCGTCAGCGACTCCAAGGATCCCTTG 7242
2234 AlaSerGlyProProAspSerMetAlaAlaSerProSerProLysLysAspValLeuSer 2253
7243 GCCTCTGGCCCCCTGACAGCATGGCTGCTCCCTCCCTCCCAAGAGATGTGCTGAGT 7302

Qy 2254 LeuSerGlyLeuSerSerAspProAlaAspLeuAspPro 2266
Db 7303 CTCTCCGGTTATCTCTGACCCAGACACCTGGACCCC 7341

RESULT 2

AAF31684
ID AAF31684 standard; cDNA; 6892 BP.
XX
AC AAF31684;
XX
DT 09-APR-2001 (first entry)
XX
DE Human alpha-IG T-type calcium channel cDNA.

XX Human; antiarrhythmic; anticonvulsant; hypotensive; cardiant; nootropic;
KW T-type calcium channel subunit; cardiac hypertrophy; cardiac arrhythmia;
KW hypertension; sleep disorder; epilepsy; alpha-IG T-type calcium channel;
KW ss.

XX Homo sapiens.

XX WO200102561-A2.

XX 11-JAN-2001.

XX 04-JUL-2000; 2000WO-CA000794.

XX 02-JUL-1999; 99US-00346794.

XX (NEUR-) NEUROMED TECHNOLOGIES INC.

XX Snutch TP, Baillie DL;

XX WPI; 2001-123111/13.

XX P-PSDB; AAB66481.

XX Novel T-type calcium channel alpha-1 subunit gene useful for treating
PT cardiac hypertrophy, cardiac arrhythmia, hypertension, sleep disorder and
PT epilepsy.

XX Example 3; Fig 6; 103pp; English.

XX The present sequence is given in a specification providing sequences and
CC partial sequences for three types of mammalian (human and rat) T-type
CC calcium channel subunits. An expression cassette has been generated which
CC comprises a nucleotide sequence encoding a T-type calcium channel alpha-1
CC subunit operably linked to control sequences to effect its expression.
CC The novel calcium channel nucleic acids and proteins are useful for
CC treating conditions characterised by undesirable levels of T-type calcium
CC channel activity such as cardiac hypertrophy, cardiac arrhythmia,
CC hypertension, sleep disorder and epilepsy

XX SQ Sequence 6892 BP; 1315 A; 2223 C; 2017 G; 1337 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 0 Length: 6892
Score: 11874.00 Matches: 2261
Percent Similarity: 99.82% Conservative: 1
Best Local Similarity: 99.78% Mismatches: 4
Query Match: 99.75% Indels: 0
DB: 5 Gaps: 0

US-09-611-257A-37 (1-2266) x AAF31684 (1-6892)

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Qy 21 ArgLeuAsnAspLeuSerGlyAlaGlyClyArgProGlyProGlySerAlaGlyLysAsp 40
Db 111 CGGCTCAACGACCTGTGGGGCGCGGGCGCGGGCGCGGGGTGAGCAAGAAAGGAC 170
Qy 41 ProGlySerAlaAspSerGluAlaGluGlyLeuProTyrProAlaLeuAlaProValVal 60

171 CCGGCGAGCGGACCTCCGAGGCGGAGGCGCTCCGCTACCGCGCGTGGCGGTGTT 230
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61 PhePheTyrLeuSerGlnAspSerArgProArgSerTyrCysLeuArgThrValCysAsn 80
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101 PheArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPhe 120
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181 ThrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeu 200
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651 GTCAAGTGTCTGCTGATACGCTGCCATGCTGGCAACGCTGCTGCTGCTGCTTCTTC 710
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401 ThrIysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAla 420

1251 ACCAAGCAGCGGGAAGACCCAGCTGATCGGGAGCAGCGGTGTGCGGTCTCTGTCTCAAGCC 1310
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481 SerCysSerArgSerHisArgArgLeuSerValHisLeuValHisHisHisHis 500
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761 GlyIleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnIle 780
Db
2331 GGCATCGATACCCAGCAGCAGCCCGGAGGCTTACCAACCGCCCTAGAAATCAGCAACATC 2390

Qy 781 ValPheThrSerLeuPheAlaLeuGluMetLeuLeuLeuValTyrGlyProPhe 800
Db 2391 GTCTTCACCAACCTCTTTGGCCCTGGAGATGCTGCTGAAGCTGCTGTGTATGGTCCCTTT 2450
Qy 801 GlyTyrIleLeuAsnProTyrAsnIlePheAspGlyValIleValIleSerValTyr 820
Db 2451 GGCTACATCAAGATCCCTACACATCTTCGATGGTGTCAATGTGGTCATCAGCGTGTGG 2510
Qy 821 GluIleValGlyGlnGlnGlyGlyLeuSerValLeuArgThrPheArgLeuMetArg 840
Db 2511 GAGATCGTGGCCAGCAGGGGGGGCGCTGCTGCTGCTGCGACCTTCGCGCTGATGCGT 2570
Qy 841 ValLeuLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetIys 860
Db 2571 GTGCTGAAGCTGGTGGCTTCCTCCCGCGCTGTCAGCGGCGAGCTGGTGGTCTCATGAAG 2630
Qy 861 ThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePheIlePheSer 880
Db 2631 ACCATGACACAGTGGCCACCTTCTGCATGCTGCTTATGCTCTTCACTTCTCATCTTCAGC 2690
Qy 881 IleLeuGlyMetHisLeuPheGlyCysIysPheAlaSerGluArgAspGlyAspThrLeu 900
Db 2691 ATCTGGGATGATCTCTTCGGCTGCAAGTTTGCCTCTGAGCGGATGGGGACACCTG 2750
Qy 901 ProAspArgIysAsnPheAspSerLeuLeuTrrAlaIleValThrValPheGlnIleLeu 920
Db 2751 CCAGACCGGAAGATTTTGACTCTCTGCTGCGGCCATCGTCACTGCTCTTCAGATCCTG 2810
Qy 921 ThrGlnGluAspTrrAsnLysValLeuTrrAsnGlyMetAlaSerThrSerTrrAla 940
Db 2811 ACCCAGAGGACTGGAAACAAAGTCTCTACAAATGGTATGGCTCCAGTCTGCTGGGCG 2870
Qy 941 AlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuVal 960
Db 2871 GCCCTTTATTTCACTTGGCTCATGACCTTCGGCAACTAGCTGCTCTTCAATTTGCTGCTC 2930
Qy 961 AlaIleLeuValGluGlyPheGlnAlaGluIleSerLysArgGluAspAlaSerGly 980
Db 2931 GCCATTCTGGTGGAGGGCTTCAGCGCGAGGAAATCAGCAACCGGAAGATGCGAGTGA 2990
Qy 981 GlnLeuSerCysIleGlnLeuProValAspSerGlnGlyGlyAspAlaAsnLysSerGlu 1000
Db 2991 CAGTTAAGCTGTATTACGCTGCCCTGTGACTCCAGCGGGGAGATGCCAACAGTCCGAA 3050
Qy 1001 SerGluProAspPheSerProSerLeuAspGlyAspGlyAspArgLysCysLeu 1020
Db 3051 TCAGAGCCCGATTTCTTCTACCCAGCTGGATGGTGTATGGGACAGGAAGTGTCTG 3110
Qy 1021 AlaLeuValSerLeuGlyGluHisProGluLeuArgIysSerLeuProProLeuIle 1040
Db 3111 GCCTTGGTGTCCCTGGGAGAGCACCGGAGCTGGCGAAGAGCTGCTGCCGCTCTCATC 3170
Qy 1041 IleHisThrAlaAlaThrProMetSerLeuProLysSerThrSerThrGlyLeuGlyGlu 1060
Db 3171 ATCCACAGGGCGCCACACCCATGCTGCTGCCAAGAGCACAGCGGGCTGGGCGAG 3230
Qy 1061 AlaLeuGlyProAlaSerArgThrSerSerSerGlySerAlaGluProGlyAlaAla 1080
Db 3231 CGCTGGGCGCTGGTCCGCGCGCACCGACAGCAGCGGGTCCGCGAGCTGGGCGGCC 3290
Qy 1081 HisGluMetLysSerProProSerAlaArgSerSerProHisSerProTrrSerAlaAla 1100
Db 3291 CACGAGATGAAGTCAACCGCCAGCGCCCGAGCTCTCCGCACAGCCCCCTGGAGCGCTGCA 3350
Qy 1101 SerSerTrrThrSerArgArgSerSerArgAsnSerLeuGlyArgAlaProSerLeuLys 1120
Db 3351 AGCAGCTGGACAGCAGCGCTCCAGCGGAAACAGCTTCGGCGCTGGACCCAGCTGAAG 3410
Qy 1121 ArgArgSerProSerGlyGluArgSerLeuLeuSerGlyGluGlnGlnSerGln 1140
Db 3411 CGGAGAGCCCAAGTGGAGAGCGGCGTCTCTGTGTGGGAGAGGCCAGGAGGCCAG 3470

Qy 1141 AspGluGluSerSerGluGluArgAlaSerProAlaGlySerAspHisArgHis 1160
Db 3471 GATGAAGAGGAGACTCAGAAGAGGAGCGGCCAGCCCTGCGGCGAGTGACATCGCCAC 3530
Qy 1161 ArgGlySerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeuGlnVal 1180
Db 3531 AGGGGGTCCCTGGAGCGGAGGCCAAGATTCCTTTGACCTGCCAGACACACTGCGAGCTG 3590
Qy 1181 ProGlyLeuHisArgThrAlaSerGlyArgGlySerAlaSerGluHisGlnAspCysAsn 1200
Db 3591 CCAGGGCTGCATCGACTGCGCAGTGGCGAGGGTCTGCTTCTGAGCACAGGACTGCAAT 3650
Qy 1201 GlyLysSerAlaSerGlyArgLeuAlaArgAlaLeuArgProAspAspProLeuLeuAsp 1220
Db 3651 CGCAAGTGGCTTCAGGGCGCTGCGCGCGCCCTGCGGCTGTAGATGACCCCCACTGAT 3710
Qy 1221 GlyAspAlaAspAspGluGlyAsnLeuSerLysGlyGluArgValArgAlaTrrIle 1240
Db 3711 GGGGATGACCGCGATGACGAGGGCAACTGAGCAAGGGGAACGGGTCCGCGCTGGATC 3770
Qy 1241 ArgAlaArgLeuProAlaCysTyrLeuGluArgAspSerTrrSerAlaTyrIlePhePro 1260
Db 3771 CGAGCCGACTCCCTGCTGCTTACTCGAGCGAGACTCTGCTGCTCACCTACATCTTCCCT 3830
Qy 1261 ProGlnSerArgPheArgLeuLeuCysHisArgIleIleThrHisLysMetPheAspHis 1280
Db 3831 CCTCAGTCCAGTTCCGCTCTGTCACCGGATCATCACCACAAAGATGTTGACCCAG 3890
Qy 1281 ValValLeuValIleIlePheLeuAsnCysIleThrIleAlaMetGluArgProLysIle 1300
Db 3891 GTGGTCTTGTATCATCTTCTTAACTGCATCACCATCGCATGGAGCGGCCCAAAAT 3950
Qy 1301 AspProHisSerAlaGluArgIlePheLeuThrLeuSerAsnTyrIlePheThrAlaVal 1320
Db 3951 GACCCACACAGCGCTGAACGCTCTTCTGACCCCTCTCCAATTACATCTTCCCGCAGTC 4010
Qy 1321 PheLeuAlaGluMetThrValLysValValAlaLeuGlyTrrCysPheGlyGluGlnAla 1340
Db 4011 TTTCTGGCTGAATGACAGTGAAGTGGTGCACTGGGCTGGTCTTCTGGGGAGCAGCG 4070
Qy 1341 TyrLeuArgSerSerTrrAsnValLeuAspGlyLeuLeuValLeuIleSerValIleAsp 1360
Db 4071 TACCTGGGAGCAGTGGACGCTGCTGACGGGCTGTGTGGTCTCATCTCGTCATCGAC 4130
Qy 1361 IleLeuValSerMetValSerAspSerGlyThrLysIleLeuGlyMetLeuArgValLeu 1380
Db 4131 ATTCTGGTGTCCATGGTCTCTGACGCGCACCAAGATCCTGGGCATGCTGAGGGTGTG 4190
Qy 1381 ArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeuLysLeu 1400
Db 4191 CGGCTGTGCGGACCCCTGCGCCGCTCAGGGTGTATCAGCGGGCGGCGAGGGCTGAAGCTG 4250
Qy 1401 ValValGluThrLeuMetSerSerLeuLysProIleGlyAsnIleValIleCysCys 1420
Db 4251 GTGGTGAAGACGTGATGTCTCTCATGAACCCATCGGCAACATTTAGTATCATCTGCTGT 4310
Qy 1421 AlaPhePheIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPhePheVal 1440
Db 4311 GCCTTCTCATCTTTCTGGCATCTTGGGGGTGCGAGCTCTTCAAAGGAAAGTTTTCTGTG 4370
Qy 1441 CysGlnGlyGluAspThrArgAsnIleThrAsnLysSerAspCysAlaGluAlaSerTyr 1460
Db 4371 TGGCAGGGCGAGGATACAGGAACATCACAATAAATCGGACTGTGGCGAGGCCAGTTTAC 4430
Qy 1461 ArgTrrValArgHisLysTyrAsnPheAspAsnLeuGlyGlnAlaLeuMetSerLeuPhe 1480
Db 4431 CGGTGGGTCCGGCAAGTACAACTTTTGACAACTTTGGCCAGGCGCTGATGCTCTGTTTC 4490
Qy 1481 ValLeuAlaSerLysAspGlyTrrValAspIleMetTyrAspGlyLeuAspAlaValGly 1500
Db 4491 GTTTTGGCTCCCAAGGATGGTGGGTGGACATCATGATACGATGGCTGGATGCTGTGGGC 4550
Qy 1501 ValAspGlnGlnProIleMetAsnHisAsnProTrrMetLeuLeuTyrPheIleSerPhe 1520

Db	4551	GTGACACAGAGCCCATCATGACACACACCCCTGGATGCTGCTACTTCATCTCGTTC	4610	Db	5631	AGCCCCCAGCCCACTCGCCACTGGGACGCCCTTCTCTGGCTGGGGTCGAGGGCCCC	5690
Qy	1521	LeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValValValGluAsnPhe	1540	Qy	1881	AspSerProAspSerProLysProGlyAlaLeuHisProAlaAlaHisAlaArgSerAla	1900
Db	4611	CTGCTCATTTGGGCTTCTTGTCTCTGAACATGTTTGTGGGTGTGGTGTGGAGAACTTC	4670	Db	5691	GACAGCCCCACAGCCCCCAAGCCTTGGGCTCTGCACCCAGCGGCCCCACGCGAGATCAGCC	5750
Qy	1541	HisLysCysArgGlnHisGlnGlnGluGluGluAlaArgArgGluGluLysArgLeu	1560	Qy	1901	SerHisPheSerLeuGluHisProThrMetGlnProHisProHisProThrGluLeuProGlyPro	1920
Db	4671	CACAAGTGTAGCGACACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	4730	Db	5751	TCCCACTTTTCCCTGGAGCACCCACGATGACAGCCCCACCCACGAGCTGCCAGGCCA	5810
Qy	1561	ArgArgLeuGluLysLysArgLysAlaGlnCysLysProTyrTyrSerAspTyrSer	1580	Qy	1921	AspLeuLeuThrValArgLysSerGlyValSerArgThrHisSerLeuProAsnAspSer	1940
Db	4731	CGAAGCTGGAGAAAAAGAGAGAAAGCCAGTGCACAACTTACTCTCCGACTACTCC	4790	Db	5811	GACTTACTGCTGTGCGGAAGTCTGGGGTCAGCGCAACGCACTCTCTGCCCAATGACGC	5870
Qy	1581	ArgPheArgLeuLeuValHisHisLeuCysThrSerHisTyrLeuAspLeuPheLeuThr	1600	Qy	1941	TyrMetCysArgHisGlySerThrAlaGluGlyProLeuGlyHisArgGlyTyrGlyLeu	1960
Db	4791	CGCTTCGGGCTCCTCGTCCACACTTGTGCACCAAGCCACTTACCTGGACCTTTCATCACA	4850	Db	5871	TACATGTGTGGCATGGGAGCACTGCCAGGGGCCCTGGGACACAGGGGCTGGGGCTC	5930
Qy	1601	GlyValIleGlyLeuAsnValValThrMetAlaMetGluHisTyrGlnGlnProGlnIle	1620	Qy	1961	ProLysAlaGlnSerGlySerValLeuSerValHisSerGlnProAlaAspThrSerTyr	1980
Db	4851	GGTGTCTCGGGCTGAACGTGTCACCATGCCATGGCAGCACTACCAAGAGCCCGAGATT	4910	Db	5931	CCCAAGCTCAGTCAGGCTCCGTCTGTTCGGTTCACTCCAGCCAGCAGATACCAAGTAC	5990
Qy	1621	LeuAspGluAlaLeuLysIleCysAsnTyrIlePheThrValIlePheValLeuGluSer	1640	Qy	1981	IleLeuGlnLeuProLysAspAlaProHisLeuLeuGlnProHisSerAlaProThrTyr	2000
Db	4911	CTGGATGAGGCTCTGAAGATCTGCAACTTACATCTTCACTGTCACTTTGTCTTGGAGTCA	4970	Db	5991	ATCCTGCGAGCTTCCCAAGATGCACTCATCTGCTCCAGCCCAAGCGCCCAACCTGG	6050
Qy	1641	ValPheLysLeuValAlaPheGlyPheArgArgPheGlnAspArgTyrAsnGlnLeu	1660	Qy	2001	GlyThrIleProLysLeuProProGlyArgSerProLeuAlaGlnArgProLeuArg	2020
Db	4971	GTITTTCAAACTTGGGCTTGGTTTCGTTCGTTCCTCCAGGACAGGTGGAACAGCTG	5030	Db	6051	GGCACATCCCAAACTGCCCCACAGAGCGTCCCTTTGGCTCAGAGGCCACTCAGG	6110
Qy	1661	AspLeuAlaIleValLeuLeuSerIleMetGlyIleThrLeuGluGluIleGluValAsn	1680	Qy	2021	ArgGlnAlaAlaIleArgThrAspSerLeuAspValGlnGlyLeuGlySerArgGluAsp	2040
Db	5031	GACCTGGCATTTGTGCTGCTCCATCATGGGCATCAGCTGGAGAGAAATCGAGTCAAC	5090	Db	6111	CGCCAGCAGCAATTAAGNACTGACTCCTTGGACGTTTCAAGGCTTGGGCGCGGAGAAC	6170
Qy	1681	AlaSerLeuProIleAsnProThrIleAlaGlnMetArgValLeuArgIleAlaArg	1700	Qy	2041	LeuLeuAlaGluValSerGlyProSerProLeuAlaArgAlaTyrSerPheTyrGly	2060
Db	5091	GCCTCGCTGCCCATCAACCCACCATCATCCGCATCATGAGGCTGCTGGCATTTGCCGA	5150	Db	6171	CTGCTGCAGAGGTGAGTGGGCTCCCGCCCTCCCGCCCTGGCGCGGCGCTACTCTTCTGGGGC	6230
Qy	1701	ValLeuLysLeuLeuLysMetAlaValGlyMetArgAlaLeuLeuAspThrValMetGln	1720	Qy	2061	GlnSerSerThrGlnAlaGlnGlnHisSerArgSerHisSerLysIleSerLysHisMet	2080
Db	5151	GTGCTGAAGCTGCTGAAGATGGTGTGGGCATGCGGGCGCTCTGGACACGGTGAAGCAG	5210	Db	6231	CAGTCAAGTACCCAGGACACAGCAGCACTCCCGAGCCACAGCAAGATCTCCAAAGCACATG	6290
Qy	1721	AlaLeuProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPhePheIlePheAla	1740	Qy	2081	ThrProAlaProCysProGlyProGluProAsnTyrGlyLysGlyProProGluThr	2100
Db	5211	GCCTCGCCCGAGTGGGGAACCTTGGGACTTCTTTCATGTTGTGTTTTTTCATCTTGA	5270	Db	6291	ACCCCGCCAGCCCTTGGCCAGCCCAAGCACTGGGGCAAGGGCCCTCCAGAGACC	6350
Qy	1741	AlaLeuGlyValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGluGly	1760	Qy	2101	ArgSerSerLeuGluLeuAspThrGluLeuSerTyrIleSerGlyAspLeuLeuProPro	2120
Db	5271	GCTCTGGGCGTGGAGCTCTTTGGAGACCTGGAGTGTGACGAGACACACCCCTGTGAGGGC	5330	Db	6351	AGAAGCAGCTTAGAGTTGGACACGGAGCTGAGCTGGATTTTCAAGAGACCTCTCTGCCCT	6410
Qy	1761	LeuGlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgVal	1780	Qy	2121	GlyGlyGlnGluProProSerProArgAspLeuLysLysCysTyrSerValGluAla	2140
Db	5331	CTGGGCGCTCATGCCACTTTGGAACTTTGGCACTTGGCATGGCCCTTCAACCTCTTCCGAGTC	5390	Db	6411	GGCGCCAGGAGGAGCCCTCCATCCCAAGGAGCTGAAAGAGTGTACAGCTGGAGGCC	6470
Qy	1781	SerThrGlyAspAsnTyrAsnGlyIleMetLysAspThrLeuArgAspCysAspGlnGlu	1800	Qy	2141	GlnSerCysGlnArgArgProThrSerTyrLeuAspGluGlnArgArgHisSerIleAla	2160
Db	5391	TCCACAGGTGACATTTGAATGGCATTTATGAAGACACACCTCCGGGACTGTGACAGGAG	5450	Db	6471	CAGAGCTGCCAGCCCGGCTTACGCTCTGGTGTGATGAGCAGAGGAGACACTCTATCGCC	6530
Qy	1801	SerThrCysTyrAsnThrValIleSerProIleTyrPheValSerPheValLeuThrAla	1820	Qy	2161	ValSerCysLeuAspSerGlySerGlnProHisLeuGlyThrAspProSerAsnLeuGly	2180
Db	5451	TCCACCTCTCAACACAGCGTCATCTCGCCTATCTACTTTGTGTCCTTGTGCTGAGCGGCC	5510	Db	6531	GTCAGCTCCCTGGACAGGGGCTCCCAACCCACCTGGGCAACAGCCCTCTAAACCTTGGG	6590
Qy	1821	GlnPheValLeuValAsnValValIleAlaValLeuMetLysHisLeuGluGluSerAsn	1840	Qy	2181	GlyGlnProLeuGlyGlyProGlySerArgProLysLysLysLeuSerProProSerIle	2200
Db	5511	CAGTTCTGTGTAGTCAACGTGTGTGTATCGCGTGTGTATGAAGCACTTGGAGGAGCAAC	5570	Db	6591	GGCCAGCCCTTGGGGGCTTGGAGCGCGGCCCAAGAAAAAACTCAGCCCGCTAGTATC	6650
Qy	1841	LysGluAlaLysGluGluAlaGluLeuGluAlaGluLeuGluMetLysThrLeu	1860	Qy	2201	ThrIleAspProProGluSerGlnGlyProArgThrProProSerProGlyIleCysLeu	2220
Db	5571	AAGAGGCCCAAGAGAGGAGCGAGCTAGAGCTGAGCTGGAGCTGGAGATGAGACCCCTC	5630	Db	6651	ACCATAGACCCCGCCAGAGCCAGGCTCTCGGACCCCGCCAGCCCTTGGTATCTGCTC	6710
Qy	1861	SerProGlnProHisSerProLeuGlySerProPheLeuTyrProGlyValGluGlyPro	1880	Qy	2221	ArgArgArgAlaProSerSerAspSerLysAspProLeuAlaSerGlyProProAspSer	2240
				Db	6711	CGGAGAGGGGCTCCGCTCCAGCGACTCCCAAGGATCCCTTGGGCTCTTGGCCCCCTGACAGC	6770

Qy 2241 MetAlaAspSerProLysValLeuSerLeuSerGlyLeuSerSerAsp 2260
Db 6771 ATGCTGCTCGCCCTCCCAAGAAAGATGCTGAGTCTCTCCGGTTTATCTCTGAC 6830

Qy 2261 ProAlaAspLeuAspPro 2266
Db 6831 CCACGACCTGGACCCC 6848

RESULT 3

ID ADQ89063
XX ADQ89063 standard; cDNA; 7648 BP.

XX AC ADQ89063;

XX DT 21-OCT-2004 (first entry)

XX DE Human urological disorder related protein 4421 encoding cDNA SEQ:15.

XX KW urological disorder; uropathic; cytostatic; urinary incontinence;

XX KW benign prostatic hyperplasia; human; gene; ss.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers
XX CDS 1..7134

XX FT /*tag= a
XX FT /product= "urological disorder related protein 4421"

XX PN WO2004065576-A2.

XX XX

XX PD 05-AUG-2004.

XX PF 14-JAN-2004; 2004WO-US000750.

XX PR 15-JAN-2003; 2003US-0440318P.

XX PR 04-FEB-2003; 2003US-0444783P.

XX PR 27-MAR-2003; 2003US-0457901P.

XX PR 08-MAY-2003; 2003US-0468775P.

XX PR 19-MAY-2003; 2003US-0471614P.

XX PR 16-JUN-2003; 2003US-047842P.

XX PR 18-JUL-2003; 2003US-0488529P.

XX PR 30-JUL-2003; 2003US-0491156P.

XX PR 02-SEP-2003; 2003US-049594P.

XX PR 26-SEP-2003; 2003US-0506332P.

XX PA (MILL-) MILLENNIUM PHARM INC.

XX PI Karicheti V, Silos-Santiago I, Eliasof SD;

XX XX

XX DR WPI; 2004-562167/54.

XX DR P-PSDB; ADQ89064.

XX PT Use of polypeptides related to urological disorders, e.g. 44390, 54181,

XX PT 211 or for identifying a compound capable of treating a urological

XX PT disorder or identifying and treating a subject having a urological

XX PT disorder.

XX PS Claim 1; SEQ ID NO 15; 542pp; English.

XX CC The present invention describes the use of polypeptides related to

XX CC urological disorders for identifying a compound capable of treating a

XX CC urological disorder, identifying a subject having a urological disorder,

CC related protein, which is used in the exemplification of the present

CC invention.

XX SQ Sequence 7648 BP; 1492 A; 2419 C; 2205 G; 1532 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 0 Length: 7648
Score: 11815.50 Matches: 2264
Percent Similarity: 95.29% Conservatives: 1
Best Local Similarity: 95.25% Mismatches: 1
Query Match: 99.26% Indels: 111
DB: 13 Gaps: 2

US-09-611-257A-37 (1-2266) x ADQ89063 (1-7648)

Qy 1 MetAspGluGluAspGlyAlaGlyAlaGluSerGlyGlnProArgSerPheMet 20

Db 1 ATGGACGAGGAGGAGGATGGAGCGGCGCGGAGTGGGACAGCCCGGAGCTTCATG 60

Qy 21 ArgLeuAsnAspLeuSerGlyAlaGlyGlyArgProGlyProGlySerAlaGluLysAsp 40

Db 61 CGGCTCAACGACCTGTGCGGGGCGGGGCGGGGCGGGGTCACGAGAAAGGAC 120

Qy 41 ProGlySerAlaAspSerGluAlaGluGluProTyrProAlaLeuAlaProValVal 60

Db 121 CCGGCGACGCGGACTCCGAGGCGGAGGGCTGCCGTACCCGGGCTGGCCCGGTGGTT 180

Qy 61 PhePheTyrLeuSerGlnAspSerArgProArgSerTrpCysLeuArgThrValCysAsn 80

Db 181 TTCTTCTACTTGGCCAGGACAGCCGCGCGGAGTGGTGTCTCCGACCGGTCTGTAAAC 240

Qy 81 ProTrpPheGluArgIleSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMet 100

Db 241 CCCTGGTTTGGCGCATCAGCATGTTGGTCTATCTTCTCAACTCGGTGACCTGGGCATG 300

Qy 101 PheArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPhe 120

Db 301 TTCGGGCGATGGAGGACATCGCTGTGACTCCAGCGGCTGCCGAGTCTTCGACGGCCTTT 360

Qy 121 AspAspPheIlePheAlaPhePheAlaValGluMetValValLysMetValAlaLeuGly 140

Db 361 GATGACTTCTCTTTGCTCTCTTTCGCGTGAGATGGTGGTGAAGATGGTGGCTTGGGC 420

Qy 141 IlePheGlyLysLysCysTyrLeuGlyAspThrTrpAsnArgLeuAspPheIleVal 160

Db 421 ATCTTTGGGAAAAAGTGTATCTTACCTGGGAGACACTTGGAAACCGGCTTGACTTTTCATCGTC 480

Qy 161 IleAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArg 180

Db 481 ATCGACGGATGCTGGAGTACTCGCTGGACCTTGAGAACGTCAGCTTCTCAGCTGTCAAG 540

Qy 181 ThrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeu 200

Db 541 ACAGTCGTGTGCTGCGACCGCTCAGGCGCATTAACCGGGTGCCAGCATCGCATCCTT 600

Qy 201 ValThrLeuLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePhe 220

Db 601 GTCAGTTGCTGTGGATACGCTGCCCATGCTGGGCAACGCTCTGCTGCTCTGCTCTTC 660

Qy 221 ValPhePheIlePheGlyIleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArg 240

Db 661 GTCTTCTTCATCTTGGCATCGTCGGGCTCGAGCTGTGGGCGGGGCTGCTTCGGAACCGA 720

Qy 241 CysPheLeuProGluAsnPheSerLeuProLeuSerValAspLeuGluArgTyrTrpGln 260

Db 721 TGCTTCTTACTGAGATTTTTCAGCTCTCCCTCGAGCGTGGACCTGGAGCGCTATTACCA 780

Qy 261 ThrGluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArg 280

Db 781 ACAGAGAACGAGGATGAGAGCCCTTTCATCTGCTCCAGCCACGCGAGACCGCATTCGG 840

Qy 281 SerCysArgSerValProThrLeuArgGlyAspGlyGlyGlyProProCysGlyLeu 300

841 TCCTGAGAAAGCTGCCACGCTGCCGGGACGGGGCGGTGCCACCTTGCCTGCTG 900
301 AspTyrGluAlaTyrAsnSerSerAsnThrThrCysValAsnTrpAsnGlnTyrTyr 320
901 GACTATGAGCCCTACAAAGCTCCAGACCAACCCACCTGTGTCACTGGGAACAGTACTAC 960
321 ThrAsnCysSerAlaGlyGluHisAsnProPheLysGlyAlaIleAsnPheAspAsnIle 340
961 ACCAACTGCTCAGCGGGGAGCAACACCCCTTCAGGGGCCCATCAACTTTGACAACATT 1020
341 GlyTyrAlaTrpIleAlaIlePheGlnValIleThrLeuGluGlyTrpValAspIleMet 360
1021 GGCTATGCTTGGATCGCACTTCAGGTCACTCAGCTGATCAGCTGAGGGCTGGGTGCACATCATG 1080
361 TyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleIle 380
1081 TACTTTGTGATGGAGTCTCATCTCTTCAAAATTCATCTTCACTCCCTCCCTCATCATC 1140
381 ValGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGlu 400
1141 GTGGGCTCTCTTCATGATCAACTGTGCTGGTGTGATTGCGACGAGTTCTCAGAG 1200
401 ThrLysGlnArgGluSerGlnLeuMetArgGlnArgValArgPheLeuSerAsnAla 420
1201 ACCAAGCAGCGGGAAGCAGCTGATGCGGAGCAGCGTGTGCGGTTCTGTCCACGCC 1260
421 SerThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLeuLysTyrLeu 440
1261 AGCACCTTGGCTAGCTTCTCTGAGCCCGCAGCTGTATGAGGAGCTGCTCAAGTACTG 1320
441 ValTyrIleLeuArgLysAlaAlaArgArgLeuAlaGlnValSerArgAlaAlaGlyVal 460
1321 GTGTACATCTTCGTAAGCAGCCCGCAGGCTGCTCAGGTTCTTCGGGCGACGAGTGTG 1380
461 ArgValGlyLeuLeuSerSerProAlaProLeuGlyGlyGlnGluThrGlnProSerSer 480
1381 CGGGTGTGGGCTGCTCAGCAGCCAGCAGCAGCCCTCGGGGCCAGGACACCGCCAGCAGC 1440
481 SerCysSerArgSerHisArgArgLeuSerValHisHisLeuValHisHisHisHis 500
1441 AGCTGTCTCTCGTCCACCGCGCTTATCCGTCACACCTGGTGACACCAACCCACAC 1500
501 HisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHis 520
1501 CATCACCAACCATCACCTGGCAATGGAGCCTCAGGCCCCCGGGCCAGCCCGGAG 1560
521 IleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProSerThrPro 540
1561 ATCCAGACAGGATGCCAATGGGTCCCGAGGCTCATGTGCGACACCCCTCGAGCGCT 1620
541 AlaLeuSerGlyAlaProProGlyGlyAlaGluSerValHisSerPheTyrHisAlaAsp 560
1621 GCCCTCTCCGGGGCCCCCTGTGGCGCAGAGTCTGTGCACAGCTTCTACCATGCCGAC 1680
561 CysHisLeuGluProValArgCysGlnAlaProProProArgSerProSerGluAlaSer 580
1681 TGCCACTTAGAGCCAGTCCGCTGCCAGCGCCCCCTCCAGGTCCCATCTGAGGCGATCC 1740
581 GlyArgThrValGlySerGlyLysValTyrProThrValHisThrSerProProProGlu 600
1741 GGCAGGACTGTGGGCGAGGGGAAGGTATCCCACTGCCAGCTGCACACCGCTCCACCGGAG 1800
601 ThrLeuLysGlyLysAlaLeuValGluValAlaAlaSerSerGlyProProThrLeuThr 620
1801 AGCTTGAAGGAGAGGACCATAGTAGAGGTGGTCCAGCTCTGGGCCCCCAACCCCTACC 1860
621 SerLeuAsnIleProProGlyProTyrSerSerMetHisLysLeuLeuGluThrGlnSer 640
1861 AGCCTCAACATCCCAACCGGGCCCTACAGCTCCATGCAAGCTGCTGGAGACACAGAT 1920
641 ThrGlyAlaCysGlnSerSerCysLysIleSerSerProCysLeuLysAlaAspSerGly 660
1921 ACAGGTGCTGCCAAGGCTCTTGCAAGATCTCCAGCCCTTGTGTAAGACGACAGTGGGA 1980

661 AlaCysGlyProAspSerCysProTyrCysAlaArgAlaGlyValaGlyValGluLeu 680
1981 GCCTGTGGTCCAGACAGCTGCCCTACTGTGCCGGCCGGGAGGAGGTGGAGCTC 2040
681 AlaAspArgGluMetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAla 700
2041 GCCGACGCTGAATGCTGACTCAGACAGCGAGGCAAGTTTATGAGTTTACACAGGATGCC 2100
701 GlnHisSerAspLeuArgAspProHisSerArgArgGlnArgSerLeuGlyProAspAla 720
2101 CAGCACAGCAGCCTCGGGACCCCAACGCGCGCGGACGAGCCTGGGCCAGATGCA 2160
721 GluProSerSerValLeuAlaPheTrpArgLeuIleCysAspThrPheArgLysIleVal 740
2161 GAGCCAGCTCTGTGCTGGCTTCTGGAGGCTAATCTGTGACACCTTCCGAAAGATTGTG 2220
741 AspSerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerMet 760
2221 GACAGCAAGTACTTTGGCCGGGGAATCATGATGCCATCTCTGGTCAACACACTCAGCATG 2280
761 GlyIleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnIle 780
2281 GCATCGAATACACGAGCAGCAGCAGCAGCTTACCAACGCCCTAGAAATCAGCAACATC 2340
781 ValPheThrSerLeuPheAlaLeuGluMetLeuLysLeuLeuValTyrGlyProPhe 800
2341 GTCTTTCACGAGCTCTTTGCCCTGGAGATGCTGCTGAAGCTGCTGTGTATGTTCCCTTT 2400
801 GlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleValIleValIleSerValTrp 820
2401 GGCTACATCAGAAATCCCTACACATCTTCGATGGTGTCTTGTGTCATCAGCGTGTGG 2460
821 GluIleValGlyGlnGlnGlyGlyLeuSerValLeuArgThrPheArgLeuMetArg 840
2461 GAGATCGTGGGCAGCAGCGGGCGGCGCTGTGGGTGCTGGCGACCTTCCGCTGATGCGT 2520
841 ValLeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetLys 860
2521 GTGCTGAAGCTGTGGCGCTTCTTCCGGCGCTGTCAGCGCAGCTGCTGCTCATAGAG 2580
861 ThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePheSer 880
2581 ACCATGGACAAACGTGGCCACCTTTCATGCTGCTGTATGCTCTTCTCATCTTCTCAGC 2640
881 IleLeuGlyMetHisLeuPheGlyCysLysPheAlaSerGluArgAspGlyAspThrLeu 900
2641 ATCTTGGGCGATGATCTTCTTGGCTGCAAGTTTGCCTCTGAGCGGATGGGACACCTG 2700
901 ProAspArgLysAsnPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIleLeu 920
2701 CCAGACCGGAAGAAATTTGACTCTTGTCTTGGGCCATGCTGCTCTTCTTCTGATCCTG 2760
921 ThrGlnGluAspTrpAsnLysValLeuTyrAsnGlyMetAlaSerThrSerSerTrpAla 940
2761 ACCCAGAGGACTGGAAACAAAGTCTTACAAATGGTATGGCTCCACGCTCCAGTGGCG 2820
941 AlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuVal 960
2821 GCCCTTTATTTTCAATGGCTCATGACCTTGGCAACTTACGTGCTCTTCAATTTGTGGTC 2880
961 AlaIleLeuValGluGlyPheGlnAlaGluIleSerLysArgGluAspAlaSerGly 980
2881 GCCATTCCTGGTGGAGGGCTTCCAGCGGAGGAATCAGCAACCGGAAGATGCGAGTGGGA 2940
981 GlnLeuSerCysIleGlnLeuProValAspSerGlnGlyAspAlaAsnLysSerGlu 1000
2941 CAGTTAAGCTGTATTTCAGCTGCCCTGCTGACCTCCAGGGGGGAGATGCCAACAGTCCGAA 3000
1001 SerGluProAspPhePheSerProSerLeuAspGlyAspGlyAspArgLysLysCysLeu 1020
3001 TCAGAGCCCGATTTCTTCTCACCAGCCTGGATGGTGTGTTGGGACAGGAAGTGTCTTG 3060

Qy 1021 AlaleuValSerLeuGlyGluHisProGluLeuArgIysSerLeuProLeuIle 1040
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Qy 1041 IleHisThrAlaAlaThrProMetSerLeuProIysSerThrSerThrGlyLeuGlyGlu 1060
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Qy 1061 AlaleuGlyProAlaSerArgThrSerSerSerGlySerAlaGluProGlyAlaAla 1080
Db 3181 GCGCTGGGCGCTCGCTCGCGCGCACACGACGAGCGGCTCGGACAGCCTTGGGCGCGCC 3240
Qy 1081 HisGluMetIysSerProProSerAlaArgSerProHisSerProTrpSerAlaAla 1100
Db 3241 CACGAGTGAAGTCAACCGCCCGAGCGCCGAGCTCTCCGACAGCCCTGGAGCGCTGCA 3300
Qy 1101 SerSerTrpThrSerArgArgSerSerArgAsnSerLeuGlyArgAlaProSerLeuIys 1120
Db 3301 AGCAGCTGGACACGACGCGCTCCAGCCGGAACAGCCTCGGCCGTGCACCCAGCCTGAAG 3360
Qy 1121 ArgArgSerProSerGlyGluArgSerLeuLeuSerGlyGlyGluGlnGlnSerGln 1140
Db 3361 CGGAGAACCCCAAGTGGAGAGCGCGCTCCCTGTTGTCGGGAGAAGCCAGAGAGCCAG 3420
Qy 1141 AspGluGluSerSerGluGluGluArgAlaSerProAlaGlySerAspHisArgHis 1160
Db 3421 GATGAAGAGGAGACTCAGAAGAGAGCGCGCCAGCCTCGCGGCGAGTGCATCGCCAC 3480
Qy 1161 ArgGlySerLeuGluArgGluAlaIysSerSerPheAspLeuProAspThrLeuGlnVal 1180
Db 3481 AGGGGGTCCCTGGAGCGGAGGCCCAAGAGTTCCTTTGACCTGCCAGACACACTGCAGGTG 3540
Qy 1181 ProGlyLeuHisArgThrAlaSerGlyArgGlySerAlaSerGluHisGlnAspCysAsn 1200
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Qy 1201 GlyIysSerAlaSerGlyArgLeuAlaArgAlaLeuArgProAspAspProProLeuAsp 1220
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Qy 1241 ArgAlaArgLeuProAlaCysTyIleuGluArgAspSerTrpSerAlaTyIlePhePro 1260
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Qy 1261 ProGlnSerArgPheArgLeuLeuLeuCysHisArgIleIleThrHisIysMetPheAspHis 1280
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Qy 1281 ValValLeuValIleIlePheLeuAsnCysIleThrIleAlaMetGluArgProIysIle 1300
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Qy 1401 ValValGluThrLeuMetSerSerLeuIysProIleGlyAsnIleValIleCysCys 1420
Db 4201 GTGGTGGAGAGCGCTGATGCTCTCACTGAACCCCATCGCAACATTTAGTATCATCTGCTGT 4260
Qy 1421 AlaphePheIleIlePheGlyIleLeuGlyValGlnLeuPheIysGlyIysPhePheVal 1440
Db 4261 GCCTTCTTCATCATTTTTCGGCATCTTGGGGTGCAGCTCTTCAAAGGGAAGTTTTTCGTG 4320
Qy 1441 CysGlnGlyGluAspThrArgAsnIleThrAsnIysSerAspCysAlaGluAlaSerTyr 1460
Db 4321 TGCAGGGCGAGGATACAGGAACATCACCNAATAATCGGACTGTGCCGAGGCCAGTTTAC 4380
Qy 1461 ArgTrpValArgHisIysTyrAsnPheAspAsnLeuGlyGlnAlaLeuMetSerLeuPhe 1480
Db 4381 CCGTGGGTCCGGCAACAGTACAACTTTTGACAACCTTGGCAGGCGCTGATGTCCCTGTTTC 4440
Qy 1481 ValLeuAlaSerIysAspGlyTrpValAspIleMetTyrAspGlyLeuAspAlaValGly 1500
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Qy 1521 LeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValValIleGluAsnPhe 1540
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Qy 1541 HisIysCysArgGlnHisGlnGluGluAlaArgArgArgGluGluGlyArgLeu 1560
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Qy 1561 ArgArgLeuGluIysIysArgArg- 1568
Db 4681 CGAAGACTGGAG 4740
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Qy 1583 ArgLeuLeuValHisHisLeuCysThrSerHisTyrLeuAspLeuPheIleThrGlyVal 1602
Db 4801 CCGCTCTCTGCTCCACCACTTGTGCACGAGCAGCTTACCTGGACCTTCTTCATCAGAGGTGC 4860
Qy 1603 IleGlyLeuAsnValValThrMetAlaMetGluHisTyrGlnGlnProGlnIleLeuAsp 1622
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Qy 1623 GluAlaLeuIysIleCysAsnTyrIlePheThrValIlePheValLeuGluSerValPhe 1642
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Db 5161 AAGTGTGAAGATGGTGTGGGCATCGGGCGCTGCTGGACACGCTGATCAGAGGCCCTG 5220
Qy 1723 ProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPheIlePheAlaAlaLeu 1742

5221 CCCAGGTGGGGAACCTGGGACTTCTCTCATGTTGTTGTTTTCATCTTTGACGCTCTG 5280
1743 GlyValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGluGlyLeuGly 1762
5281 GGGGTGGAGCTCTTTGGAGACCTTGGAGTGTGACAGACACACCCCTGTGAGGGCTGGGC 5340
1763 ArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgValSerThr 1782
5341 CGTCATGCCACCTTTCGGAACCTTGGCATGGCCCTCTCTAACCCCTTTCGAGTCTCCACA 5400
1783 GlyAspAsnTrpAsnGlyIleMetLysAspThrLeuArgAspCysAspGlnGluSerThr 1802
5401 GGTGACAAATTGGAATGCAATTATGAGGACACCCCTCCGGGACTGTGACCAAGGATGCCACC 5460
1803 CysTrpAsnThrValIleSerProIleTyrPheValSerPheValLeuThrAlaGlnPhe 1822
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5521 GTGCTAGTCAACGTGGTGTATCGCGCTGCTGATGAAGCACCTGGAGGAGAGCAACAAGAG 5580
1843 AlalyGluGluAlaGluLeuGluAlaGluLeuGluMetLysThrLeuSerPro 1862
5581 GCCAAGGAGGAGGCGGAGCTAGAGCTCAGCTGAGCTGAGATGAAGACCCCTCAGCCCC 5640
1863 GlnProHisSerProLeuGlySerProPheLeuTrpProGlyValGluGlyProAspSer 1882
5641 CAGCCCCACTCGCACCTGGGAGGAGCCCTTCTCTGGGCTGGGGTGGAGGGCCCCGACAGC 5700
1883 ProAspSerProLysProGlyValAlaLeuHisProAlaHisAlaArgSerAlaSerHis 1902
5701 CCCGACAGCCCCAAGCCTGGGGCTCTGCACCCAGCGGCCCAAGGATCAGCTCCAC 5760
1903 PheSerLeuGluHisProThr----- 1909
5761 TTTTCCCTGGAGCACCACCGCAGGAGCTGTTTGACACCATATCCCTGCTGATCCAG 5820
1909 ----- 1909
5821 GGCTCCCTGGAGTGGGAGCTGAAGCTGATGACAGCTGGCAGGCCCGGAGGAGCAAT 5880
1909 ----- 1909
5881 TCTGCTTCCCTTCTGCTGACCTCAGAGATTGTGTGAACCGTCTCTCTAGCTCTG 5940
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5941 ATGGAGGCTCTGCTCTGACCTCAGAGATTGTGTGAACCGTCTCTCTAGCTCTG 6000
1909 ----- 1909
6001 ACGGATGACTTTTGGCTGATGACATGACACACATCTTACTTAGTGCCCTGGAGGCAAT 6060
1910 MetGlnProHisProThrGluLeuProGlyProAspLeuLeuThrValArgLysSerGly 1929
6061 ATGAGCCCCACCCACGAGCTGGCAGGACAGACATTTACTCACTGTGCGGAAGTCTGGG 6120
1930 ValSerArgThrHisSerLeuProAsnAspSerTyrMetCysArgHisGlySerThrAla 1949
6121 GTCAGCGAAGCAGCACTCTCTGCCCCAATGACAGCTACATGTGCGGATGGGAGACTGCC 6180
1950 GluGlyProLeuGlyHisArgGlyTrpGlyLeuProLysAlaGlnSerGlySerValLeu 1969
6181 GAGGGGCCCCCTGGGACACAGGGCTGGGGCTCCCCAAGCTCAGTCAAGCTCCGCTCTG 6240
1970 SerValHisSerGlnProAlaAspThrSerTyrIleLeuGlnLeuProLysAspAlaPro 1989
6241 TCCGTTCACTCCAGCCAGCAGATACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 6300
1990 HisLeuLeuGlnProHisSerAlaProThrTrpGlyThrIleProLysLeuProPro 2009
6301 CATCTGCTCCAGCCCCACAGCGCCCCAACCTGGGGGACCATCTCCCAAACTGCCCCACCA 6360

2010 GlyArgSerProLeuAlaGlnArgProLeuArgArgGlnAlaAlaIleArgThrAspSer 2029
6361 GGAGCGCTCCCTTTGGCTCAGAGGCGCACTCAGGCGCCAGGCAATAAGGACTGACTCC 6420
2030 LeuAspValGlnGlyLeuGlySerArgGluAspLeuLeuAlaGluValSerGlyProSer 2049
6421 TTGGAGCTTTGAGGTCTGGGCGAGCGGGAGACCTGCTGGCAGAGTGTAGTGGGCCCTCC 6480
2050 ProProLeuAlaArgAlaTyrSerPheTrpGlyGlnSerSerThrGlnAlaGlnGlnHis 2069
6481 CGCCCTCCCTGGCCCGGCCCTACTCTTTCTGGGGCAGTCAAGTACCAGGACAGAGCAGC 6540
2070 SerArgSerHisSerLysIleSerLysHisMetThrProProAlaProCysProGlyPro 2089
6541 TCCCGCAGCCACAGCAAGATCTCCAAGCACATGATCCCGCCGCGCCCTTGCCAGGCCCA 6600
2090 GluProAsnTrpGlyLysGlyProProGluThrArgSerSerLeuGluLeuAspThrGlu 2109
6601 GAACCCAACTGGGGCAAGGGCCCTCCAGAGACCAGAGAGCAGTGTAGAGTTGGACAGGAG 6660
2110 LeuSerTrpIleSerGlyAspLeuLeuProProGlyGlyGlnGluProProSerPro 2129
6661 CTGAGCTGGATTTTCAGAGACCTCTCTGCCCCCTGGCGCCAGGAGGCCCTCCCA 6720
2130 ArgAspLeuLysLysCysTyrSerValGluAlaGlnSerCysGlnArgArgProThrSer 2149
6721 CGGAGCTGAAGAAGTGTACAGCTGGAGGCCCGCAGAGCTGCCAGGCGCGCCCTAGCTCC 6780
2150 TrpLeuAspGluGlnArgHisSerIleAlaValSerCysLeuAspSerGlySerGln 2169
6781 TGCTGGATGAGCAGAGGAGACACTCTATCGCTGAGCTGCTGGACAGCGCTCCCA 6840
2170 ProHisLeuGlyThrAspProSerAsnLeuGlyGlyGlnProLeuGlyGlyProGlySer 2189
6841 CCCACCTGGCACAGACCCCTCTAACCTTGGGGCGCCAGCTCTTGGGGCGCTGGGAGC 6900
2190 ArgProLysLysLysLeuSerProProSerIleThrIleAspProProGluSerGlnGly 2209
6901 CGGCCCAAGAAAAAATCTAGCCCGCTGTATCATCATTAGACATAGACATAGACATAGACAT 6960
2210 ProArgThrProProSerProGlyIleCysLeuArgArgAlaProSerSerAspSer 2229
6961 CCTCGAGACCCCGCCCGCCCTGATCTGCTCTCGGAGGAGGCTCGCTCCAGGACTCC 7020
2230 LysAspProLeuAlaSerGlyProProAspSerMetAlaAlaSerProSerProLysLys 2249
7021 AAGGATCCCTTGGCTCTGGCCCTGCGCCCTGACAGCATGGCTGCTCGCCCTCCCAAGAAA 7080
2250 AspValLeuSerLeuSerGlyLeuSerSerAspProAlaAspLeuAspPro 2266
7081 GATGTGCTGATCTCTCCGGTTTATCTCTGTGACCCAGCAGCTGGACCCC 7131

RESULT 4

ADS16298 standard; DNA; 7648 BP.

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Human voltage-dependent alpha 1G subunit calcium channel (CACNA1G) DNA.
Voltage-dependent ion channel; drug candidate;
aberrant electrical activity; muscle contraction; epilepsy; arrhythmia;
anticonvulsant; antiarrhythmic; human; alpha 1G subunit; ds.

Homo sapiens.

US2004175761-A1.

09-SEP-2004.

PF 01-MAR-2003; 2003US-003771139.
 XX
 PR 01-MAR-2003; 2003US-003771139.
 XX
 PA (MACK/) MACKINNON R.
 PA (MACK/) MACKINNON A L.
 PA (JIAN/) JIANG Y.
 PA (RUTA/) RUTA V.
 XX
 PI Mackinnon R, Mackinnon AL, Jiang Y, Ruta V;
 XX
 DR WPI; 2004-642122/62.
 DR REFSEQ; NM_018896.
 XX
 XX Screening drug candidates that target voltage dependent ion channel
 PT protein, involves contacting screening protein with chemical compound,
 PT which is drug candidate and determining whether chemical compound binds
 PT to screening protein.
 XX
 PS Disclosure; SEQ ID NO 10; 61bp; English.
 XX
 CC The invention relates to the composition of matter suitable for use in
 CC identifying chemical compounds that bind to voltage-dependent ion channel
 CC proteins. The composition comprises a screening protein that consists of
 CC an ion channel voltage sensor domain of the ion channel protein
 CC immobilised on a solid support. The invention is useful for identifying
 CC chemical compounds (drug candidate) that bind to voltage-dependent ion
 CC channel proteins. The drug candidate of the invention is utilised for
 CC treating a condition mediated by aberrant electrical activity that
 CC initiates uptake or release of neurotransmitters and contraction of
 CC muscles. The drug candidate of the invention is also utilised for
 CC treating epilepsy and arrhythmia. The present sequence is a voltage-
 CC dependent calcium channel DNA.
 XX
 SQ Sequence 7648 BP; 1492 A; 2419 C; 2205 G; 1532 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 0 Length: 7648
 Score: 11815.50 Matches: 2264
 Percent Similarity: 95.29% Conservative: 1
 Best Local Similarity: 95.25% Mismatches: 1
 Query Match: 99.26% Indels: 111
 DB: 13 Gaps: 2
 US-09-611-257A-37 (1-2266) x ADS16298 (1-7648)
 QY 1 MetAspGluGluGluAspGlyAlaGluGluSerGlyGlnProArgSerPheMet 20
 DB 1 ATGACGAGGAGGAGGATGGAGCGGGCCCGGAGGATCGGACAGCCCGGAGCTTCATG 60
 QY 21 ArgLeuAsnAspLeuSerGlyAlaGlyGlyArgProGlyProGlySerAlaGluLysAsp 40
 DB 61 CGGCTCAACGACCTGTTCGGGGCGGGGGCGGGCGGGGGCGGGGTCAGCAGAGAAAGGAC 120
 QY 41 ProGlySerAlaAspSerGluAlaGluGlyLeuProTyrProAlaLeuAlaProValVal 60
 DB 121 CCGGGCAGCGGAGCTCCGAGCGGAGGGGCTGCCGTACCCGGCGCTGGCCCGGGTGT 180
 QY 61 PhePheTyrLeuSerGlnAspSerArgProArgSerTyrPheLeuArgThrValCysAsn 80
 DB 181 TTCTTCTACTTGACGACGACAGCGCCCGGGAGCTGGTGTCTCCGACCGCTCTGTAAC 240
 QY 81 ProTrpPheGluArgIleSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMet 100
 DB 241 CCCTGGTTGAGCGCATCAGCATGTGGTTCATCTTCTCACTCGGTGACCTCGGCATG 300
 QY 101 PheArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPhe 120
 DB 301 TTCGGGCATCGGAGGACATCCCTGTGACTCCAGCGGCTCCCGGATCCTCGAGCGCTTT 360
 QY 121 AspAspPheIlePheAlaPhePheAlaValGluMetValValLysMetValAlaLeuGly 140
 DB 361 GATGACTTCATCTTTGGCCCTCTTTTGGCCGTGGAGATGGTGGTGAAGATGGTGGCCCTTGGGC 420
 QY 141 IlePheGlyLysLysCysTyrLeuGlyAspThrTrpAsnArgLeuAspPhePheIleVal 160
 DB 421 ATCTTTGGGAAAAAGTGTACCTGGGACACACTTGGAAACCGGCTTGACTTTTTCATCGTC 480
 QY 161 IleAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArg 180
 DB 481 ATCGCAGGATGCTGGAGTACTCGCTGGACTCGAGAACGTCAGCTTCTCAGCTGTCAAG 540
 QY 181 ThrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeu 200
 DB 541 ACAGTCCGTGTGCTGGACCGCTCAGGGCCATTAAACCGGGTGCCAGCATGGCATCTTT 600
 QY 201 ValThrLeuLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePhe 220
 DB 601 GTCACTGTGTGTGATACGCTGCCATGCTGGGCAACGCTCCTGCTCTGCTCTCTTC 660
 QY 221 ValPhePheIlePheGlyIleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArg 240
 DB 661 GTCTTCTTCATCTTCGGCATCGTGGCGTCCAGCTGTGGCGAGGCTGCTTCGGAACCGA 720
 QY 241 CysPheLeuProGluAsnPheSerLeuProLeuSerValAspLeuGluArgTyrTyrGln 260
 DB 721 TGCTTCTTACTGAGATTTTTCAGCTCCCTCTGAGCGTGGACCTGGAGCGCTATTACGAG 780
 QY 261 ThrGluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArg 280
 DB 781 ACAGAGAACGAGGATGAGAGCCCTTCTATCTGCTCCAGCCAGCGAGAACGGCATGGCG 840
 QY 281 SerCysArgSerValProThrLeuArgGlyAspGlyGlyGlyProProCysGlyLeu 300
 DB 841 TCCTGCAAGAGCGTGGCCACGCTCGGGGGGACCGGGGGCGGTGGCCACCTTGGGGTCTG 900
 QY 301 AspTyrGluAlaTyrAsnSerSerSerAsnThrThrCysValAsnTrpAsnGlnTyrTyr 320
 DB 901 GACTATGAGGCTTACACAGCTCCAGCAACACCACTGTGTCACTGGAACCACTACTACTAC 960
 QY 321 ThrAsnCysSerAlaGlyGluHisAsnProPheLysGlyAlaIleAsnPheAspAsnIle 340
 DB 961 ACCAACTGTCTCAGCGGGGAGCACAACCCCTTCAAGGGCGGCATCAACTTTGACAACTT 1020
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 QY 361 TyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleIle 380
 DB 1081 TACTTTGTGATGGATGCTCATTCCTTCTACAAATTTCACTTCTTCTCTCTCTCTCATC 1140
 QY 381 ValGlySerPhePheMetIleAsnLeuValValIleAlaThrGlnPheSerGlu 400
 DB 1141 GTGGGCTCTTCTTTCATGATCAACCTGTGCTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1200
 QY 401 ThrIysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAla 420
 DB 1201 ACCAAGCAGCGGGAAGACAGCTGATCGGAGCAGCGTGTGGCGTTCCTGTCCAACGCC 1260
 QY 421 SerThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLysTyrLeu 440
 DB 1261 AGCACTCTGGCTAGCTTCTCTGAGCCCGGAGCTGCTATGAGGAGCTGCTCAAGTACCTG 1320
 QY 441 ValTyrIleLeuArgLysAlaIleArgArgLeuAlaGlnValSerArgAlaAlaGlyVal 460
 DB 1321 GTGTACATCTTGTGAAGGAGCCCGGAGCTGGCTCAGGTCTCTCGGGCAGCAGGTGTG 1380
 QY 461 ArgValGlyLeuLeuSerSerProAlaProLeuGlyGlnGluThrGlnProSerSer 480
 DB 1381 CGGGTTGGGTGTCTCAGACGCCAGCAGCCCTCTCGGGGGCCAGGAGATCCAGCCAGCAGC 1440
 QY 481 SerCysSerArgSerHisArgArgLeuSerValHisIleLeuValHisHisHisHis 500
 DB 1441 AGCTGTCTCTGCTTCCACCCCGGCTTATCCGTCCACCACTTGGTGGACCAACCAACCA 1500

QY 501 HieHisHisTyrHisLeuGlyAsnGlyThrLeuArgAlaProArgAlaSerProGlu 520
DB 1501 CATCACCACTACCACTGGGCAATGGGAGCTCAGGGCCCCCGGGCAGCCCGAG 1560
QY 521 IleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProSerThrPro 540
DB 1561 ATCCAGGACAGGAGTGCATGGGTCCCGAGGCTCATGTGCCACCACTCGAGCCCT 1620
QY 541 AlaLeuSerGlyAlaProProGlyGlyAlaGluSerValHisSerPheTyrHisAlaAsp 560
DB 1621 GCCCTCTCCGGGGCCCCCTGGTGGCGCAGAGCTGTGCACAGCTTCTACCAATGCCGAC 1680
QY 561 CysHisLeuGluProValArgCysGlnAlaProProProArgSerProSerGluAlaSer 580
DB 1681 TGCCACTTAGAGCCAGTCCGCTGCCAGGGCCCCCTCCAGGTCCCATCTGAGGCATCC 1740
QY 581 GlyArgThrValGlySerGlyLysValTyrProThrValHisThrSerProProProGlu 600
DB 1741 GGCAGGACTGTGGGCAGCGGAGGTGTATCCCACTCCAGCCGTCACACAGCCCTCCACCGGAG 1800
QY 601 ThrLeuLysGluLysAlaLeuValGluValAlaAlaSerSerGlyProThrLeuThr 620
DB 1801 ACGCTGAAGGAGAGGACATAGTAGAGGTGCTCCAGCTCTGGGCCCCCAACCTCAC 1860
QY 621 SerLeuAsnIleProProGlyProTyrSerSerMetHisLysLeuLeuGluThrGlnSer 640
DB 1861 AGCCTCAACATCCCAACCGGGCCCTACAGCTCCATGCACAAAGCTGTGGAGACACAGT 1920
QY 641 ThrGlyAlaCysGlnSerSerCysLysIleSerSerProCysLysLysAlaAspSerGly 660
DB 1921 ACAGTGCTGCCAAAGCTCTTGAAGATCTTCCAGCCCTTGCCTTGAAGCAGACAGTGA 1980
QY 661 AlaCysGlyProAspSerCysProTyrCysAlaArgAlaGlyAlaGlyGluValGluLeu 680
DB 1981 GCCTGTGTGCAGACAGTGCCTCTACTGTGCCCGGGCGGAGGAGGTGGAGCTC 2040
QY 681 AlaAspArgGluMetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAla 700
DB 2041 GCCGACCGTGAATGCCTGACTCAGACAGCGAGGAGCTTATGATGTTTACACAGGATGCC 2100
QY 701 GlnHisSerAspLeuArgAspProHisSerArgGlnArgSerLeuGlyProAspAla 720
DB 2101 CAGCACAGCAGACCTCCGGGACCCCAAGCGCGGCAACAGGAGCTTGGGCCAGATGCA 2160
QY 721 GluProSerValLeuAlaPheTrpArgLeuIleCysAspThrPheArgLysIleVal 740
DB 2161 GAGCCCACTGTGTGTGGCCCTTCTGGAGGCTATCTGTGCACCTTCCGNAAGTTGTG 2220
QY 741 AspSerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerMet 760
DB 2221 GACAGCAAGTACTTTGGCCGGGGAATCATGATGCCATCTCTGGTCAACACACTCAGCATG 2280
QY 761 GlyIleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnIle 780
DB 2281 GGCAATCGAATACCAAGCAGCAGCCCGAGAGCTTACCAACGCCCTTAGAAATCAGCAACATC 2340
QY 781 ValPheThrSerLeuPheAlaLeuGluMetLeuLysLeuLeuValTyrGlyProPhe 800
DB 2341 GTCTTACCAGCTCTTTGGCCCTGGAGNATGTGTGAGTGTCTGTGTATGTGTCCCTTT 2400
QY 801 GlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleValIleSerValTrp 820
DB 2401 GGCTATACCAAGAAATCCCTACAAATCTTCATGTGTGTCTTGTGTGTGTGTGTGTGTGTG 2460
QY 821 GluIleValGlyGlnGlnGlyGlyLeuSerValLeuArgThrPheArgLeuMetArg 840
DB 2461 GAGATCGTGGGCCAGCAGCGGGGGCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2520
QY 841 ValLeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetLys 860
DB 2521 GTGCTGAAGCTGT 2580
QY 861 ThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePheSer 880

DB 2581 ACCATGGACAACGTGGCCACCTTCTGCATGCTGCTTATGCTCTTCTCATCTTCTTCTCAGC 2640
QY 881 IleLeuGlyMetHisLeuPheGlyCysLysPheAlaSerGluArgAspGlyAspThrLeu 900
DB 2641 ATCCTGGGATGATCTCTTGGCTGCAAGTTTGGCTCTGAGCGGATGGGACACCTG 2700
QY 901 ProAspArgLysAsnPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIleLeu 920
DB 2701 CCAGACCGGAGAAATTTTGCCTTCTGGCCATCGTCACTGTCTTTCAGATCCTG 2760
QY 921 ThrGlnGluAspTrpAsnLysValLeuTyrAsnGlyMetAlaSerThrSerSerTrpAla 940
DB 2761 ACCCAGGAGACTGGAAACAAAGTCTCTACAATGGTATGGCTCCACGCTGCTGGGCG 2820
QY 941 AlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuVal 960
DB 2821 GCCCTTATTTTCAATTCGCCCTCATGACCTTCGGCACTACGTGCTCTTCAATTTGCTGTC 2880
QY 961 AlaIleLeuValGluGlyPheGlnAlaGluGluIleSerLysArgGluAspAlaSerGly 980
DB 2881 GCCATTTCTGTGGAGGCTTCCAGCGGAGGAAATCAGCAACCGGAAGATCGAGTGA 2940
QY 981 GlnLeuSerCysIleGlnLeuProValAspSerGlnGlyClyAspAlaAsnLysSerGlu 1000
DB 2941 CAGTTAAGCTGTATTTCAGCTGCTGTGACTCCCGAGGGGAGATGCCAACAGTCCGAA 3000
QY 1001 SerGluProAspPhePheSerProSerLeuAspGlyAspGlyAspArgLysLysCysLeu 1020
DB 3001 TCAGAGCCCAATTTCTTCTCACCCAGCTGGATGGTATGGGACAGGAAGATGCTTG 3060
QY 1021 AlaLeuValSerLeuGlyGluHisProGluLeuArgLysSerLeuLeuProLeuIle 1040
DB 3061 GCCTTGTGTCTTGGGAGAGCACCCGAGCTCGGAAGAGCTGTGTCGCCCTCTCATC 3120
QY 1041 IleHisThrAlaAlaThrProMetSerLeuProLysSerThrSerThrGlyLeuGlyGlu 1060
DB 3121 ATCCACAGCCGCCACACCATGTCTGCTGCCCAAGAGCACCGAGCTTGGGGCGAG 3180
QY 1061 AlaLeuGlyProAlaSerArgArgThrSerSerSerGlySerAlaGluProGlyAlaAla 1080
DB 3181 GCCTTGGGCCCTGCTGCTGCGCCGCCACAGCAGCAGCGGTTCGCGAGAGCTTGGGGCGCC 3240
QY 1081 HisGluMetLysSerProProSerAlaArgSerSerProHisSerProTrpSerAlaAla 1100
DB 3241 CACGAGATGAAGTCAACGCCCGAGCGCTCTCCGACAGCCCTCGAGCGCTGCA 3300
QY 1101 SerSerTrpThrSerArgArgSerSerArgAsnSerLeuGlyValArgAlaProSerLeuLys 1120
DB 3301 AGCAGCTGGACCAAGAGCGCTCCAGCGGAACAGCCCTCGGCCGTGACCCAGCTGAAG 3360
QY 1121 ArgArgSerProSerGlyGluArgArgSerLeuLeuSerGlyGluGlyGlnGluSerGln 1140
DB 3361 CGGAGAACCCCAAGTGGAGAGCGCGGTCTCTGTGTGGGAGAGGCCAGGAGCCAG 3420
QY 1141 AspGluGluGluSerSerGluGluArgAlaSerProAlaGlySerAspHisArgHis 1160
DB 3421 GATGAAGAGGAGAGCTCAGAAGAGGAGCGGCCAGCCCTCGGGCAGTGCATCGCCAC 3480
QY 1161 ArgGlySerLeuGluArgGluAlaLysSerPheAspLeuProAspThrLeuGlnVal 1180
DB 3481 AGGGGGTCTTGGAGCGGAGGCCAAGATTTCTTTTACCTGCCAGACACACTGCAGGTG 3540
QY 1181 ProGlyLeuHisArgThrAlaSerGlyArgGlySerAlaSerGluHisGlnAspCysAsn 1200
DB 3541 CCAGGGCTGCATCGCACTGCCAGTGGCCGAGGGTCTCTTCTTTCAGCACACAGGAGTCAAT 3600
QY 1201 GlyLysSerAlaSerGlyArgLeuAlaArgAlaLeuArgProAspAspProProLeuAsp 1220
DB 3601 GGCAAGTCCGCTTTCAGGGCGCTTGGGCCCGGCTGTGAGTGCATGATGATGATGATGAT 3660
QY 1221 GlyAspAspAlaAspAspGluGlyAsnLeuSerLysGlyGluArgValArgAlaTrpIle 1240

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Qy 1 MetAspGluGluAspGlyAlaGlyAlaGluGluSerGlyGlnProArgSerPheMet 20
Db 1 ATGCACGAGGAGGAGTGGAGCGGGCCCGGAGGATCGGACACGCCCGGAGCTTCATG 60
Qy 21 ArgLeuAsnAspLeuSerGlyAlaGlyGlyArgProGlyProGlySerAlaGluLysAsp 40
Db 61 CGGCTCAACGACCTGTGCGGGGGCGGGGGCGGGGGCGGGGGCTCAGCAGAAAGGAC 120
Qy 41 ProGlySerAlaAspSerGluAlaGluGlyLeuProTyrProAlaLeuAlaProValVal 60
Db 121 CCGGGCAGCGGGACTCCGAGCGGGAGGGGGTGGCTACCGGGCGCTGGCCCCGGTGGTT 180
Qy 61 PhePheTyrLeuSerGlnAspSerArgProArgSerTyrCysLeuArgThrValCysAsn 80
Db 181 TTCTTCTACTTGAAGCAGACAGCGCGCGCGGAGCTGGTGTCTCCGACCGGTCTGTAAC 240
Qy 81 ProTyrPheGluArgIleSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMet 100
Db 241 CCCTGGTTGAGCGCATCAGCATGTTGGTCACTTCTTCAACTCGGTGACCCCTGGGCATG 300
Qy 101 PheArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPhe 120
Db 301 TTCGGCCATCGGAGGACATCGCTGTGACTCCACAGCGCTCCGGATCCTCGACGGCCTTT 360
Qy 121 AspAspPheIlePheAlaPheAlaValGluMetValValLysMetValAlaLeuGly 140
Db 361 GATGACTTCACTTTGCGCTCTTTGGCGTGAGATGGTGGTGAAGATGGTGGCTTGGGC 420
Qy 141 IlePheGlyLysLysCysTyrLeuGlyAspThrTrpAsnArgLeuAspPheIleVal 160
Db 421 ATCTTTGGGAAAAAGTGTACTCGGAGACACTTGGAAACCGGCTTGACTTTTTCATCGTC 480
Qy 161 IleAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArg 180
Db 481 ATCGAGGGATGCTGGAGTACTCGCTGGACTGCTGAGACGTCAGCTTCTCAGCTGTCCAGG 540
Qy 181 ThrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeu 200
Db 541 ACAGTCCGTGTGCTGCGACCGCTCAGGGCCATTAAACCGGGTCCCGAGCATCGCATCCTT 600
Qy 201 ValThrLeuLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePhe 220
Db 601 GTCAAGTGTGCTGGATACGCTGCCATGCTGGGCAACGCTGCTGCTGCTGCTGCTCTTC 660
Qy 221 ValPhePheIlePheGlyIleValGlyValGlnLeuTyrAlaGlyLeuLeuArgAsnArg 240
Db 661 GTCTTCTTCACTTCGGCATCGTGGCGTCCAGCTGTGGGCGAGGCTGCTTCGGAAACCGA 720
Qy 241 CysPheLeuProGluAsnPheSerLeuProLeuSerValAspLeuGluArgTyrTyrGln 260
Db 721 TGCTTCTTACCTGAGAAATTCAGCTCCCTCCCTGAGCGTGGACCTGGAGCGCTATTACCAG 780
Qy 261 ThrGluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArg 280
Db 781 ACAGAGAACGAGGATGAGAGCCCTTCACTGCTCCAGCCACGCGACGAGCAACGCGATGCGG 840
Qy 281 SerCysArgSerValProThrLeuArgGlyAspGlyGlyGlyGlyProProCysGlyLeu 300
Db 841 TCCTGCAAGCGGTGCCCCCGCTGGCGGGGACCGGGGGCGGTGGCCCCACCTTTCGGGTCTG 900
Qy 301 AspTyrGluAlaTyrAsnSerSerAsnThrThrCysValAsnTrpAsnGlnTyrTyr 320
Db 901 GACTATGAGCGCTACAACAGCTCCAGCAACACCACTCTGTGTCACTGGAAACGAGTACTAC 960
Qy 321 ThrAsnCysSerAlaGlyGluHisAsnProPheLysGlyAlaIleAsnAspAsnIle 340
Db 961 ACCAACTCTCAGCGGGGGAGCACAAACCCCTTCAAGGGCGGCATCAACTTTGACAAACATT 1020
Qy 341 GlyTyrAlaTrpIleAlaIlePheGlnValIleThrLeuGluGlyTyrValAspIleMet 360
Db 1021 GGCTATGCTGATCGCCATCTTCCAGGTCAACGCTGGAGGGCTGGGTGCACATCATG 1080
Qy 361 TyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIle 380
Db 1081 TACTTTGTGATGGATGCTCATTTCTTACAAATTTCACTACTTTCATCTCTCTCATCATC 1140
Qy 381 ValGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGlu 400
Db 1141 GTGGGCTCTTCTTTCATGATCAACTGTGCTGTGGTGGATGGCCACGAGTTCTTCAGAG 1200
Qy 401 ThrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAla 420
Db 1201 ACCAAGCAGCGGAAAGCCAGCTCATGCGGGAGCAGCGGTGTGCGGTTCTTGTCCAACGCC 1260
Qy 421 SerThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLeuLysTyrLeu 440
Db 1261 AGCACCTTGGCTAGCTTCTTGTAGCCCGCAGCTGTATGAGGAGCTGCTCAAGTACCTG 1320
Qy 441 ValTyrIleLeuArgLysAlaAlaArgArgLeuAlaGlnValSerArgAlaAlaGlyVal 460
Db 1321 GTGTACATCTTCTGTAAGGACGCCCGCAGGCTGGCTCAGGTCTCTCGGGCAGCAGGTGTG 1380
Qy 461 ArgValGlyLeuLeuSerSerProAlaProLeuGlyGlyGlnGluThrGlnProSerSer 480
Db 1381 CGGCTTGGCTGTCTCAGCAGCCAGCACCTCTCGGGGCCAGAGACCCAGCCAGCAGC 1440
Qy 481 SerCysSerArgSerHisArgArgLeuSerValHisLeuValHisHisHisHis 500
Db 1441 AGCTGCTCTCGCTCCACCGCGCTATCCGTCACCACTTGGTGGTGCACACCAACCCAC 1500
Qy 501 HisHisHisHisTyrHisLeuGlyAsnGlyThrLeuArgAlaProArgAlaSerProGlu 520
Db 1501 CATCACCACTACTACCCTGGGCAATGGGACGCTCAGGGCCCCCGGGCCAGCCCGGAG 1560
Qy 521 IleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProProSerThrPro 540
Db 1561 ATCCAGGACAGGATGCCAATGGTCCCGCGGCTCATGCTGCCACCACTCCAGCGCT 1620
Qy 541 AlaLeuSerGlyAlaProProGlyGlyAlaGluSerValHisSerPheTyrHisAlaAsp 560
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Qy 561 CysHisLeuGluProValArgCysGlnAlaProProProArgSerProSerGluAlaSer 580
Db 1681 TGCCACTTAGAGCAGTCCGCTGCGAGCGCCCCCTCCAGGTCCCCATCTGAGGACATCC 1740
Qy 581 GlyArgThrValGlySerGlyLysValTyrProThrValHisThrSerProProProGlu 600
Db 1741 GGCAAGACTGTGGCAGCGGGAAGGTGTATCCCACTGTCACACAGCGCTCCACCGGAG 1800
Qy 601 ThrLeuLysGluLysAlaLeuValGluValAlaAlaSerSerGlyProProThrLeuThr 620
Db 1801 ACCTGGAAGGAGAGGACACTAGTAGAGTGGTGCAGCTCTGGGCCCCCAACCTCCACC 1860
Qy 621 SerLeuAsnIleProProGlyProTyrSerSerMetHisLysLeuLeuGluThrGlnSer 640
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Qy 641 ThrGlyAlaCysGlnSerSerCysLysIleSerSerProCysLeuLysAlaAspSerGly 660
Db 1921 ACAGTGTCTGCCAAAGCTCTTTCAGATCTTCCAGCCCTTCTTGAAGAGACAGATGGA 1980
Qy 661 AlaCysGlyProAspSerCysProTyrCysAlaArgAlaGlyAlaGlyGluValGluLeu 680
Db 1981 GCCTGTGTCCAGACAGCTGCCCTTACTGTGCCGGGCGGGGAGGAGGTGGAGCTC 2040
Qy 681 AlaAspArgGluMetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAla 700
Db 2041 GCCCAGCGTGAATGCTCTGACTCAGACGAGGAGCGGTTATGATTTTCCACAGAGATGCC 2100
Qy 701 GlnHisSerAspLeuArgAspProHisSerArgArgGlnArgSerLeuGlyProAspAla 720
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QY 721 GluProSerValLeuAlaPheTrpArgLeuIleCysAspThrPheArgIlyIleVal 740
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 QY 761 GlyIleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnIle 780
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 QY 781 ValPheThrSerLeuPheAlaLeuGluMetLeuLysLeuValTyrGlyProPhe 800
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 QY 861 ThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePheSer 880
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 QY 981 GlnLeuSerCysIleGlnLeuProValAspSerGlnGlyValAspAlaAsnLysSerGlu 1000
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 QY 1041 IleHisThrAlaAlaThrProMetSerLeuProLysSerThrSerThrGlyLeuGlyGlu 1060
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 Db 3112 GCGCTGGGCCCTTGGTCTGCGCGCCGACCCAGCAGAGGGGTGCGCAGAGGCTGGGGCGGC 3171

QY 1081 HisGluMetLysSerProProSerAlaArgSerSerProHisSerProTrpSerAlaAla 1100
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 QY 1101 SerSerTrpThrSerArgArgSerSerArgAsnSerLeuGlyArgAlaProSerLeuLys 1120
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 QY 1141 AspGluGluGluSerSerGluGluGluArgAlaSerProAlaGlySerAspHisArgHis 1160
 Db 3352 GATGAAGAGGAGAGCTCAGAAGAGAGCGGGCCAGCTTCGGCGCAGTGCATTCGCCAC 3411
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 QY 1381 ArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeuLysLeu 1400
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 QY 1401 ValValGlnThrLeuMetSerSerLeuLysProIleGlyAsnIleValIleCysCys 1420
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 QY 1421 AlaPhePheIleIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPheVal 1440
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 QY 1441 CysGlnGlyGluAspThrArgAsnIleThrAsnLysSerAspCysAlaGluAlaSerTyr 1460

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Db 4312 CGGTGGGTCCGGCACAAGTACAACTTTGACAACTTTGGCCAGGCCCTGATGTCTCTGTTT 4371
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Qy ValAspGlnProIleMetAsnHisAsnProTrpMetLeuLeuTyPheIleSerPhe 1520
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Db 4552 CACAAGTGTCCGACAGCACAGAGAGAGAGAGGCCCGCGCGGGAGGAGAAAGCGCCTA 4611
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Qy ValLeuLysLeuLeuLysMetAlaValGlyMetArgAlaLeuLeuAspThrValMetGln 1720
Db 5032 GTGCTGAAGCTCTGAAGATGGCTGGGATGGCGGCTGCTGGACACCGTGTATGCAG 5091
Qy AlaLeuProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPhePheIlePheAla 1740
Db 5092 GCCCTGCCAGGTGGGGAACCTGGGACTTCTCTCATGTGTGTTGTTTTCATCTTTGCA 5151
Qy AlaLeuGlyValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGluGly 1760
Db 5152 GCTCTGGCGGTGGAGCTCTTTGGAGACCTGGAGTGTGACGAGACACACCCCTGTGAGGGC 5211
Qy LeuGlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgVal 1780
Db 5212 CTGGCCCTCATGCCACCTTTCCGNACTTTGGCATGGCTTCCTAACCCCTCTTCGAGTC 5271
Qy SerThrGlyAspAsnTrpAsnGlyIleMetLysAspThrLeuArgAspCysAspGlnGlu 1800
Db 5272 TCCAGAGTGACAAATGGAATGGCAATTATGAAGACACCCCTCCGAGACTGTGACCCAGGAG 5331
Qy SerThrCysTyAsnThrValIleSerProIleTyPheValSerPheValLeuThrAla 1820

Db 5332 TCCACCTGCTACAACACGGTCATCTCGCCTATCTACTTTGTGTCTCTTCTGCTGACGGCC 5391
Qy GlnPheValLeuValAsnValIleAlaValLeuMetLysHisLeuGluGluSerAsn 1840
Db 5392 CAGTTCTGTCTAGTCAACAGTGGTGTATCCCGCTGTGTATGAAGCACCTGGAGGAGCAAC 5451
Qy LysGluAlaLysGluAlaGluLeuGluAlaGluLeuGluLeuGluMetLysThrLeu 1860
Db 5452 AAGAGAGCCCAAGGAGGAGCGAGCTAGAGCTGAGCTGGAGCTGGAGATGAAGACCCCTC 5511
Qy SerProGlnProHisSerProLeuGlySerProPheLeuTrpProGlyValGluGlyPro 1880
Db 5512 AGCCCCCAGCCCCACTGGCCACTGGGCAGCCCCCTTCTTGGCCTGGGGTCCAGGGGCCCC 5571
Qy AspSerProAspSerProLysProGlyAlaLeuHisProAlaAlaHisAlaArgSerAla 1900
Db 5572 GACAGCCCGACAGACCCCAAGCCTGGGCTCTGCACCCAGCGGGCCACCGCAGATCAGCC 5631
Qy SerHisPheSerLeuGluHisProThrMetGlnProHisProThrGluLeuProGlyPro 1920
Db 5632 TCCCACTTTTCCCTGGAGCACCCCAAGATGAGCGGCCCAACCCAGCGAGCTGCCAGGACCA 5691
Qy AspLeuLeuThrValArgLysSerGlyValSerArgThrHisSerLeuProAsnAspSer 1940
Db 5692 GACTTACTGACTGTGCGAAGTCTGGGTGAGCCGACGACACTCTCTGCCCAATGACAGC 5751
Qy TyrMetCysArgHisGlySerThrAlaGluGlyProLeuGlyHisArgGlyTrpGlyLeu 1960
Db 5752 TACATGTGTGGCATGGAGCACTGCCAGGGGCCCTCTGGGACACAGGGCTGGGGGCTC 5811
Qy ProllysAlaGlnSerGlySerValHisSerGlnProAlaAspThrSerTy 1980
Db 5812 CCCAAAGCTCAGTCAGCTCCGTCTTGTCCGTTCACCTCCAGCCAGCAGATACCAAGTAC 5871
Qy IleLeuGlnLeuProLysAspAlaProHisLeuLeuGlnProHisSerAlaProThrTrp 2000
Db 5872 ATCTCTGAGCTTCCAAAGATGACCTCATCTGTCCAGCCCCACAGCGCCCAACCTGG 5931
Qy GlyThrIleProLysLeuProProGlyArgSerProLeuAlaGlnArgProLeuArg 2020
Db 5932 GGCACCATCCCAAACTGCCCCCAAGGAGCTCCCTCTTGGTCTCAGAGCCACTCAGG 5991
Qy ArgGlnAlaIleAlaIleArgThrAspSerLeuAspValGlnGlyLeuGlySerArgGluAsp 2040
Db 5992 CGCCAGCAGCAATTAAGGACTCCTCTTGGACCTTCCAGGCTCTGGGCGAGCCGGGAAGAC 6051
Qy LeuLeuAlaGluValSerGlyProSerProProLeuAlaArgAlaTySerPheTrpGly 2060
Db 6052 CTGCTGGCAGAGGTGAGTGGGCCCTCCCGCCCTCTGGCCGGGCTACTCTTTCTGGGGC 6111
Qy GlnSerSerThrGlnAlaGlnGlnHisSerArgSerHisSerLysIleSerLysHisMet 2080
Db 6112 CAGTCAAGTACCCAGGCACAGCAGCACTCCCGCAGCCACAGCAAGATCTCCAAGCACAATG 6171
Qy ThrProAlaProCysProGlyProGluProAsnTrpGlyLysGlyProProGluThr 2100
Db 6172 ACCCGCCAGCCCTTCCCGAGGCCCAACCCCAACTGGGGCAAGGGCCCTCCAGAGACC 6231
Qy ArgSerSerLeuGluLeuAspThrGluLeuSerTrpIleSerGlyAspLeuLeuProPro 2120
Db 6232 AGAAGCAGCTTAGAGTTGGACACGAGCTGAGCTGGATTTTCAGGAGACCTCTCTGCCCT 6291
Qy GlyGlyGlnGluProProSerProArgAspLeuLysLysCysTySerValGluAla 2140
Db 6292 GGCAGCCAGGAGGAGCCCACTCCCAAGGAGCTGAGTGAAGAGTGTCTACAGCTGGAGGCC 6351
Qy GlnSerCysGlnArgArgProThrSerTrpLeuAspGluArgArgHisSerIleAla 2160
Db 6352 CAGAGCTGCCAGCCCGCCCTACGTCTCTGGCTGATGAGCAGAGAGACACTCTATTCGCC 6411
Qy ValSerCysLeuAspSerGlySerGlnProHisLeuGlyThrAspProSerAsnLeuGly 2180
Db 6412 GTCAGCTGCCCTGGACAGCGGCTCCCAACCCCACTGGGACACAGACCCCTCTTAACCTTGGG 6471

QY 2181 GlycInProLeuGlyGlyProGlySerArgProLySylsLeuSerProProSerIle 2200
Db 6472 GGCAGGCTCTTGGGGGCTGGAGCGCGCCCAAGAAAACTCAGCCGCTAGTATC 6531
QY 2201 ThrIleAspProGluSerGlnGlyProArgThrProProSerProGlyIleCysLeu 2220
Db 6532 ACCATAGACCCCGGAGCCAGGCTCTGGACCCCGCCAGCCCTGGTATCTGCCCTC 6591
QY 2221 ArgArgAlaProSerSerAspSerLysAspProLeuAlaSerGlyProProAspSer 2240
Db 6592 CGGAGGAGGCTCGTCCAGGACTCCAGGATCCCTTGGCCCTCTGGCCCGCCCTGACAGC 6651
QY 2241 MetAlaAspProSerProLySylsAspValLeuSerLeuSerGlyIleSerSerAsp 2260
Db 6652 ATGGCTGCTCGCCCTCCCAAGAAAGATGTGCTGAGTCTCTCCGGTTTATCCTCTGAC 6711
QY 2261 ProAlaAspLeuAspPro 2266
Db 6712 CCAGAGACCTGGACCCC 6729
RESULT 6
ID AAX83481 standard; cDNA; 6750 BP.
XX AAX83481;
AC AAX83481;
XX 07-DEC-1999 (first entry)
DT Human T-type voltage-gated Ca channel alpha-1-G (hCavT1a) cDNA.
DE Human; T-type voltage-gated calcium channel; membrane; pore; ion;
KW activation; current; rat; screen; drug; cardiomyopathy; epilepsy; ds.
XX Homo sapiens.
XX WO9299847-A1.
XX 17-JUN-1999.
XX 30-OCT-1998; 98WO-US023161.
XX 05-DEC-1997; 97US-00985809.
XX (LOYO) UNIV LOYOLA CHICAGO.
XX Perez-Reyes E, Cribbs LL;
PI WPI; 1999-394972/33.
DR P-PSDB; AAV14586.
XX New T-type voltage-gated calcium channels.
PT Disclosure; Page 31-40; 138pp; English.
PS
XX This sequence represents the coding region for a human T-type voltage-gated calcium (Ca) channel alpha-1-G designated hCavT1a. Voltage gated channels are membrane bound glycosylated proteins formed of several subunits. The large alpha subunits form a pore in the membrane that is selective for a given ionic species. Each alpha subunit contains 4 domains (I, II, III and IV) and each domain contains 6 putative transmembrane helical segments (S1-S6). T-type Ca channels are activated at a lower voltage than L- or N-type channels. Characteristics of T-type channels include short current time, slow activation kinetics near threshold, fast inactivation kinetics and slow tail current. The sequences AAX83481-X83492 represent novel T-type voltage-gated Ca channel genes from humans and rats. Each of the novel Ca-channels contains a putative IVS4 region comprising the amino acid sequence AAY14598. Cells expressing the T-type voltage-gated calcium channel proteins can be used to screen for drugs which affect calcium channels. Methods are also disclosed for treating a disease or disorder associated with a deficiency in a native T-type calcium channel nucleic acid, e.g. to treat cardiomyopathy, epilepsy, etc

XX SQ Sequence 6750 BP; 1290 A; 2170 C; 1306 G; 1306 T; 0 U; 0 Other;
Alignment Scores: 0 Length: 6750
Pred. No.: 11741.00 Matches: 2241
Score: 98.64% Conservatives: 1
Percent Similarity: 98.59% Mismatches: 1
Best Local Similarity: 98.63% Indels: 30
Query Match: 2 Gaps: 2
DB: 2
US-09-611-257A-37 (1-2266) x AAX83481 (1-6750)
QY 1 MetAspGluGluAspGlyAlaGluSerGlyGlnProArgSerPheMet 20
Db 1 ATGGACGAGGAGGATGGAGCGCGCGCGGAGGAGTCCGGACAGCCCGAGCTTCATG 60
QY 21 ArgLeuAsnAspLeuSerGlyAlaGlyGlyArgProGlyProGlySerAlaGlyLysAsp 40
Db 61 CGGCTCAACGACCTGTCCGGGGCCCGGGGGCGCGGGGCGGGGTGACGAGAAAGGAC 120
QY 41 ProGlySerAlaAspSerGluAlaGluGlyLeuProTyrProAlaLeuAlaProValVal 60
Db 121 CCGGGCAGCGCGGACTCCGAGGCGGAGGGGCTGCGGTACCCGGCGCTGCCCGGTGTT 180
QY 61 PhePheTyrLeuSerGlnAspSerArgProArgSerTyrCysLeuArgThrValCysAsn 80
Db 181 TTCTTCTACTTGAGCCAGGACAGCCCGCGGAGCTGGTGTCTCCGACGGTCTGTAAAC 240
QY 81 ProTyrPheGluArgIleSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMet 100
Db 241 CCTGTGTTTGGAGCCATCAGCATGTGTGTCTCTCACTGGGTGACCTGGGCGATG 300
QY 101 PheArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPhe 120
Db 301 TTCGGCCCATGCGAGGACATCGCTGTGACTCCGAGCGCTGCCGATCTCGAGGCTTT 360
QY 121 AspAspPheIlePheAlaPheAlaValGluMetValValLysMetValAlaLeuGly 140
Db 361 GATGACTTCTATCTTTCCTTCTTTCCTTTCCTTTCCTTTCCTTTCCTTTCCTTTCCT 420
QY 141 IlePheGlyLysCysTyrLeuGlyAspThrTyrAsnArgLeuAspPhePheIleVal 160
Db 421 ATCTTTGGGAAAAGTGTACCTGGGAGACACTTGGAAACCGGCTTGACTTTTTCATCGTC 480
QY 161 IleAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArg 180
Db 481 ATCGCAGGATGCTGGAGTACTCGCTGGACCTGCAGAACGCTCAGCTTCTCAGCTGTACG 540
QY 181 ThrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeu 200
Db 541 ACAGTCCGTGTGTGCGACCGCTCAGGGCCATTAAACCGGGTCCCGAGCATGCGCATCCTT 600
QY 201 ValThrLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePhe 220
Db 601 GTCAGCTTGTCTGGATACGCTGCCCATCTCGGCAACGCTCCTGTGCTGTCTGCTTCTTC 660
QY 221 ValPhePheIlePheGlyIleValGlyValGlnLeuTyrAlaGlyLeuLeuArgAsnArg 240
Db 661 GTCTTCTTCTTCTTTCGGCATCGTCCGGCTCAGCTGTGGCAGGGGCTGCTTCGGAACCGA 720
QY 241 CysPheLeuProGluAsnPheSerLeuProLeuSerValAspLeuGluArgTyrTyrGln 260
Db 721 TGCTTCTTCTTCTTTCAGGATTTTCAGCTTCCCTGAGCTGGACCTGGAGCGCTATTACAG 780
QY 261 ThrGluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArg 280
Db 781 ACAGAAACGAGGATGAGAGCCCTTCTATCTGCTCCAGCCACCGAGAACCGCATCGCG 840
QY 281 SerCysArgSerValProThrLeuArgGlyAspGlyGlyGlyProProCysGlyLeu 300
Db 841 TCCTGCAAGACGCTGCCCAACGCTGCGGGGAGCGGGGCGGTGGCCACCTTGGGCTGTG 900

QY 301 AspTyrGluAlaTyrAsnSerSerSerAsnThrThrCysValAsnTrpAsnGlnTyrTyr 320
DB 901 GACTATGAGGCTTACACAGCTCCAGCAACACCCTGTGTCAACTGGAAACAGTACTAC 960
QY 321 ThrAsnCysSerAlaGlyGluHisAsnProPheLysGlyAlaIleAsnPheAsnIle 340
DB 961 ACCAACTGCTCAGCGGGGAGCACAAACCCCTTCAAGGGCGCATCAACTTTGACACATT 1020
QY 341 GlyTyrAlaTrpIleAlaIlePheGlnValIleThrLeuGluGlyTyrValAspIleMet 360
DB 1021 GGCTATGCTGGATGCCATCTTCCAGGTATCATCGTGGAGGGGTGGGTGCACATCATG 1080
QY 361 TyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIle 380
DB 1081 TACTTTGTGTGATGCTCATCTTCTTACAAATTTTCATCTCTTCTCATCATC 1140
QY 381 ValGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGlu 400
DB 1141 GTGGGCTCTTCTCATCATCAACCTGTGCTGGTGGTGAATGGCCAGCAGTTCTCAGAG 1200
QY 401 ThrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAla 420
DB 1201 ACCAAGCAGCGGAAAGCAGCTGATGCGGAGCAGCGTGTGCGGTTCTCTCCAAACGCC 1260
QY 421 SerThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLysTyrLeu 440
DB 1261 AGCACCTTGGCTAGCTTCTCTGAGCCCGGAGCTGTATGAGGAGCTGCTCAAGTACCTG 1320
QY 441 ValTyrIleLeuArgLysAlaAlaArgArgLeuAlaGlnValSerArgAlaAlaGlyVal 460
DB 1321 GTGTACATCTTCTGAAGCAGCCCGCAGGCTGGCTCAGGTCTCTCGGGCAGCAGGTGTG 1380
QY 461 ArgValGlyLeuLeuSerSerProAlaProLeuGlyGlyGlnGluThrGlnProSerSer 480
DB 1381 CGGGTGGGCTGCTCAGCAGCCAGCAGCCCTCGGGGCGCAGGACCCAGCCAGCAGC 1440
QY 481 SerCysSerArgSerHisArgArgLeuSerValHisHisLeuValHisHisHisHis 500
DB 1441 AGCTGCTCTCCCTCCACCGCGCTATCTGTCACCACTTGGTGGTGCACACACACCCAC 1500
QY 501 HisHisHisTyrHisLeuGlyAsnGlyThrLeuArgAlaProArgAlaSerProGlu 520
DB 1501 CATCACCACTACCTACCTGGGCAATGGGAGCTCAGGGCCCCCGGGCCAGCCCGAG 1560
QY 521 IleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProProSerThrPro 540
DB 1561 ATCCAGGACAGGATGCCAATGGGTCCCGCGGCTCATGCTGCCACCACTCCAGCGCT 1620
QY 541 AlaLeuSerGlyAlaProProGlyGlyAlaGluSerValHisSerPheTyrHisAlaAsp 560
DB 1621 GCCCTCTCCGGGGCCCCCTGGTGGGCGCAGTCTGTGCACAGCTTCTACCATGCCGAC 1680
QY 561 CysHisLeuGluProValArgCysGlnAlaProProArgSerProSerGluAlaSer 580
DB 1681 TGCCACTTAGAGCCAGTCCGCTGCCAGGCCCCCTCCAGGTCCCCATCTGAGGCATCC 1740
QY 581 GlyArgThrValGlySerGlyLysValTyrProThrValHisThrSerProProGlu 600
DB 1741 GGCAGGACTGTGGGCGAGCGGAAGGTATCCACCGTGCAACACAGCCCTCCACCGGAG 1800
QY 601 ThrLeuLysGluLysAlaLeuValGluValAlaAlaSerSerGlyProProThrLeuThr 620
DB 1801 ACGCTGAAGGAGAGGCACTAGTAGGTGCTGCCAGCTCTGGGGCCCCAACCTCACC 1860
QY 621 SerLeuAsnIleProProGlyProTyrSerSerMetHisLysLeuLeuGluThrGlnSer 640
DB 1861 AGCTCAACATCCACCCCGGCCCCCTACAGCTTCCATGCAAGCTGTGTGGAGACACAGAGT 1920
QY 641 ThrGlyAlaCysGlnSerSerCysLysIleSerSerProCysLeuLysAlaAspSerGly 660
DB 1921 ACAGTGCTGCCAAAGCTCTTGAAGATCTCCAGCATCTCCAGCCCTTCTTGAAGACAGATGGA 1980
QY 661 AlaCysGlyProAspSerCysProTyrCysAlaArgAlaGlyAlaGlyGluValGluLeu 680

DB 1981 GCCTGTGTTCAGACAGCTGCCCTTACTGTGCCCGGGCGGAGGAGGTGGAGCTC 2040
QY 681 AlaAspArgGluMetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAla 700
DB 2041 GCCGACCGTGAATGCCTGACTCAGACAGCAGGAGCAGTTTATGAGTTTACACAGGATGCC 2100
QY 701 GlnHisSerAspLeuArgAspProHisSerArgArgGlnArgSerLeuGlyProAspAla 720
DB 2101 CAGCACAGCAGCTCCCGGACCCACACAGCGGGCGCAACGAGCCTCGGGCCAGATGCA 2160
QY 721 GluProSerSerValLeuAlaPheTrpArgLeuIleCysAspThrPheArgLysIleVal 740
DB 2161 GAGCCAGCTCTGTGTGGCCTTCTGGAGGCTAATCTGTGACACCTTCCGAAAGATTGTG 2220
QY 741 AspSerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerMet 760
DB 2221 GACAGCAAGTACTTTGGCCGGGAATCATGATGCCATCTTGGTCAACACACTCAGCATG 2280
QY 761 GlyIleGluTyrHisGluGlnProGluGluThrAsnAlaLeuGluIleSerAsnIle 780
DB 2281 GGCATCGAATACCAAGCAGCAGCAGCGGAGCTTACCAACGCGCCTAGAAATCAGCAACATC 2340
QY 781 ValPheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuValTyrGlyProPhe 800
DB 2341 GTCTTCCAGCCCTCTTGGCCTGGAGATGCTGTGAAGCTGCTTGTGTATGTGCCCTTT 2400
QY 801 GlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleValIleSerValTrp 820
DB 2401 GGCTACATCAAGATCCCTACCAACATCTTCATGGTGTTCATTTGGTTCATCAGCGTGTG 2460
QY 821 GluIleValGlyGlnGlnGlyGlyLeuSerValLeuArgThrPheArgLeuMetArg 840
DB 2461 GAGATCGTGGCCAGCAGCAGGGGGCGGCTGTGCGTGTGTCGCGACCTTCCGCTGTATGCT 2520
QY 841 ValLeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetLys 860
DB 2521 GTGCTGAAGCTGTGTGGCTTCTGCGCGCTGAGCGCGAGCTGGTGTCTCATGAAG 2580
QY 861 ThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePheSer 880
DB 2581 ACCATGACACAGTGGCCACCTTCTGCATGCTGTTCATGCTTTCATCTTCATC 2640
QY 881 IleLeuGlyMetHisLeuPheGlyCysLysPheAlaSerGluArgAspGlyAspThrLeu 900
DB 2641 ATCTTGGGCATGCTCTCTTCCGCTGCAAGTTTGCCTCTGAGCGGGATGGGGACACCTG 2700
QY 901 ProAspArgLysAsnPheAspSerLeuTrpAlaIleValThrValPheGlnIleLeu 920
DB 2701 CCAGACCGAAGAAATTTGACTCTTGTCTGGGCCCATCTGCTCTTTCAGATCTCTG 2760
QY 921 ThrGlnGluAspTrpAsnLysValLeuTyrAsnGlyMetAlaSerThrSerTrpAla 940
DB 2761 ACCCAGGAGGACTGGAACAAAGTCTCTTACAAATGGTATGGCTCCACGCTGCTGGGCG 2820
QY 941 AlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuVal 960
DB 2821 GCCCTTTATTTTCTTCTTCCACCGCTCATGCTTCCGCAACTACGCTCTTCAATTTGTGCTC 2880
QY 961 AlaIleLeuValGluGlyPheGlnAlaGluIleSerLysArgGluAspAlaSerGly 980
DB 2881 GCCATCTGTGGTGGAGGCTTCCAGCGGAG----- 2910
QY 981 GlnLeuSerCysIleGlnLeuProValAspSerGlnGlyGlyAspAlaAsnLysSerGlu 1000
DB 2911 -----GGAGATGCCCAACAGTCCGAA 2931
QY 1001 SerGluProAspPhePheSerProSerLeuAspGlyAspGlyAspArgLysCysLeu 1020
DB 2932 TCAGAGCCGATTTCTTCTTCCACCGCTGATGGTGTGATGGGACAGGAAGTGTG 2991
QY 1021 AlaLeuValSerLeuGlyGluHisProGluLeuArgLysSerLeuLeuProLeuIle 1040

Db 2992 GCCTTGCTGTCCTGGAGAGCACCAGGAGCTGGGAGAGCCTGCTGCGCCCTCTCATC 3051
Qy 1041 IleHisThrAlaAlaThrProMetSerLeuProLysSerThrSerThrGlyLeuGlyGlu 1060
Db 3052 ATCCACACGCGCGCCACACCATGTGCTGCCAAGAGACACAGCAGCGCGCTGGCGAG 3111
Qy 1061 AlaLeuGlyProAlaSerArgArgThrSerSerSerGlySerAlaGluProGlyAlaAla 1080
Db 3112 GCGCTGGCGCTGCTGCTGCGCGCCAGCAGCAGCAGCGGGTCGGCAGAGCCTGGGGCGGCC 3171
Qy 1081 HisGluMetLysSerProProSerAlaArgSerSerProHisSerProTrpSerAlaAla 1100
Db 3172 CACGAGATGAGTCACTCCGCCAGCGCCCGCAGCTCTCCGACACGCCCTCGAGCGCTGCA 3231
Qy 1101 SerSerTrpThrSerArgArgSerSerArgAsnSerLeuGlyArgAlaProSerLeuLys 1120
Db 3232 AGCAGCTGGACAGCGCGCTCCAGCGGAAACAGCCTCGCGCGTGCACCGCCTGAAG 3291
Qy 1121 ArgArgSerProSerGlyGluArgArgSerLeuLeuSerGlyGluGlyGlnGluSerGln 1140
Db 3292 CGGAGAACCCCAAGTGGAGAGCGCGGTCTCTGTTGCGGAGAGAGCCAGGAGCGAG 3351
Qy 1141 AspGluGluGluSerSerGluGluGluArgAlaSerProAlaGlySerAspHisArgHis 1160
Db 3352 GATGAGAGGAGAGCTCAGAGAGAGAGCGGCCAGCCTCGCGGCGAGTGCATCGCCAC 3411
Qy 1161 ArgGlySerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeuGlnVal 1180
Db 3412 AGGGGGTCCCTGGAGCGGGAGGCCAAGAGTTCCTTGACCTGCCAGACACACTCGAGGTG 3471
Qy 1181 ProGlyLeuHisArgThrAlaSerGlyArgGlySerAlaSerGluHisGlnAspCysAsn 1200
Db 3472 CCAGGGCTGCACTCCGACCTCCAGTGGCGCGCGGTCTGCTTCTGAGCACCGAGCTGCAAT 3531
Qy 1201 GlyLysSerAlaSerGlyArgLeuAlaArgAlaLeuArgProAspAspProProLeuAsp 1220
Db 3532 GGCAGTCCGGCTTCAGGGCGCTGCGCCGGCGCTGCGCGCTGTATGACCCCGCCTGAT 3591
Qy 1221 GlyAspAspAlaAspAspGluGlyAsnLeuSerLysGlyGluArgValArgAlaTrpIle 1240
Db 3592 GGGGATGACGGATGACAGGGCAACCTGAGCAAGGGGAAACGGGTCCGCGCGTGGATC 3651
Qy 1241 ArgAlaArgLeuProAlaCysTrpLeuGluArgAspSerTrpSerAlaTrpIlePhePro 1260
Db 3652 CGAGCCCGACTCCCTGCTGCTGCTCGAGCGAGACTCTGCTGACGCTACATCTTCCT 3711
Qy 1261 ProGlnSerArgPheArgLeuLeuCysHisArgIleIleThrHisLysMetPheAspHis 1280
Db 3712 CCTCAGTCCAGGTTCGGCTCTGTCGTACCGGATCATCACCAAGATGTTGACCCAC 3771
Qy 1281 ValValLeuValIlePheLeuAsnCysIleThrIleAlaMetGluArgProLysIle 1300
Db 3772 GTGGTCTCTGTATCATCTTCTTTAATGTGCATCACATCGCATCGAGCGGCCCAAAATT 3831
Qy 1301 AspProHisSerAlaGluArgIlePheLeuThrLeuSerAsnTrpIlePheThrAlaVal 1320
Db 3832 GACCCCCACAGCGCTGAACGCATCTCTGACCTCTCCAAATTACATCTTCAACCGCAGTC 3891
Qy 1321 PheLeuAlaGluMetThrValLysValAlaLeuGlyTrpCysPheGlyGluGlnAla 1340
Db 3892 TTTCTGGCTGAATGACATGAGGAGGGTGGCACCTGGGTGTGTCTCGGAGACAGCGG 3951
Qy 1341 TyrLeuArgSerSerTrpAsnValLeuAspGlyLeuLeuValLeuIleSerValIleAsp 1360
Db 3952 TACCTCGGAGCAGTTGGAACTGTGGACGGGTGTGGTGTCTCATCTCCGCTCATCGAC 4011
Qy 1361 IleLeuValSerMetValSerAspSerGlyThrLysIleLeuGlyMetLeuArgValLeu 1380
Db 4012 ATTCTGGTGTCCATGTCTCTGACAGCGGCACCAAGATCTCTGGGCATGTGAGGGTGTG 4071
Qy 1381 ArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeuLysLeu 1400
Db 4072 CGGCTGCTCGGAGACCTGCGCCCGCTCAGGGTGATCAGCGGGCGCAGGGGCTGAAGCTG 4131

Qy 1401 ValValGluThrLeuMetSerSerLeuLysProIleGlyAsnIleValValIleCysCys 1420
Db 4132 GTGGTGGAGACGCTCATGTCTCTCACTGAACCCATCGGCAACATTTAGTATCATCTGCTGT 4191
Qy 1421 AlaPhePheIleIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPheVal 1440
Db 4192 GCCTTCTTCATCATTTTCGGCATCTTGGGGTGGAGCTCTTCAAAGGGAAGTTTTTCGTG 4251
Qy 1441 CysGlnGlyGluAspThrArgAsnIleThrAsnLysSerAspCysAlaGluAlaSerTrp 1460
Db 4252 TCCAGGGCGAGATACCAAGAACATCAACATAAATCGGACTGTGCCGAGCCAGTTAC 4311
Qy 1461 ArgTrpValArgHisLysTrpAsnPheAspAsnLeuGlyGlnAlaLeuMetSerLeuPhe 1480
Db 4312 CGGTGGTCCGGCACACAGTACAACTTTGACAACCTTGGCAGCGCTGATGCTCCCTGTTTC 4371
Qy 1481 ValLeuAlaSerLysAspGlyTrpValAspIleMetTrpAspGlyLeuAspAlaValGly 1500
Db 4372 GTTTTGGCCTCCAAGGATGTTGGGTGGACATCATGTACGATGGGTGGATGCTGTGGGC 4431
Qy 1501 ValAspGlnGlnProIleMetAsnHisAsnProTrpMetLeuLeuTrpPheIleSerPhe 1520
Db 4432 GTGGACAGCGCCCATCATGAACCAACCCCTGGATGCTGCTGTACTTCACTTCGTTTC 4491
Qy 1521 LeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValValValGluAsnPhe 1540
Db 4492 CTGCTCATTTGGCTTCTTGTCTGAACATGTTTGTGGGTGTGGTGGAGAACTTC 4551
Qy 1541 HisLysCysArgGlnHisGlnGluGluGluAlaArgArgGluGluLysArgLeu 1560
Db 4552 CACAGTGTGGCAGCACCGAGGAGAGAGGCCCGCGCGGAGGAGAGCGCCCTA 4611
Qy 1561 ArgArgLeuGluLysLysArgArg-----LysAlaGlnCysLys 1573
Db 4612 CGAAGACTGGAGAAAAGAGAGAGTAAAGAGAGAGTGGCTGAAGCCAGTCAAA 4671
Qy 1574 ProTrpTrpSerAspTrpSerArgPheArgLeuLeuValHisLysCysThrSerHis 1593
Db 4672 CCTTACTACTCCGACTACTCCGCTTCCGGCTCCTCGTCCACCATTTGTGCACCGCCAC 4731
Qy 1594 TyrLeuAspLeuPheIleThrGlyValIleGlyLeuAsnValValThrMetAlaMetGlu 1613
Db 4732 TACTTGACCTCTTCATCAGAGTGTCTGCGGCTGACGCTGTCACCATGGCATGGAG 4791
Qy 1614 HisTrpGlnGlnProGlnIleLeuAspGluAlaLeuLysIleCysAsnTrpIlePheThr 1633
Db 4792 CACTTACCAGCAGCCCGCAGATTTCTGGATGAGGCTCTGAAGATCTGCAACTACATCTTCAC 4851
Qy 1634 ValIlePheValLeuGluSerValPheLysLeuValAlaPheGlyPheArgArgPhePhe 1653
Db 4852 GTCATCTTGTCTTGGAGTCAGTTTTCAAACCTTGTGGCCCTTGGTTTCCGTCGGTTCCTC 4911
Qy 1654 GlnAspArgTrpAsnGlnLeuAspLeuAlaIleValLeuLeuSerIleMetGlyIleThr 1673
Db 4912 CAGACAGGTGGAAACAGCTGGACCTGGCCATTTGCTGCTGCTCATCATGGGCATCACG 4971
Qy 1674 LeuGluGluLeuGluValAsnAlaSerLeuProIleAsnProThrIleIleArgIleMet 1693
Db 4972 CTGGAGGAAATCGAGGTCAACGCCCTCGCTGCCATCAACCCCAACCATCATCCGCATCATG 5031
Qy 1694 ArgValLeuArgIleAlaArgValLeuLysLeuLysMetAlaValGlyMetArgAla 1713
Db 5032 AGGGTGTCTGCCATTTGCCGAGTGTCTGAGATGGCTGTGGGATGGCTGTGGGCGCGG 5091
Qy 1714 LeuLeuAspThrValMetGlnAlaLeuProGlnValGlyAsnLeuGlyLeuLeuPheMet 1733
Db 5092 CTGCTGGACACGGTGTGTCAGGCTGTGAGATGGCTGTGGGATGGCTGTGGGCGCGG 5151
Qy 1734 LeuLeuPhePheIlePheAlaAlaLeuGlyValGluLeuPheGlyAspLeuGluCysAsp 1753
Db 5152 TTGTTGTTTTTTCATCTTTCAGCTCTGGGGCTGGAGCTCTTTGGAGACCTGGAGTGTGAC 5211

1754 GluThrHisProCysGluGlyValArgHisAlaThrPheArgAsnPheGlyMetAla 1773
|||||
5212 GAGACACACCCCTGTGAGGGCTGGCGCTCATGCCACCTTTTCGAACTTTGGCATGGCC 5271
|||||
1774 PheLeuThrLeuPheArgValSerThrGlyAspAsnTrpAsnGlyIleMetLysAspThr 1793
|||||
5272 TTCCTAACCCCTCTCCGAGTCTCCACAGGTGACAAATTCGAATGGCAATATTAAGAGACACC 5331
|||||
1794 LeuArgAspCysAspGlnGluSerThrCysThrAsnThrValIleSerProIleThrPhe 1813
|||||
5332 CTCGGGACTGTGACAGAGTCCACCTGTGTACACACGGTATCGCCCTATCTACTTT 5391
|||||
1814 ValSerPheValLeuThrAlaGlnPheValLeuValLeuValIleAlaValLeuMet 1833
|||||
5392 GTGTCTTCTGTGTGACGGCCAGTTCTGTCTAGTCAACGTGGTGATCGCCGTGTGATG 5451
|||||
1834 LysHisLeuGluGluSerAsnLysGluAlaLysGluGluAlaGluLeu 1853
|||||
5452 AAGCACCTGGAGGAGAGCAACAAGAGGCCAAGAGGAGGCCGAGCTAGAGCTGAGCTG 5511
|||||
1854 GluLeuGluMetLysThrLeuSerProGlnProHisSerProLeuGlySerProPheLeu 1873
|||||
5512 GAGCTGGAGATGAAGACCTCAGCGCCCGACCTCGCCACTGGCGAGCCCTTCCTC 5571
|||||
1874 TrpProGlyValGluGlyProAspSerProAspSerProLysProGlyAlaLeuHisPro 1893
|||||
5572 TGGCTGGGGTGGAGGGCCCCGACAGCCCCGACAGCCCCCAAGCCCTGGGGCTCTGCACCCA 5631
|||||
1894 AlaAlaHisAlaArgSerAlaSerHisPheSerLeuGluHisProThrMetGlnProHis 1913
|||||
5632 CGGGCCACGCGAGATCAGCTCCCACTTTTCCCTGGAGCACCCACGATCGAGCCCCAC 5691
|||||
1914 ProThrGluLeuProGlyProAspLeuThrValArgLysSerGlyValSerArgThr 1933
|||||
5692 CCCACGGAGCTGCAGGAGCACAGCTTACTGACTGTGCGAAGTCTGGGGTCTGCGAAGC 5751
|||||
1934 HisSerLeuProAsnAspSerTyrMetCysArgHisGlySerThrAlaGluGlyProLeu 1953
|||||
5752 CACTCTCTGCCCAATGACAGCTAGATGTGCGCATGGAGCACTGCGAGGGGCCCTGTG 5811
|||||
1954 GlyHisArgGlyTTPGlyLeuProLysAlaGlnSerGlySerValLeuSerValHisSer 1973
|||||
5812 GGACACAGGGGCTGGGGCTCCCCAAGAGCTCAGTCAGGCTCCGTCTGCTGCTCACTCC 5871
|||||
1974 GlnProAlaAspThrSerTyrIleLeuGlnLeuProLysAspAlaProHisLeuLeuGln 1993
|||||
5872 CAGCCAGCAGATACAGCTACATCTGCAGCTTCCAAAGATGCACCTCATCTGCTCCAG 5931
|||||
1994 ProHisSerAlaProThrTrpGlyThrIleProLysLeuProProGlyValArgSerPro 2013
|||||
5932 CCCACAGCGCCCCCAACCTGGGGCACCATCCCCAAACTGCCCCCACCAGGAGCGTCCCT 5991
|||||
2014 LeuAlaGlnArgProLeuArgArgGlnAlaAlaIleArgThrAspSerLeuAspValGln 2033
|||||
5992 TTGGCTCAGAGGCCACTCAGCGGCCAGCAGCAATAGAGCTGACTCTTGAGAGTTGAG 6051
|||||
2034 GlyLeuGlySerArgGluAspLeuAlaGluValSerGlyProSerProProLeuAla 2053
|||||
6052 GGTCTGGCGACCGGGAAGACCTGTGGCAGAGGTAGTGGGCCCTCCCCCGCCCTGGCC 6111
|||||
2054 ArgAlaTyrSerPheThrGlyGlnSerSerThrGlnAlaGlnGlnHisSerArgSerHis 2073
|||||
6112 CGGGCCCTACTCTTTCTGGGGCCAGTCAAGTACCAGGCAGCAGCACTCCCGCAGGCCAC 6171
|||||
2074 SerLysIleSerLysHisMetThrProAlaProCysProGlyProGluProAsnTrp 2093
|||||
6172 AGCAGATCTCCAGACATGATACCCCGCCAGCCCTTGGCCAGGCCCCAGAACCCCACTGG 6231
|||||
2094 GlyLysGlyProProGluThrArgSerSerLeuGluLeuAspThrGluLeuSerTrpIle 2113
|||||
6232 GGCAAGGGCCCTCCAGAGACCAAGACGCTTAGAGTTGGACACGGAGCTGAGCTGGATT 6291
|||||
2114 SerGlyAspLeuLeuProProGlyGlyGlnGluProProSerProArgAspLeuLys 2133
|||||

6292 TCAGGAGACCTCTGCCCCCTGGCGGCAGAGAGAGCCCCCATCCCCACGGGACTGAG 6351
|||||
2134 LysCysTyrSerValGluAlaGlnSerCysGlnArgArgProThrSerTrpLeuAspGlu 2153
|||||
6352 AAGTGCTACAGCGTGGAGGCCAGAGCTGCCAGCGCGGCTACGCTCTGGCTGGATGAG 6411
|||||
2154 GlnArgArgHisSerIleAlaValSerCysLeuAspSerGlySerGlnProHisLeuGly 2173
|||||
6412 CAGAGGAGACACTTATCGCGCTCAGCTGCTGGACAGCGGCTCCCAACCCCACTGGGC 6471
|||||
2174 ThrAspProSerAsnLeuGlyGlnProLeuGlyProGlySerArgProLysLys 2193
|||||
6472 ACAGACCCCTCTAACCTTGGGGGCCAGCTCTTGGGGGGCTGGAGCGGCCGCCAAGAAA 6531
|||||
2194 LysLeuSerProProSerIleThrIleAspProGluSerGlnGlyProArgThrPro 2213
|||||
6532 AACTCAGCGCGCTAGTATCACCATAGACCCCCCGAGAGGCCAAGGTCTCGAGCCCG 6591
|||||
2214 ProSerProGlyIleCysLeuArgArgAlaProSerSerAspSerLysAspProLeu 2233
|||||
6592 CCCAGCCCTGGTATCTGCTCCGAGAGGAGCTCCGTCCAGCGACTCCAGGATCCCTTG 6651
|||||
2234 AlaSerGlyProProAspSerMetAlaAspProSerProLysLysAspValLeuSer 2253
|||||
6652 GCCTCTGGCCCCCTGACGATGGCTGCTCGCCCTCCCAAGAAAGATGCTGCTGAGT 6711
|||||
2254 LeuSerGlyLeuSerSerAspProAlaAspLeuAspPro 2266
|||||
6712 CTCTCCGGTTTATCTCTGACCCAGAGACTGCGACCC 6750
|||||
RESULT 7
AAX83482
ID AAX83482 standard; cDNA; 6783 BP.
AC AAX83482;
XX 07-DEC-1999 (first entry)
DT Human T-type voltage-gated Ca channel alpha-1-G (hCav1b) cDNA.
DE Human; T-type voltage-gated calcium channel; membrane; pore; ion;
KW activation; current; rat; screen; drug; cardiomyopathy; epilepsy; ds.
XX Homo sapiens.
OS WO9929847-A1.
XX 17-JUN-1999.
XX 30-OCT-1998; 98WO-US023161.
XX 05-DEC-1997; 97US-00985809.
XX (LOYO) UNIV LOYOLA CHICAGO.
XX Perez-Reyes E, Cribbs LL;
XX WPI; 1999-394972/33.
XX P-PSDB; AAY14587.
XX New T-type voltage-gated calcium channels.
XX Disclosure; Page 40-49; 138pp; English.
XX This sequence represents the coding region for a human T-type voltage-gated calcium (Ca) channel alpha-1-G designated hCav1b. Voltage gated channels are membrane bound glycosylated proteins formed of several subunits. The large alpha subunits form a pore in the membrane that is selective for a given ionic species. Each alpha subunit contains 4 domains (I, II, III and IV) and each domain contains 6 putative transmembrane helical segments (S1-S6). T-type Ca channels are activated at a lower voltage than L- or N-type channels. Characteristics of T-type

CC channels include short current time, slow activation kinetics near
 CC threshold, fast inactivation kinetics and slow tail current. The
 CC sequences AAX83481-X83492 represent novel T-type voltage-gated Ca channel
 CC genes from humans and rats. Each of the novel Ca-channels contains a
 CC putative IVS4 region comprising the amino acid sequence AAY14598. Cells
 CC expressing the T-type voltage-gated calcium channel proteins can be used
 CC to screen for drugs which affect calcium channels. Methods are also
 CC disclosed for treating a disease or disorder associated with a deficiency
 CC in a native T-type calcium channel nucleic acid, e.g. to treat
 CC cardiomyopathy, epilepsy, etc
 XX
 SQ Sequence 6783 BP; 1294 A; 2182 C; 1990 G; 1317 T; 0 U; 0 Other;

Alignment Scores:
 Pred. NO.: 0 Length: 6783
 Score: 11735.50 Matches: 2241
 Percent Similarity: 98.16% Conservative: 1
 Best Local Similarity: 98.12% Mismatches: 1
 Query Match: 98.58% Indels: 41
 DB: 2 Gaps: 2

US-09-611-257A-37 (1-2266) x AAX83482 (1-6783)

QY	1	MetAspGluGluGluAspGlyAlaGluSerGlyGlnProArgSerPheMet	20
DB	1	ATGACAGGAGGAGGATGGAGCGGCGCCGAGGATCGGACACGCCCGGAGCTTCATG	60
QY	21	ArgLeuAsnAspLeuSerGlyAlaGlyArgProGlyProGlySerAlaGluLysAsp	40
DB	61	CGGCTCAACGACCTGTTCGGGGCGCGGGCGCGCGGGGTCAGCAGAAAGGAC	120
QY	41	ProGlySerAlaAspSerGluAlaGluLysLeuProTyrProAlaLeuAlaProVal	60
DB	121	CGGGACGCGGAGCTCCGAGCGGAGGGGTGCGTACCCGCGCTGGCCCGGGTGT	180
QY	61	PhePheTyrLeuSerGlnAspSerArgProArgSerTyrPysLeuArgThrValCysAsn	80
DB	181	TTCCTCTACTTGAGCGCATCAGCATGTGTGTCATCTCTCACTCGGCAGCGTCTGTAAC	240
QY	81	ProTyrPheGluArgIleSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMet	100
DB	241	CCCTGGTTGAGCGCATCAGCATGTGTGTCATCTCTCACTCGGTGACCCCTGGGATG	300
QY	101	PheArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPhe	120
DB	301	TTCGGGCATGCGAGGACATCGCTGTGACTCCAGCGCTGCGGATCTTCAGGCGCTTT	360
QY	121	AspAspPheIlePheAlaPhePheAlaValGluMetValValLysMetValAlaLeuGly	140
DB	361	GATGACTTCATCTTTGCTCTCTTTCGCGTGGAGATGGTGGTGAAGATGGTGGCTTGGGC	420
QY	141	IlePheGlyLysLysCysTyrIleuGlyAspThrTyrAsnArgLeuAspPheIleVal	160
DB	421	ATCTTTGGGAAAAGTTTACCTGGGAGACATCTGGAAACCGCTTGACTTTTCATGCTC	480
QY	161	IleAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArg	180
DB	481	ATCGCAGGGATGCTGGAGTACTCGTGGACCTGCAGAACGTCAGCTTCTCAGCTGTGAG	540
QY	181	ThrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeu	200
DB	541	ACAGTCCGTGTGTGCGACCGCTCAGGGCCATTAACCGGGTTCGCCAGATGCGCATCTT	600
QY	201	ValThrLeuLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhe	220
DB	601	GTACAGTTCGCTGATGATAGCTGCCATCTGCTGGGCAAGCTCTGCTGCTGCTCTTC	660
QY	221	ValPhePheIlePheGlyIleValGlyValGlnLeuTyrAlaGlyLeuLeuArgAsnArg	240
DB	661	GTCTTCTTCATCTTCGGCATCTGTCGGCGTCCAGCTGTGGCAGGGGTGCTTCGGAACCGA	720
QY	241	CysPheLeuProGlnAsnPheSerLeuProLeuSerValAspLeuGluArgTyrTyrGln	260

DB	721	TGCTTCTTACCTGAGATTTTCAGCCTCCCTCGAGCGTGGACCTGGAGCGGCTATTACGAG	780
QY	261	ThrGluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArg	280
DB	781	ACAGAGACGAGGATGAGAGCCCTTTCATCTGCTCCAGCCACCGAGACCGCATCGG	840
QY	281	SerCysArgSerValProThrLeuArgGlyAspGlyGlyGlyGlyProCysGlyLeu	300
DB	841	TCCTGACGAGGCTGCCAGCGTGGCGGAGCGGGCGGTGGCCACCTTGGCGGTCTG	900
QY	301	AspTyrGluAlaTyrAsnSerSerSerAsnThrThrCysValAsnTyrAsnGlnTyrTyr	320
DB	901	GACTATGAGGCTTACACAGAGCTCCAGCAACACCACTGTGTCACTGGAACAGTACTAC	960
QY	321	ThrAsnCysSerAlaGlyGluHisAsnProPheLysGlyAlaIleAsnPheAspAsnIle	340
DB	961	ACCACTGCTGAGCGGGGAGGACCAACCCCTTCAAGGGCGCCATCACTTTGACAACATT	1020
QY	341	GlyTyrAlaTyrIleAlaIlePheGlnValIleThrLeuGluGlyTyrValAspIleMet	360
DB	1021	GGCTATGCTGATGCCATCTTCCAGGTTCATCGCTGGAGGGTGGGTCCACATCATG	1080
QY	361	TyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleIle	380
DB	1081	TACTTTGTGATGATGCTCATCTCTTCAAAATTTCACTACTTCACTCTCTCATCATC	1140
QY	381	ValGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGlu	400
DB	1141	GTGGGCTCTTCTTCTCATGATCAACCTGTGCTGGTGGTGGTGGTGGTGGTGGTGGT	1200
QY	401	ThrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAla	420
DB	1201	ACCAAGCAGCGGAAAGCAGCTGATGCGGAGCAGCGTGGGTGCTGCTGCTGCTGCTGCTG	1260
QY	421	SerThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLysTyrLeu	440
DB	1261	AGCACCTTGGCTAGCTTCTCTGAGCCCGGAGCTGTATGAGGAGCTGCTCAAGTACCTG	1320
QY	441	ValTyrIleLeuArgLysAlaAlaArgArgLeuAlaGlnValSerArgAlaAlaGlyVal	460
DB	1321	GTGTACATCTTCTTAAAGCAGCGCCGAGCTGCTCAGGTCTCTCGGCGAGCAGGTGTG	1380
QY	461	ArgValGlyLeuLeuSerSerProAlaProLeuGlyGlyGlnThrGlnProSerSer	480
DB	1381	CGGTTGGGCTGTCTGAGCAGCCCGAGCCCTCGGGGGCGAGGAGACCCAGCCAGCAGC	1440
QY	481	SerCysSerArgSerHisArgArgLeuSerValHisHisLeuValHisHisHisHis	500
DB	1441	AGCTGCTCTGCTCCACCGCCCTATCGTCCACCTGCTGTCACCCACCCACCCACCCAC	1500
QY	501	HisHisHisHisHisHisLeuGlyAsnGlyThrLeuArgAlaProArgAlaSerProGlu	520
DB	1501	CATCACCCACTTACCTTGGGCAATGGGACGCTCAGGGCCCCCGGGCGAGCCCGGAG	1560
QY	521	IleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProSerThrPro	540
DB	1561	ATCCAGACAGGATGCCATGGTCCCGCGGCTCATGTGCCACCCACCCCTCGAGCCT	1620
QY	541	AlaLeuSerGlyAlaProProGlyGlyAlaGluSerValHisSerPheTyrHisAlaAsp	560
DB	1621	GGCTCTCCGGGGCCCCCTTGGTGGCGAGAGTCTGTGCACAGCTTCTACCATGCCGAC	1680
QY	561	CysHisLeuGluProValArgCysGlnAlaProProArgSerProSerGluAlaSer	580
DB	1681	TGCCACTTAGAGCCAGTCCCTGCGAGCGCCCCCTCCAGGTCCCATCTGAGGCATCC	1740
QY	581	GlyArgThrValGlySerGlyLysValTyrProThrValHisThrSerProProGlu	600
DB	1741	GGCAGGACTGTGGCAGCGGAGGTGTATCCACCGTGCACACCCAGCCCTCCACCCGAG	1800
QY	601	ThrLeuLysGluLysAlaLeuValGluValAlaAlaSerSerGlyProProThrLeuThr	620
DB	1801	ACGCTGAAGGAGAGGCACTAGTAGAGGTGCTGCCAGCTTGGGGCCCCCAACCTCACC	1860

QY 621 SerLeuAsnIleProProGlyProTyrSerSerMetHisLysLeuLeuGluThrGlnSer 640
DB 1861 AGCTCTCAACATCCACCGCGGCCCTTACAGCTCCATGCAACAGCTGCTGGAGACACAGAT 1920
QY 641 ThrGlyAlaCysGlnSerSerCysLysIleSerSerProCysLeuLysAlaAspSerGly 660
DB 1921 ACAGGTGCTGCCAAAGCTCTTGCAAGATCTCCAGCCCTTCTTGAAAGCAGACAGTGA 1980
QY 661 AlaCysGlyProAspSerCysProTyrCysAlaArgAlaGlyAlaGlyValGluLeu 680
DB 1981 GCCTGTGTGCAGACAGCTGCCCTTACTGTGCCGGCGGGCAGGGAGGTGGAGCTC 2040
QY 681 AlaAspArgGluMetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAla 700
DB 2041 GCCGACCGTGAATGCTCTGACTCAGACAGCGAGCGAGTTATGATTTACACACAGATGCC 2100
QY 701 GlnHisSerAspLeuArgAspProHisSerArgArgGlnArgSerLeuGlyProAspAla 720
DB 2101 CAGCACAGGACCTCCGGGACCCCAACGCGGGCGGACAGAGCCTGGGCCAGATGCA 2160
QY 721 GluProSerSerValLeuAlaPheTrpArgLeuIleCysAspThrPheArgLysIleVal 740
DB 2161 GAGCCAGCTCTGTGTGCTGCTTCTGGAGGCTAATCTGTGACACCTTCGGAAGATTGTG 2220
QY 741 AspSerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerMet 760
DB 2221 GACAGCAAGTACTTTGGCGGGGAATCATGATGCCATCTCTGGTCAACACACTCAGCATG 2280
QY 761 GlyIleGluTyrHisGluGlnProGluLeuThrAsnAlaLeuGluIleSerAsnIle 780
DB 2281 GGCAATGANTACACAGACAGCCCGAGAGCTTACCAACGCCCTTAGAAATCAGCAACATC 2340
QY 781 ValPheThrSerLeuPheAlaLeuGluMetLeuLysLeuValTyrGlyProPhe 800
DB 2341 GTCTTACCAGCCTCTTTGCCCTCGAGATGCTGCTGAAGCTGCTGTGTATGTCCTTT 2400
QY 801 GlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleValIleSerValTrp 820
DB 2401 GGCTACATCAAGAAATCCCTACAAATCTTCATGATGCTGTCATTGTGGTCAACAGCGTGG 2460
QY 821 GluIleValGlyGlnGlnGlyGlyLeuSerValLeuArgThrPheArgLeuMetArg 840
DB 2461 GAGATCTGGGCCAGCAGGGGGGGCGCTGCTGCTGCGGACCTTCGCGCTGATGCT 2520
QY 841 ValLeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetLys 860
DB 2521 GTGCTGAAGCTGGTGGCTTCTTCCGCGCGCTGCAGCGGACGCTGGTGGTCTCATGAAG 2580
QY 861 ThrMetAspAsnValAlaThrPheCysMetLeuMetLeuPheIlePhePheSer 880
DB 2581 ACCATGGACACAGTGGCCACCTTCTGCATGCTGCTTATGCTCTTTCATCTTCATCTTCAGC 2640
QY 881 IleLeuGlyMetHisLeuPheGlyCysLysPheAlaSerGluArgAspGlyAspThrLeu 900
DB 2641 ATCTGGCATGCAATCTCTCGCTGCAAGTTTGCTTCTGAGCGGGAGTGGGACACCCCTG 2700
QY 901 ProAspArgLysAsnPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIleLeu 920
DB 2701 CCAGACCGAAGATTTTGACTCTGCTTGGGCCCATCGTCACTGCTTTTCAGATCTCTG 2760
QY 921 ThrGlnGluAspTrpAsnLysValLeuTyrAsnGlyMetAlaSerThrSerSerTrpAla 940
DB 2761 ACCCAGGAGGACTGGAAACAAAGTCTCTACAAATGGTATGGCTCCACGTCCTCGTGGCG 2820
QY 941 AlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuVal 960
DB 2821 GCCCTTTATTTCATTTGGCCCTCATGACCTTCGGCACTACGTCGCTTCAATTTCTGGTGC 2880
QY 961 AlaIleLeuValGluGlyPheGlnAlaGluIleSerLysArgGluAspAlaSerGly 980
DB 2881 GCCATTCTGTGGAGGGCTTCAGCGGGAG----- 2910

QY 981 GlnLeuSerCysIleGlnLeuProValAspSerGlnGlyGlyAspAlaAsnLysSerGlu 1000
DB 2911 -----GGAGATGCCAAACAAGTCCGAA 2931
QY 1001 SerGluProAspPhePheSerProSerLeuAspGlyAspGlyAspArgLysCysLeu 1020
DB 2931 TCAGAGCCCGATTCTTCTCACCCAGCTGGATGGTATGGGACAGAGAAGTGTCTTG 2991
QY 1021 AlaLeuValSerLeuGlyGluHisProGluLeuArgLysSerLeuLeuProLeuIle 1040
DB 2991 GCCTTGTGTCTCTGGGAGAGCACCGGAGCTCGGAAGAGCCTGCTGCCCTCTCATC 3051
QY 1041 IleHisThrAlaAlaThrProMetSerLeuProLysSerThrSerThrGlyLeuGlyGlu 1060
DB 3051 ATCCACACGGCCGCCACACCATGCTGCTGCCAAGAGCACACAGCGGGCTGGCGGAG 3111
QY 1061 AlaLeuGlyProAlaSerArgThrSerSerGlySerAlaGluProGlyAlaAla 1080
DB 3111 GCGCTGGGCCCTGCTGCGCGCCGACACAGCAGCAGCGGTCGGCAGAGCCTGGGGCGGCC 3171
QY 1081 HisGluMetLysSerProProSerAlaArgSerSerProHisSerProTrpSerAlaAla 1100
DB 3171 CACGAGATGAAGTCAACCGCCAGCGCCGAGCTCTCCGACAGCCCTGGAGCGCTGCA 3231
QY 1101 SerSerTrpThrSerArgArgSerSerArgAsnSerLeuGlyArgAlaProSerLeuLys 1120
DB 3231 AGCAGCTGGACACAGAGCGCTCCAGCCGGAACAGCCTCGGCCGTGACCCAGCCTGAAG 3291
QY 1121 ArgArgSerProSerGlyGluArgArgSerLeuLeuSerGlyGluGlyGlnGluSerGln 1140
DB 3291 CGGAGAACCCCNAGTGGAGAGCGCGCTCTCTGTGTCGGGAGAGGCGCAGAGAGCNG 3351
QY 1141 AspGluGluGluSerSerGluGluArgAlaSerProAlaGlySerAspHisArgHis 1160
DB 3351 GATGAAGAGAGAGCTCAGAAGAGAGAGCGGCCAGCCTCGCGGAGTGACCATCGCCAC 3411
QY 1161 ArgGlySerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeuGlnVal 1180
DB 3411 AGGGGGTCCCTGGAGCGGAGGCGCAAGATTTCTTTTACCTGCGCAGACACACTGCAGGTG 3471
QY 1181 ProGlyLeuHisArgThrAlaSerGlyArgGlySerAlaSerGluHisGlnAspCysAsn 1200
DB 3471 CCAGGGTGTGATCGCACTGCCAGTGGCGGAGGCTGCTCTTCTGAGCACCAGGACTGCAAT 3531
QY 1201 GlyLysSerAlaSerGlyArgLeuAlaArgAlaLeuArgProAspAspProProLeuAsp 1220
DB 3531 GGCAAGTCCGCTTCAGGGCGCTGGCCCGCGCCCTGCGGCTGATGATACCCCCACTGAT 3591
QY 1221 GlyAspAspAlaAspAspGluGlyAsnLeuSerLysGlyGluArgValArgAlaTrpIle 1240
DB 3591 GGGGATGACCCGATGACGAGGGCACTGAGCAAGGGGAAACGGGTCGCGCGGTGGATC 3651
QY 1241 ArgAlaArgLeuProAlaCysTyrLeuGluArgAspSerTrpSerAlaTyrIlePhePro 1260
DB 3651 CGAGCCCGACTCCCTGTGCTGCTGCTGAGGAGACTCTCTGCTGAGCTGATCTTCCCT 3711
QY 1261 ProGlnSerArgPheArgLeuLeuCysHisArgIleIleThrHisLysMetPheAspHis 1280
DB 3711 CCTCAGTCCAGGTTCGCTCTGTCGCGGATCATCCCAAGATGTTCCAGCCAC 3771
QY 1281 ValValLeuValIleIlePheLeuAsnCysIleThrIleAlaMetGluArgProLysIle 1300
DB 3771 GTGGTCTCTGTATCATCTTCTTAACATGATCATCCATCGCCATGCGGAGCGCCCAAAAT 3831
QY 1301 AspProHisSerAlaGluArgIlePheLeuThrLeuSerAsnTyrIlePheThrAlaVal 1320
DB 3831 GACCCCAACAGCGCTGAACGATCTTCTGACCTCTTCCAAATTTACATCTTCCAGCGAGTC 3891
QY 1321 PheLeuAlaGluMetThrValLysValAlaLeuGlyTrpCysPheGlyGluGlnAla 1340
DB 3891 TTTCTGCTCAATGACAGTGAAGTGTGTCAGCTGGGTGCTTTCGGGGAGCAGCGC 3951
QY 1341 TyrLeuArgSerSerTrpAsnValLeuAspGlyLeuLeuValLeuIleSerValIleAsp 1360

Db	3952	TACCTGGGAGCAGTTCGACGGCTGTGGTCTCATCTCCGTCATCGAC	4011
Qy	1361	IleLeuValSerMetValSerAspSerGlyThrIysIleLeuGlyMetLeuArgValLeu	1380
Db	4012	ATTCTGGTGTCCATGCTCTGACAGCGGCACCAAGATCCCTGGGCATGTGAGGGTGCTG	4071
Qy	1381	ArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeuLysLeu	1400
Db	4072	CGGTCTGTGGGACCCCTGGCCCGCTCAGGGTGNATCAGCGGGCGACGGGGCTGAAGCTG	4131
Qy	1401	ValValGluThrLeuMetSerSerLeuLysProIleGlyAsnIleValValIleCysCys	1420
Db	4132	GTGGTGGAGACGCTGATGCTCTCACTGAACCCCATCGCAACATTGTAGTCACTGCTGT	4191
Qy	1421	AlaPhePheIleIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPheVal	1440
Db	4192	GCCTTCTTCATCATTTTTCGGCATCTTGGGGTGCAGCTCTTCAAGGGAAAGTTTTTCGTG	4251
Qy	1441	CysGlnGlyGluAspThrArgAsnIleThrAsnLysSerAspCysAlaGluAlaSerTyr	1460
Db	4252	TGCCAGGGCGAGATACAGGAACATCACCAATAATCGGACTGTGCGAGGCCAGTTAC	4311
Qy	1461	ArgTrpValArgHisLysTyrAsnPheAspAsnLeuGlyGlnAlaLeuMetSerLeuPhe	1480
Db	4312	CGGTGGGTCCGGCACAAAGTACAACTTTGCACAACTTGGCCAGGCCCTCATGTCTCTTTC	4371
Qy	1481	ValLeuAlaSerLysAspGlyTrpValAspIleMetTyrAspGlyLeuAspAlaValGly	1500
Db	4372	GTTTTGGCTCCAAAGGATGGTTGGTGACATCATGATGAGTGGCTGGATGCTGTGGGC	4431
Qy	1501	ValAspGlnGlnProIleMetAsnHisAsnProTrpMetLeuLeuTyrPheIleSerPhe	1520
Db	4432	GTGNACAGACGCCCATCATGAACCAACACCTGGATGCTGCTGCTCATCTCGTTC	4491
Qy	1521	LeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValValValGluAsnPhe	1540
Db	4492	CTGCTCATTTGTGGCTTCTTGTCTGCAACATGTTTGTGGTGTGGTGGTGGAACTTC	4551
Qy	1541	HisLysCysArgGlnHisGlnGluGluGluAlaArgArgGluGluLysArgLeu	1560
Db	4552	CACAAAGTGTCCGACGACACAGAGAGAGAGAGGCCCGCGCGGAGGAGAGCGGCTA	4611
Qy	1561	ArgArgLeuGluLysLysArgArg	1568
Db	4612	CGAAGACTGGAGAAAAAGAGAGGAATCTAATGCTGGACGATGTAATTGCTTCGGCGAGC	4671
Qy	1569	-----LysAlaGlnCysLysProTyrTyrSerAspTyrSerArgPhe	1582
Db	4672	TCAGCAGCGCTGCGTCAAGAGCCCGAGTGCAGAACTTACTACTCCGACTCTCCGCTTC	4731
Qy	1583	ArgLeuLeuValHisHisLeuCysThrSerHisTyrLeuAspLeuPheIleThrGlyVal	1602
Db	4732	CGGTCTCTCGTCCACCATCTGTGCACAGCCACTACTCTGGACCTTTCATCACAGGTGTC	4791
Qy	1603	IleGlyLeuAsnValValThrMetAlaMetGluHisTyrGlnGlnProGlnIleLeuAsp	1622
Db	4792	ATCCGGCTGAACTGGTCAACATGCCATGAGACACTACAGCAGCCCGCAGATTCTGGAT	4851
Qy	1623	GluAlaLeuLysIleCysAsnTyrIlePheThrValIlePheValLeuGluSerValPhe	1642
Db	4852	GAGGCTCTGAAGACTCGAACTTACATCTCTACTGTCTTGTCTTGGAGTCAGTTTTTC	4911
Qy	1643	LysLeuValAlaPheGlyPheArgArgPheGlnAspArgTrpAsnGlnLeuAspLeu	1662
Db	4912	AAACTTGTGGCTTTTGGTTTCGTTCGTTCCTCCAGGACAGTGGAAACAGTGGACCTG	4971
Qy	1663	AlaIleValLeuLeuSerIleMetGlyIleThrLeuGluGluIleGluValAsnAlaSer	1682
Db	4972	GCAATTGTGCTGCTGTCATCATGAGGATCAGCTGGAGGAATCGAGTCAACGCCCTCG	5031
Qy	1683	LeuProIleAsnProThrIleIleArgIleMetArgValLeuArgIleAlaArgValLeu	1702

Db	5032	CTGCCCATCAACCCCAACCATCATATCCGCATCATAGAGGGTCTCGGCATTCGCCAGTGTCTG	5091
Qy	1703	LysLeuLeuLysMetAlaValGlyMetArgAlaLeuLeuAspThrValMetGlnAlaLeu	1722
Db	5092	AGCTGTCTGAAGATGGCTGTGGGCATGGGGCGCTGCTGGACACCGTGTATGAGGCCCTG	5151
Qy	1723	ProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPhePheIlePheAlaAlaLeu	1742
Db	5152	CCCCAGTGGGAAACCTGGGACTTCTCTTCATGTGTGTGTGTTCATCTTTTCAGAGCTCTG	5211
Qy	1743	GlyValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGluGlyLeuGly	1762
Db	5212	GGGTGGAGCTCTTTGGAGACCTGGAGTGTGAGACACACCCCTGTGAGGGCTGGGC	5271
Qy	1763	ArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgValSerThr	1782
Db	5272	CGTCAATGCCACCTTTTCGGAACCTTGGCATGGCTTCTTAACCTCTTCCGAGTCTCCACA	5331
Qy	1783	GlyAspAsnTrpAsnGlyIleMetLysAspThrLeuArgAspCysAspGlnGluSerThr	1802
Db	5332	GGTGAACAATTGGAAATGGCAATATGAAGGACACCCCTCCGGGACTGTACAGGAGTCCACC	5391
Qy	1803	CysTyrAsnThrValIleSerProIleTyrPheValSerPheValLeuThrAlaGlnPhe	1822
Db	5392	TGCTACAAACAGGTCTATCTCGCTATCTACTTGTCTCTTCTGTGTGACGGCCAGTTTC	5451
Qy	1823	ValLeuValAsnValValIleAlaValLeuMetLysHisLeuGluGluSerAsnLysGlu	1842
Db	5452	GTCTAGTCAACGTGTGTATCGCCGTGTGATGAAGCACCTGGAGGAGAGCAACAAGGAG	5511
Qy	1843	AlaLysGluGluAlaGluLeuGluAlaGluLeuGluMetLysThrLeuSerPro	1862
Db	5512	GCCAAAGGAGGAGGCCAGCTAGAGGTGAGCTGAGCTGGAGTGGAGTGAAGACCTTCACCCC	5571
Qy	1863	GlnProHisSerProLeuGlySerProPheLeuTrpProGlyValGlyProAspSer	1882
Db	5572	CAGCCCCACTCGGCACCTGGGCACCCCTTCTCTGACCTGGGTGGGGCCCCGACAGC	5631
Qy	1883	ProAspSerProLysProGlyAlaLeuHisProAlaAlaHisAlaArgSerAlaSerHis	1902
Db	5632	CCCGACAGCCCAAGCTGGGGCTCTGCACCCACCGCGGCCACCGAGATCAGGCTCCCCAC	5691
Qy	1903	PheSerLeuLysIleProThrMetGlnProHisProThrGluLeuProGlyProAspLeu	1922
Db	5692	TTTTTCTCGAGCACCCACGATGACGCCCCACCCACCGAGGTGCCAGGACCCAGACTTA	5751
Qy	1923	LeuThrValArgLysSerGlyValSerArgThrHisSerLeuProAsnAspSerTyrMet	1942
Db	5752	CTGACTGTGGGAAGTCTGGGTGAGCCGAACGACTCTCTGCCCAATGACAGTACATG	5811
Qy	1943	CysArgHisGlySerThrAlaGluGlyProLeuGlyHisArgGlyTyrGlyLeuProLys	1962
Db	5812	TGTGGCATGGGACACTGCCGAGGGGCCCTGGGACACAGGGGGTGGGGGCTCCCCAAA	5871
Qy	1963	AlaGlnSerGlySerValLeuSerValHisSerGlnProAlaAspThrSerTyrIleLeu	1982
Db	5872	GCTCAGTCAGGCTCCGTTCTTGTCCGTTCACTCCAGGACGACAGATACAGTACATCTG	5931
Qy	1983	GlnLeuProLysAspAlaProHisLeuLeuGlnProHisSerAlaProThrTrpGlyThr	2002
Db	5932	CAGCTTCCCAAGATGACCTCATCTGCTCCAGCCCCACAGCGCCCCCAAGCTGGGGCACC	5991
Qy	2003	IleProLysLeuProProGlyArgSerProLeuAlaGlnArgProLeuArgArgGln	2022
Db	5992	ATCCCCAACTGGCCCCCAGGAGCGCTCCCTTTGGCTCAGAGGGCCACTCAGGCGCAG	6051
Qy	2023	AlaAlaIleArgThrAspSerLeuAspValGlnGlyLeuGlySerArgGluAspLeuLeu	2042
Db	6052	GCAGCAATAGGACTGACTCTTTGGAGCTTCAGGCTCTGGGACCGCGGAGAGCTGCTG	6111
Qy	2043	AlaGluValSerGlyProSerProProLeuAlaArgAlaIleTyrSerPheTrpGlyLysSer	2062
Db	6112	GCAGAGGTGAGTGGGGCTCTCCCGCCCTCTGGCGGGCTACTCTTTCTGGGGCCAGTCA	6171

181 ThrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeu 200
Db ACAGTCCGTGTGCTGCGACCGCTCAGGGCCATTAAACGGGTGCCAGCATCCTT 600
201 ValThrLeuLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhe 220
Db GTACAGTGTGCTGTGGATACGCTCCCATGCTGGGCAACGCTCTGCTGTCTTCTTC 660
221 ValPhePheIlePheGlyIleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArg 240
Db GTCTTCTTCATCTTCGGCATCGTCGGGTCCAGCTGTGGGAGGGCTGTCTCGGAACCGA 720
241 CysPheLeuProGluAsnPheSerLeuProLeuSerValAspLeuGluArgTyrGln 260
Db TGTCTTCTTACCTGAGAAATTCAGCTCCCTCTGAGCGTGGACCTGGAGCGCTATTACCAG 780
261 ThrGluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArg 280
Db ACAGAGAACGAGGATGAGAGCCCTTCATCTGCTCCAGCCACGCGAGAAACGCGATCGG 840
281 SerCysArgSerValProThrLeuArgGlyAspGlyGlyGlyProProCysGlyLeu 300
Db TCCTGCAAGACGTCGCCACCTCGCGGGACCGGGGGCGGTGGCCACCTTTCGGGTCTG 900
301 AspTyrGluAlaTyrAsnSerSerAsnThrThrCysValAsnTrpAsnGlnTyrTyr 320
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321 ThrAsnCysSerAlaGlyGluHisAsnProPheLysGlyAlaIleAsnPheAspAsnIle 340
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341 GlyTyrAlaTrpIleAlaIlePheGlnValIleThrLeuGluGlyTrpValAspIleMet 360
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361 TyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIle 380
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381 ValGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGlu 400
Db GTGGGCTCCTTCTTCATGATCAACCTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGT 1200
401 ThrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAla 420
Db ACCAAGACGCGGAAGCCAGCTGATCGGGAGCAGCGTGTGCGGTTCTGTCTCAACGCC 1260
421 SerThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLeuLysTyrLeu 440
Db AGCACCTGGCTAGCTTCTGTAGCCCGGACGCTGTATGAGGAGCTGTCAAGTACCTG 1320
441 ValTyrIleLeuArgLysAlaAlaArgArgLeuAlaGlnValSerArgAlaAlaGlyVal 460
Db GTGTACATCTCTTGTAAAGCAGCCCGCAGGCTGCTCAGGTCTCTCGGGCAGCAGGTGTG 1380
461 ArgValGlyLeuLeuSerSerProAlaProLeuGlyGlyGlnGluThrGlnProSerSer 480
Db CGGGTGGGCTGCTCAGCAGCCAGCAGCCCTCGGGGCGAGAGAGCCAGCCAGCCAGCAG 1440
481 SerCysSerArgSerHisArgArgLeuSerValHisIleValHisHisHisHisHis 500
Db AGCTGCTCTGCTCCACCGCGGCTATCCGTCCACCACTGGTGTGACCAACCAACCAAC 1500
501 HisHisHisHisTyrHisLeuGlyAsnGlyThrLeuArgAlaProArgAlaSerProGlu 520
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521 IleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProProSerThrPro 540
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1621 GCCCTCTCCGGGGCCCCCTGTGTGCGCAGAGTCTGTGTCACAGCTTCTTACCATTGCCGAC 1680
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Db TGCACCTTAGAGCAGTCGCTGCCAGGGCCCCCTCCAGGTCCCCCATCTGAGGCACTCC 1740
581 GlyArgThrValGlySerGlyLysValTyrProThrValHisThrSerProProProGlu 600
Db GGAGAGCTGTGGGCGGCGGAGAGGTGTATCCACCGTGCACACCGAGCCCTCCACCGGAG 1800
601 ThrLeuLysGluLysAlaLeuValGluValAlaAlaSerSerGlyProProThrLeuThr 620
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621 SerLeuAsnIleProProGlyProTyrSerSerMetHisLysLeuLeuGluThrGlnSer 640
Db AGCTTCAACATCCACCGGGCCCTACAGCTCCATGTCACAAAGCTGTGGAGACACAGT 1920
641 ThrGlyAlaCysGlnSerSerCysLysIleSerSerProCysLeuLysAlaAspSerGly 660
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661 AlaCysGlyProAspSerCysProTyrCysAlaArgAlaGlyAlaGlyGluValGluLeu 680
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681 AlaAspArgGluMetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAla 700
Db GCCGACCGTGAATGCTGACTCAGACAGCGAGCGAGTATATGAGTTTCAACAGGATGCC 2100
701 GlnHisSerAspLeuArgAspProHisSerArgArgGlnArgSerLeuGlyProAspAla 720
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Qy 981 GlnLeuSerCysIleGlnLeuProValAspSerGlnGlyGlyAspAlaAsnLysSerGlu 1000
Db 2911 -----GGAGATGCCAAACAAAGTCCGAA 2931
Qy 1001 SerGluProAspPheSerProSerLeuAspGlyAspGlyAspArgLysCysLeu 1020
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Qy 1896 HisAlaArgSerAlaSerHisPheSerLeuGluHisProThrMetGlnProHisProThr 1915
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Qy 1916 GluLeuProGlyProAspLeuThrValArgLysSerGlyValSerArgThrHisSer 1935
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Qy 1936 LeuProAsnAspSerTyrMetCysArgHisGlySerThrAlaGluGlyProLeuGlyHis 1955
Db 5812 CTGCCCAATGACAGTACATGTGTGGCATGGGAGCACTGCGGAGGGGCCCTTGGGACAC 5871
Qy 1956 ArgGlyTrpGlyLeuProLysAlaGlnSerGlySerValLeuSerValHisSerGlnPro 1975
Db 5872 AGGGGCTGGGGGCTCCCCAAGACTCAGTCAGGCTCCGCTTGTCCGTTCATCTCCAGCCA 5931
Qy 1976 AlaAspThrSerTyrIleLeuGlnLeuProLysAspAlaProHisLeuLeuGlnProHis 1995

Db 5932 GCAGATACCAAGCTACATCTCTGCAGCTTCCCAAAGATGCACCTCATCTGCTCCAGCCAC 5991
Qy 1996 SerAlaProThrTrpGlyThrIleProLysLeuProProGlyArgSerProLeuAla 2015
Db 5992 AGCGCCCCAACCTTGGGGCACCATCCCCAACTCCCCACCCAGAGCGCTCCCCCTTTGGCT 6051
Qy 2016 GlnArgProLeuArgArgGlnAlaAlaIleArgThrAspSerLeuAspValGlnGlyLeu 2035
Db 6052 CAGAGGCCATCTAGGCGCCAGGAGCAATPAAGACTGACTCTCTTGGAGCTTCAAGGCTG 6111
Qy 2036 GlySerArgGluAspLeuLeuAlaGluValSerGlyProSerProProLeuAlaArgAla 2055
Db 6112 GGCAGCGCGGAGACCTGCTGGCAGAGGTGAGTGGGCCCTTCCCGCCCTTGGCCGCGGCC 6171
Qy 2056 TyrSerPheTrpGlyGlnSerSerThrGlnAlaGlnGlnHisSerArgSerHisSerLys 2075
Db 6172 TACTCTTTTGGGGCCAGTCAAGTACCAGGACAGCAGCAGCTCCCGCAGCCACAGCAAG 6231
Qy 2076 IleSerLysHisMetThrProAlaProCysProGlyProGluProAsnTrpGlyLys 2095
Db 6232 ATCTCAAGCACATGACCCCGCCAGCCCTTGGCCAGGCCAGAACCCCAACTGGGGCAAG 6291
Qy 2096 GlyProProGluThrArgSerSerLeuGluLeuAspThrGluLeuSerTrpIleSerGly 2115
Db 6292 GGGCCTCCAGAGACCAAGAGCAGCTTAGAGTTGGACACGAGCTGAGCTGGATTTCAAGGA 6351
Qy 2116 AspLeuLeuProProGlyGlyGlnGluProProSerProArgAspLeuLysLysCys 2135
Db 6352 GACCTCTGCCCCCTGGCGCCAGGAGGAGCCCCATCCCCACGGACCTGAGAGAGTGC 6411
Qy 2136 TyrSerValGluAlaGlnSerCysGlnArgArgProThrSerTrpLeuAspGluGlnArg 2155
Db 6412 TACAGCGTGGAGGCCAGAGCTGCCAGCGCCGCGCTACGCTCTGGCTGGATGAGCAGAG 6471
Qy 2156 ArgHisSerIleAlaValSerCysLeuAspSerGlySerGlnProHisLeuGlyThrAsp 2175
Db 6472 AGACACTCTATCGCCGTGAGTGCCTGGACAGCGGCTCCCAACCCCACTGGGCGCACAGC 6531
Qy 2176 ProSerAsnLeuGlyGlyGlnProLeuGlyGlyProGlySerArgProLysLysLysLeu 2195
Db 6532 CCTCTAACCTTGGGGGCCAGCTCTTGGGGGCCCTGGGAGCCGCGCCCAAGAAAACTC 6591
Qy 2196 SerProProSerIleThrIleAspProGluSerGlnGlyProArgThrProProSer 2215
Db 6592 AGCCCGCTAGTATCACCATAGACCCCGCCAGAGCCAGGCTCTCGGACCCCGCCAGC 6651
Qy 2216 ProGlyIleCysLeuArgArgAlaProSerSerAspSerLysAspProLeuAlaSer 2235
Db 6652 CCTGGTATCTGCTCCGAGAGGGGCTCCGCTCCAGCGACTCCAAGGATCCCTTGGCCCTCT 6711
Qy 2236 GlyProProAspSerMetAlaAlaSerProSerProLysLysAspValLeuSerLeuSer 2255
Db 6712 GGGCCCCCTGACAGATGGCTGCTGCTGCTCCCTCCCAAGAAAGATGTGCTGCTCTCC 6771
Qy 2256 GlyLeuSerSerAspProAlaAspLeuAspPro 2266
Db 6772 GGTATTCTCTGACCCAGCAGACCTGGAGCCCC 6804

RESULT 9

AAH98402
ID AAH98402 standard; cDNA; 8002 BP.

XX AC AAH98402;

XX DT 12-OCT-2001 (first entry)

XX DE Human EST-derived coding sequence SEQ ID NO: 259.

XX KW Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
XX KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
XX KW diagnostics; forensic test; gene mapping; genetic disorder; biodiversity;
XX KW gene therapy; nutrition; ss.

Db 1936 AGCTGCTCTCGCTCCCAACCGCGCTATCCGTCACCAACCTGGTGCACCAACCAACCAAC 1995
Qy 501 HishishistyrHisLeuGlyAsnGlyThrLeuArgAlaProArgAlaSerProGlu 520
Db 1996 CATCACCACTACCACTGGGCAATGGGACGCTCAGGGCCCCCGGGCCAGCCCGGAG 2055
Qy 521 IleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProProSerThrPro 540
Db 2056 ATCCAGAGACAGGATGCCATGGGTCCCGCGGCTCATGCTGCCACCAACCTCCAGCGCT 2115
Qy 541 AlaleuSerGlyAlaProProGlyGlyAlaGluSerValHisSerPheThrHisAlaAsp 560
Db 2116 GCCCTCTCCGGGGCCCCCTGGTGGCGCAGAGTCTGTGCACAGCTTCTACCAATGCCGAC 2175
Qy 561 CysHisLeuGluProValArgCysGlnAlaProProProArgSerProSerGluAlaSer 580
Db 2176 TGCCACTTAGACGACAGTCCGCTGCAGGGCGCCCTCCAGGTCCCATCTGAGGCATCC 2235
Qy 581 GlyArgThrValGlySerGlyLysValTyProThrValHisThrSerProProProGlu 600
Db 2236 GGCAGGACTGTGGGCAGCGGAGGTATCCACCGTGCACACAGCCCTCCACCGGAG 2295
Qy 601 ThrLeuLysGluLysAlaLeuValGluValAlaAlaSerSerGlyProProThrLeuThr 620
Db 2296 ACCTGAAGGAGAGGCACTAGTAGAGGTGGCTGCCAGCTCTGGGCCCCCAACCTCACC 2355
Qy 621 SerLeuAsnIleProProGlyProTySerSerMetHisLysLeuLeuGluThrGlnSer 640
Db 2356 AGCTCTCAACATCCACCGGGCCCTACAGCTCCATGCACAGCTGCTGGAGACACAGT 2415
Qy 641 ThrGlyAlaCysGlnSerSerCysLysIleSerSerProCysLysLeuLysAlaAspSerGly 660
Db 2416 ACAGTGCTGCCAAAGCTCTTGCAAGATCTCCAGCCCTTGCTTGAAGCAGACAGTGA 2475
Qy 661 AlaCysGlyProAspSerCysProTyCysAlaArgAlaGlyGluValGluLeu 680
Db 2476 GCCTGTGTGCAGACAGCTGCCCTCTACTGTCCCGGGCGGGCAGGGAGGTGGAGCTC 2535
Qy 681 AlaAspArgGluMetProAspSerAspSerGluAlaValTyGluPheThrGlnAspAla 700
Db 2536 GCCGACCGTGAATGCCCTGACTCAGACAGCAGGACAGTTATGATTCACACAGATGCC 2595
Qy 701 GlnHisSerAspLeuArgAspProHisSerArgArgGlnArgSerLeuGlyProAspAla 720
Db 2596 CAGCACAGCAGCTCCGGGACCCACAGCGCGGCGCAACGAGCCTGGGCGCCAGATGCA 2655
Qy 721 GluProSerSerValLeuAlaPheThrArgLeuIleCysAspThrPheArgLysIleVal 740
Db 2656 GAGCCCAAGCTCTGTGCTGGCCCTCTGGAGGCTAATCTGTGACACCTTCCGAAAGATTGTG 2715
Qy 741 AspSerLysTyPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerMet 760
Db 2716 GACAGCAAGTACTTGGCCGGGGAAATCATGATGCCATCTCTGGTCAACACACTCAGCATG 2775
Qy 761 GlyIleGluTyHisGluGlnProGluLeuThrAsnAlaLeuGluIleSerAsnIle 780
Db 2776 GGCATCGAATACCAACAGCAGCCGAGAGCTTACCAACGCCCTAGAAATCAGCAACATC 2835
Qy 781 ValPheThrSerLeuPheAlaLeuGluMetLeuLysLeuValTyGlyProPhe 800
Db 2836 GTCCTTCCAGCCCTTTGGCCCTGGAGATGCTGTGAAGCTGCTGTGTATGGTCCCTTT 2895
Qy 801 GlyTyIleLysAsnProTyAsnIlePheAspGlyValIleValIleSerValTrp 820
Db 2896 GGCTACATCAAGATCCCTACACATCTTCGATGGTGTGTCATTTGGTTCATCAGCGTGTGG 2955
Qy 821 GluIleValGlyGlnGlnGlyGlyLeuSerValLeuArgThrPheArgLeuMetArg 840
Db 2956 GAGATCGTGGGCCAGCAGCGGGGGCGCTGTGGTGTGTGGTGTGTGGTGTGTGGTGTGTGGT 3015
Qy 841 ValLeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetLys 860
Db 3016 GTGCTGAAGCTGGTGGCTTCTTCCCGCGCTGCAGCGGACGCTGTGGTGTCTCATGAAG 3075

Qy 861 ThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePheSer 880
Db 3076 ACCATGGACAACCTGGCCACTTCTGCTGCTGCTTATGCTCTTCTATCTTCTTCTCAGC 3135
Qy 881 IleLeuGlyMetHisLeuPheGlyCysLysPheAlaSerGluArgAspGlyAspThrLeu 900
Db 3136 ATCCTGGGCATGCTCTCTTCGGCTGCAAGTTTGGCTCTGAGCGGATGGGGACACCTG 3195
Qy 901 ProAspArgLysAsnPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIleLeu 920
Db 3196 CAGACCCGGAAGAATTTTGAATCTTCTGCTCTGGGCCATCTGCTCTTTCAGATCCTG 3255
Qy 921 ThrGlnGluAspTrpAsnLysValLeuTyAsnGlyMetAlaSerThrSerSerTrpAla 940
Db 3256 ACCCAGGAGACTGGAACAAGTCTCTACAATGGTATGGCTCCACGTCGCTCGTGGCG 3315
Qy 941 AlaIleuTyPheIleAlaLeuMetThrPheGlyAsnTyPheValLeuPheAsnLeuVal 960
Db 3316 GCCCTTTATTTCAATGCTTCCCTCATGACCTTCGGAACCTACGCTCTTCAATTTGCTGCTC 3375
Qy 961 AlaIleLeuValGluGlyPheGlnAlaGluGluIleSerLysArgGluAspAlaSerGly 980
Db 3376 GCCATCTGTGGAGGGCTTCCAGGGCGAG----- 3405
Qy 981 GlnLeuSerCysIleGlnLeuProValAspSerGlnGlyAspAlaAsnLysSerGlu 1000
Db 3406 -----GGAGATGCCAACAAAGTCGAA 3426
Qy 1001 SerGluProAspPhePheSerProSerLeuAspGlyAspGlyAspArgLysLysCysLeu 1020
Db 3427 TCAGAGCCGATTTCTTCTCACCCAGCTGGATGGTATGGGACAGGAAGTAGTGTG 3486
Qy 1021 AlaLeuValSerLeuGlyGluHisProGluLeuArgLysSerLeuLeuProLeuIle 1040
Db 3487 GCCTTGTGTCTCTGGAGAGCACCAGGAGCTGGGAAGAGCTGTGCGCTCTCATC 3546
Qy 1041 IleHisThrAlaAlaThrProMetSerLeuProLysSerThrSerThrGlyLeuGlyGlu 1060
Db 3547 ATCCACACGGCCGCCACCATGTGCTGCCAACAGACACAGCAGCGGCTGGGCGAG 3606
Qy 1061 AlaLeuGlyProAlaSerArgArgThrSerSerGlySerAlaGluProGlyAlaAla 1080
Db 3607 GCCTGGGCTCTGCTGCGCCGCCAGCAGCAGCAGCGGGTGGCAGAGCTTGGGGCGGCC 3666
Qy 1081 HisGluMetLysSerProProSerAlaArgSerSerProHisSerProTrpSerAlaAla 1100
Db 3667 CACGAGATGAAGTCAACGCCGCCAGCGCCGAGCTCTCCGACAGCCCTTGAGCGCTGCA 3726
Qy 1101 SerSerTrpThrSerArgArgSerSerArgAsnSerLeuGlyArgAlaProSerLeuLys 1120
Db 3727 AGCAGCTGGACAGCAGCGCTCCAGCGGAAACAGCTCTCGCGCTGACCCAGCTGAAG 3786
Qy 1121 ArgArgSerProSerGlyGluArgArgSerLeuLeuSerGlyGluGlyGlnGluSerGln 1140
Db 3787 CGGAGAACCCCAAGTAGGAGCGCGGTCTCTGTGTGGGAGAGCCAGGAGGAGCCAG 3846
Qy 1141 AspGluGluGluSerSerGluGluArgAlaSerProAlaGlySerAspHisArgHis 1160
Db 3847 GATGAAGAGAGAGCTCAGAAAGAGGAGCGGCCAGCCCTGGGGCAGTGCACCTCGCCAC 3906
Qy 1161 ArgGlySerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeuGlnVal 1180
Db 3907 AGGGGGTCCCTGGAGCGGAGGCGCAAGATTTCTTTTTCACCTGCGGACACACTGCAGGTG 3966
Qy 1181 ProGlyLeuHisArgThrAlaSerGlyArgGlySerAlaSerGlnHisGlnAspCysAs 1200
Db 3967 CCAGGGCTGTCATCGCATGCGGCGGAGGGTCTCTCTTCTGAGCAGCAGGAGTGCAG 4026
Qy 1200 nGlyLysSerAlaSerGlyArgLeuAlaArgAlaLeuArgProAspAspProProLeuAs 1220
Db 4027 TGGCAAGTCCGCTTCAGGGCGCTTGGCCCGGGCCCTGCGGCTGATGACCCCCCACTGGA 4086

QY 1220 pGlyAspAlaAspGluGlyValAsnLeuSerLysGlyGluArgValArgAlaTrpI1 1240
DB 4087 TGGGGATGACGCCGATGACGAGGGACACTGAGCAAGAGGGATCCGGCGGTGGAT 4146
QY 1240 eArgAlaArgLeuProAlaCysTyrLeuGluArgAspSerTrpSerAlaTrpIlePhePr 1260
DB 4147 CCGAGCCGAGTCCCTGCTGCTGCTCGAGGAGACTCCTGGTCAGCTACATCTTCCC 4206
QY 1260 oProGlnSerArgPheArgLeuLeuCysHisArgIleIleThrHisLysMetPheAspHi 1280
DB 4207 TCCCTCAGTCCAGGTTCCGCCCTCTGTGTCCGGGATCATCCCAAGATGTTTCGACCA 4266
QY 1280 sValValLeuValIleIlePheLeuAsnCysIleThrIleAlaMet-GluArgProLysI 1300
DB 4267 CGTGGTCTTGTTCATCATCTTCTTAATCTCATCAACCATCGCCATGGAGGCGCCCAAAA 4326
QY 1300 le-AspProHisSerAlaGluArgIlePheLeuThrLeuSerAsnTyrIlePheThrAla 1319
DB 4327 TTTGACCCCCACAGCGTTGAAGCATCTTCTGACCCCTCTCCAATTACATCTTCACGCA 4386
QY 1320 ValPheLeuAlaGluMetThrValLysValValAlaLeuGlyTyrCypPheGlyGluGln 1339
DB 4387 GTCCTTCTGGGTGAAATGACAGTGAAGGTGGTGGCACTGGGTGGTCTTCCGGGAGCAG 4446
QY 1340 AlaTyrLeuArgSerTrpAsnValLeuAspGlyLeuValLeuValLeuIleSerValIle 1359
DB 4447 GCGTACCTGCGGAGCAGTGTGAACGTGCTGACCGGCTGTGGTGGTCTCATCTCCGTGATC 4506
QY 1360 AspIleLeuValSerMetValSerAspSerGlyThrLysIleLeuGlyMetLeuArgVal 1379
DB 4507 GACATTCGTGGTGTCCATGCTCTGACAGCGGCACCAAGATCCTGGGCATGCTGAGGGTG 4566
QY 1380 LeuArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeuLys 1399
DB 4567 CTGGGCTGCTGCGGCCCTCGCCGCTCAGGGTGTATCAGCGGGCGCAGGGGCTGAAG 4626
QY 1400 LeuValValGluThrLeuMetSerLeuLysProIleGlyAsnIleValIleCys 1419
DB 4627 CTGGTGGGAGAGCGCTGATGCTCTGCTGAAACCCATCGGCAACATTTGATGATCTGTC 4686
QY 1420 CysAlaPhePheIleIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPhePhe 1439
DB 4687 TGTGCTTCTTCATATTTTCGGCATCTTGGGGTGACAGCTCTTCAAGGAGAGTTTTC 4746
QY 1440 ValCysGlnGlyGluAspThrArgAsnIleThrAsnLysSerAspCysAlaGluAlaSer 1459
DB 4747 GTGTGCCAGGCGAGGATACCAGGAACATACCAATAATCGGACTGTGCCGAGGCCAGT 4806
QY 1460 TyrArgTrpValArgHisLysTyrAsnPheAspAsnLeuGlyGlnAlaLeuMetSerLeu 1479
DB 4807 TACCGGTGGTCCGGCACAGTACAACTTTGACAACTTTGGCCAGGCCCTGATGTCCCTG 4866
QY 1480 PheValLeuAlaSerLysAspGlyTyrValAspIleMetTyrAspGlyLeuAspAlaVal 1499
DB 4867 TTCGTTTGGCTCCAGGATGTTGGTGGACATCATGTACATGGGCTGGATGCTGTG 4926
QY 1500 GlyValAspGlnProIleMetAsnHisAsnProTrpMetLeuLeuTyrPheIleSer 1519
DB 4927 GCGGTGGACAGCAGCCCATCATGAACCAACCAACCCCTGGATGCTGCTACTTTCATCTCG 4986
QY 1520 PheLeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValValValGluAsn 1539
DB 4987 TTCCTGCTCATTTGGCCCTCTTTGCTGTAACATGTTTGGGTGGTGGTGGAGAAC 5046
QY 1540 PheHisLysCysArgGlnHisGlnGluGluAlaArgArgArgGluGluLysArg 1559
DB 5047 TTCACAGTGTCCGACACACAGAGAGAGAGGAGGCCCGCGCGGAGAGAGAGCGC 5106
QY 1560 LeuArgArgLeuGluLysLysArgArg----- 1568
DB 5107 CTACGAGACTGGAGAGAGAGAGAGAGAACTAATGCTGGACGATGTAATTGCTTCGGC 5166
QY 1569 -----LysAlaGlnCysLysProTyrTyrSerAspTyrSerArg 1581

DB 5167 AGCTCAGCCAGCGCTGCGTCAAGACCCAGTGCACAACTTACTACTCGACTACTCCGC 5226
QY 1582 PheArgLeuLeuValHisHisLeuCysThrSerHisTyrLeuAspLeuPheIleThrGly 1601
DB 5227 TTCGGCTCTCTGTCACCACTTGTGCACAGCAGCACTACCTGAGACTCTTTCATCAGGT 5286
QY 1602 ValIleGlyLeuAsnValValThrMetAlaMetGluHisTyrGlnGlnProGlnIleLeu 1621
DB 5287 GTCATCGGGCTGAAACGTTGCTCACCATGGCCATGGAGCACTACCCAGACGCCAGATTCTG 5346
QY 1622 AspGluAlaLeuLysIleCysAsnTyrIlePheThrValIlePheValLeuGluSerVal 1641
DB 5347 GATGAGGCTCTGAGAGATCTGCAACTACATCTTCACTGTCACTTGTCTTGGAGTCAGTT 5406
QY 1642 PheLysLeuValAlaPheGlyPheArgPhePheGlnAspArgTyrAsnGlnLeuAsp 1661
DB 5407 TTCAAACTGTGGCTTTGGTTTCGTCGGTTCCTCCAGGACAGGTGGAACCCAGCTGAC 5466
QY 1662 LeuAlaIleValLeuLeuSerIleMetGlyIleThrLeuGluIleGluValAsnAla 1681
DB 5467 CTGGCCATTTGCTGCTGCTCATCATGGGCATCAGCTGGAGGAATCGAGGTCAACGCC 5526
QY 1682 SerLeuProIleAsnProThrIleIleArgIleMetArgValLeuArgIleAlaArgVal 1701
DB 5527 TCGTTCGCCATCAACCCACCATCATCCGCATCATGAGGGTCTGCGCATTTGCCGAGTG 5586
QY 1702 LeuLysLeuLeuLysMetAlaValGlyMetArgAlaLeuLeuAspThrValMetGlnAla 1721
DB 5587 CTGAAGCTGCTGAAGATGGCTGTGGGCATCGGGCGCTGCTGGACACCGTGCAGGCC 5646
QY 1722 LeuProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPhePheIlePheAlaAla 1741
DB 5647 CTGCCCCAGGTGGGGAACCTGGGACTTCTCTTCATCTTGTGTTTTCATCTTTCAGCT 5706
QY 1742 LeuGlyValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGluGlyLeu 1761
DB 5707 CTGGGCTGGAGCTCTTTGGAGACTGGAGTGTGACGAGACACACCCCTGTGAGGGCTG 5766
QY 1762 GlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgValSer 1781
DB 5767 GGCCGCTCATGCCCTTTCCGAACTTTGGCATGGCTTCTTAAACCTCTTCCGAGTCTCC 5826
QY 1782 ThrGlyAspAsnTrpAsnGlyIleMetLysAspThrLeuArgAspCysAspGlnGluSer 1801
DB 5827 ACAGGTGACATTTGGAATGGCATTTATGAAGACACCCCTCCGGGACTGTGACAGGAGTCC 5886
QY 1802 ThrCysTyrAsnThrValIleSerProIleTyrPheValSerPheValLeuThrAlaGln 1821
DB 5887 ACCTGCTACAAACAGCGTCATCTCGCCTATCTTGTGTTGCTCTGCTGAGGCCCCAG 5946
QY 1822 PheValLeuValAsnValIleAlaValLeuMetLysHisLeuGluGluSerAsnLys 1841
DB 5947 TTCGTGCTAGTCAACGTGGTGATCGCGCTGCTGATGAGCACCCTGGAGAGAGCAACAAG 6006
QY 1842 GluAlaLysGluGluAlaGluLeuGluAlaGluLeuGluMetLysThrLeuSer 1861
DB 6007 GAGGCCAAGGAGGAGGCGGAGCTAGAGCTGAGCTGGAGTGGAGATGAAGACCCCTCAGC 6066
QY 1862 ProGlnProHisSerProLeuGlySerProPheLeuTrpProGlyValGluGlyProAsp 1881
DB 6067 CCCAGGCCCACTCGCACACTGGGCGAGCCCTTCTCTGCTGGGCTGGAGGCCGCCAGC 6126
QY 1882 SerProAspSerProLysProGlyAlaLeuHisProAlaAlaHisAlaArg-SerAlaSer 1901
DB 6127 AGCCCCAGACGCCCAAGCCTGGGGCTCTGCACCCAGCGGCCCGCCAGGATCAGCCTC 6186
QY 1901 rHisPheSerLeuGluHisProThrMetGlnProHisProThrGluLeuProGlyProAs 1921
DB 6187 CCACCTTTTCCCTGGAGCACCCACGATGACGCCCCACCCAGGAGTGCAGGAGCAGCA 6246
QY 1921 pLeuLeuThrValArgLysSerGlyValSerArgThrHisSerLeu-ProAsnAspSerT 1941

CC influx through L type calcium channels in cells

SQ Sequence 7286 BP; 1467 A; 2224 C; 2064 G; 1531 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 0 Length: 7286
Score: 11111.00 Matches: 2135
Percent Similarity: 94.80% Conservative: 35
Best Local Similarity: 93.27% Mismatches: 95
Query Match: 93.34% Indels: 24
DB: 3 Gaps: 5

US-09-611-257A-37 (1-2266) x AA252309 (1-7286)

Qy 1 MetAspGluGluAspGlyAlaGluGluSerGlyGlnProArgSerPheMet 20
Db 158 ATGGACGAGGAGGATGGAGCGGGCGCGGAGAGTCGGGACACGCCGCTACAG 217
Qy 21 ArgLeuAspLeuSerGlyAlaGlyGlyArgProGlyProGlySerAlaGluLeuAsp 40
Db 218 CAGCTCAACGACCTGTCCGGGGCGGGGGCGCGGAGGGGCGGGGTCCAGCAAAAGGAC 277
Qy 41 ProGlySerAlaAspSerGluAlaGluGlyLeuProTyrProAlaLeuAlaProVal 60
Db 278 CCGGGCAGCGGACTCCGAGCGGAGGGGCTGCCGTACCCGGCGCTAGCCCCGGTGGTT 337
Qy 61 PhePheTyrLeuSerGlnAspSerArgProArgSerTyrCysLeuArgThrValCysAsn 80
Db 338 TTCTTTACTTGAACGACGACGCGCGCGGAGCTGGTCTCCGACCGCTCTGTAAC 397
Qy 81 ProTyrPheGluArgIleSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMet 100
Db 398 CCGTGGTTCGAGCGAGTCAGTATGCTGTCAATTTCTCAACTGTGTGACTCTGGGTATG 457
Qy 101 PheArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPhe 120
Db 458 TTCAGCGGTGTGAGGACATTCCTGTGACTCCAGCGCTGCCGGATCCTCGAGCGCTTC 517
Qy 121 AspAspPheIlePheAlaPheAlaValGluMetValValCysMetValAlaLeuGly 140
Db 518 GATGACTTCATCTTGGCTTCTTGTGCTGGAATGGTGTGAAGATGGTGGCTTGGGC 577
Qy 141 IlePheGlyIleValCysCysTyrLeuGlyAspThrTrpAsnArgLeuAspPheIleVal 160
Db 578 ATCTTTGGGAAGAATGTACTCGGGAGACACTTGGAAACCGGCTTGACTTTTTCATTGTC 637
Qy 161 IleAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArg 180
Db 638 ATTGACGGATGCTGGAGTATTCGCTGGACCTGCAGAACCTCAGCTTCTCCGACGTCAGG 697
Qy 181 ThrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeu 200
Db 698 ACAGTCGGTGTGTCGACCGCTCAGGGCCATTAAACCGGGTGCACGATCGCATTCCTC 757
Qy 201 ValThrLeuLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePhe 220
Db 758 GTCACATTTACTGTGGACACCTTGCTATGCTGGGCAACGCTTCGCTGCTCTGTTTCTTC 817
Qy 221 ValPhePheIlePheGlyIleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArg 240
Db 818 GTCTTTTTCATCTTGGCATCGTGGCGCTCAGCTGTGGGACGAGCTGCTTCGCAACCGA 877
Qy 241 CysPheLeuProGluAsnPheSerLeuProLeuSerValAspLeuGluArgTyrGln 260
Db 878 TGCTTCTCCCGAGAACTTCAGGCTCCCTGAGCGTGGACCTGGAGCCCTATTACCA 937
Qy 261 ThrGluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArg 280
Db 938 ACAGAGATGAGGACGAGAGCCCTTCATCTGCTCTCAGCCTCGGGAGATGGCATGAGA 997
Qy 281 SerCysArgSerValProThrLeuArgGlyAspGlyGlyGlyProProCysGlyLeu 300
Db 998 TCCTGCGAGAGTGTGCCACACTCGGTGGGGAAGGGGGTGTGGCCCAACCCCTGAGTCTG 1057

Qy 301 AspTyrGluAlaTyrAsnSerSerSerAsnThrThrCysValAsnTrpAsnGlnTyrTyr 320
Db 1058 GACTATGAGACCTATAACAGTTCAGCAACACCACTGTGTGTCACTGGAACAGTACTAT 1117
Qy 321 ThrAsnCysSerAlaGlyGluGluAsnProPhePheGlyAlaIleAsnPheAspAsnIle 340
Db 1118 ACCAATCTGCTCTGGGGGAGCACAACCCCTTCAAGAGCGCATCACTTTTGACAACT 1177
Qy 341 GlyTyrAlaTrpIleAlaIlePheGlnValIleThrLeuGluGlyTyrValAspIleMet 360
Db 1178 GGCTATGCTGGATCGCATCTTCCAGTCAATCACACTGGAGGGCTGGGTGACATCATG 1237
Qy 361 TyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleIle 380
Db 1238 TACTTCGTAAATGGACGCTCACTCTCTTCAAACTTCACTTCACTTCTTCTCATCATC 1297
Qy 381 ValGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGlu 400
Db 1298 GTGGGCTCTCTTCTCATGATCACTGTGCTGTGTGTGATGTCACGAGTCTTCCGAG 1357
Qy 401 ThrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAla 420
Db 1358 ACCAAACAGCGGAGAGTCAGCTGATCGGGAGCAGCGTGTACGATTCTCTCCAATGCT 1417
Qy 421 SerThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLeuLysTyrLeu 440
Db 1418 AGCACCTTGGCAAGCTTCTCTGAGCCAGCGAGCTGTATGAGGAGCTACTCAAGTACCTG 1477
Qy 441 ValTyrIleLeuArgIleValAlaArgArgLeuAlaGlnValSerArgAlaAlaGlyVal 460
Db 1478 GTGTACATCTCTCCAAAGCAGCCCGAAGGCTGCCCGAGGCTCTAGGGCTATAGCGGTG 1537
Qy 461 ArgValGlyLeuLeuSerSerProAlaProLeuGlyGlyGlnGluThrGlnProSerSer 480
Db 1538 CGGGCTGGCTGCTCAGCAGCCAGTGGCCGCTAGTGGGAGGAGCCGCCAGCTGGC 1597
Qy 481 SerCysSerArgSerHisArgArgLeuSerValHisHisLeuValHisHisHisHis 500
Db 1598 AGCTGCACCTCGCTCACACCGCTGTCTGTCTGCCACCACCTGGTCCACACCATCACAC 1657
Qy 501 HisHisHisTyrHisLeuGluValAsnGlyThrLeuArgAlaProArgAlaSerProGlu 520
Db 1658 CACCATCACCATCACCATCTGGGTAATGGGAGCTCAGAGTTCCCGGGCGAGCCAGAG 1717
Qy 521 IleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProSerThrPro 540
Db 1718 ATCCAGACAGGGATGCCAATGGCTCTCGCGGCTCATGTCTACCAACCCCTCTACACCC 1777
Qy 541 AlaLeuSerGlyAlaProProGlyGlyAlaGluSerValHisSerPheTyrHisAlaAsp 560
Db 1778 ACTCCCTCTGGGGGCGCTCCGAGGGGTGCGGAGTCTGTACACAGCTTCTTACCATGTGAC 1837
Qy 561 CysHisLeuGluProValArgCysGlnAlaProProProArgSerProSerGluAlaSer 580
Db 1838 TGCCACTTGGAGCCAGTCCGTTGCCAGGACCCCTCCAGATGCCATGCCAGGAGCATCT 1897
Qy 581 GlyArgThrValGlySerGlyLysValTyrProThrValHisThrSerProProProGlu 600
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Qy 601 ThrLeuLysGluLysAlaLeuValGluValAlaAlaSerSerGlyProProThrLeuThr 620
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Qy 641 ThrGlyAlaCysGlnSerSerCysLysIleSerSerProCysLeuLysAlaAspSerGly 660
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661 AlaCysGlyProAspSerCysProTyrCysAlaArgAlaGlyAlaGlyGluValGluLeu 680
2138 GCCTGCGGGCGGACAGTGTCTCCTACTGTGCGCGACAGGACGAGGAGCCAGAGTCC 2197
681 AlaAspArgGluMetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAla 700
2198 GCTGACCATGTCATGCTGACTCAGACAGCGAGGCTGTGTATGAGTTTACACAGGACGCT 2257
701 GlnHisSerAspLeuArgAspProHisSer--ArgArgGlnArgSerLeuGlyProAsp 719
2258 CAGCACAGTACCTCCCGGATCCCAACAGCGCGCGGACGAGCGGAGCCCTGGGCGCCAGAT 2317
720 AlaGluProSerSerValLeuAlaPheTyrArgLeuIleCysAspThrPheArgLysIle 739
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740 ValAspSerIleTyrPheGlyArgGlyIleValMetIleAlaIleValAsnThrLeuSer 759
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Qy 1499 ValGlyValAspGlnGlnProIleMetAsnHisAsnProTTPMetLeuLeuTyrPheIle 1518
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Qy 461 ArgValGlyLeuLeuSerSerProAlaProLeuGlyGlyGlnGluThrGlnProSerSer 480
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3172 GCCCACCATGAGATGAAATGTCGCCCAAGTGCCCGCAGCTCCCGCACAGTCCCTGGAGT 3231
1099 AlaAlaSerSerTrpThrSerArgArgSerSerArgAsnSerLeuGlyArgAlaProSer 1118
Db : : : : :
3232 CGCGCAAGCAGCTGGACCGCAGCGCTCCAGCAGGAACAGCCTGGGCGCGGCCCCAGC 3291
1119 LeuLysArgArgSerProSerGlyGluArgArgSerLeuSerGlyGluGlnGlu 1138
Db : : : : :
3292 CTAAAGCGGAGAGCCCGAGCGGAGCGGAGGTCCCTGTCTGGAGAGGGCCAGAG 3351
1139 SerGlnAspGluGluSerSerGluGluArgAlaSerProAlaGlySerAspHis 1158
Db : : : : :
3352 AGTCAGGATGAGGAGGAAAGTTTCAGAGAGAGCCCGGCGCAGCCAGCGGAGTGCACAT 3411
1159 ArgHisArgGlySerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeu 1178
Db : : : : :
3412 CGCCACAGGGGTCTCTTGGAACTGTGAGCCCAAGAGTTCTTTTGACCTGCCTGACACTCTG 3471
1179 GlnValProGlyLeuHisArgThrAlaSerGlyArgGlySerAlaSerGluHisGlnAsp 1198
Db : : : : :
3472 CAGTGC CGGGCTGACCGCACAGCCAGCGCGGAGCTCTGCTCTGAGCACCAAGAC 3531
1199 CysAsnGlyLysSerAlaSerGlyArgLeuAlaArgAlaLeuArgProAspAspPro 1218
Db : : : : :
3532 TGTAATGGCAAGTCGGCTTCAGGGCGTTTGGCCCGCACCTTGAGGACTGATGACCCCAA 3591
1219 LeuAspGlyAspAspAlaAspAspGluGlyAsnLeuSerLysGlyGluArgValArgAla 1238
Db : : : : :
3592 CTGGATGGGGATGATGACAATGATGAGGGAATCTGAGCAAAAGGGGAACGATACAAAGCC 3651
1239 TrpIleArgAlaArgLeuProAlaCysTyrLeuGluArgAspSerTrpSerAlaTyrIle 1258
Db : : : : :
3652 TGGGTGAGATCCCGGCTTCCTGCTGTCGCGAGCGAGATTCTGTGTCGCGCTATATC 3711
1259 PheProGlnSerArgPheArgLeuLeuCysHisArgIleIleThrHisLysMetPhe 1278
Db : : : : :
3712 TTTCTCTCAGTCAAGGTTTCGTCTCTGCTGTACCCGATCATCCACCAAGATGTTT 3771
1279 AspHisValValLeuValIlePheLeuAsnCysIleThrIleAlaMetGluArgPro 1298
Db : : : : :
3772 GACCATGTGGTCCCTCGTATCATCTTCTCACTGTATCACCATCGCTATGGAGCGCCCC 3831
1299 LysIleAspProHisSerAlaGluArgIlePheLeuThrLeuSerAsnTyrIlePheThr 1318
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3832 AAAATGACCCCCAGCGCTGAGCGCATCTTCCTGACCCCTCTCAACTACATCTTCAGC 3891
1319 AlaValPheLeuAlaGluMetThrValLysValValAlaLeuGlyTrpCysPheGlyGlu 1338
Qy

3892 GCAGTCTTTTCTAGCTGAAATGACAGTGAAGGTGGTGCCACTGGGCTGGTCTTTGGGGAG 3951
Qy GlnAlaTyrLeuArgSerSerTrpAsnValLeuAspGlyLeuLeuValLeuIleSerVal 1358
Db CAGGCCCTACTCGCGCAGCAGCTGGAATGTCTGGACGGCTTGTGGTGCTCATCTCCGTC 4011
Qy IleAspIleLeuValSerMetValSerAspSerGlyThrLysIleLeuGlyMetLeuArg 1378
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Qy ValLeuArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeu 1398
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Qy LysLeuValValGluThrLeuMetSerSerLeuLysProIleGlyAsnIleValValIle 1418
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Qy SerTyrArgTrpValArgHisLysTyrAsnPheAspAsnLeuGlyGlnAlaLeuMetSer 1478
Db AGTACCGATGGGTCCGGCACAAGTACAACTTTGACAACTGGCGCAGGCTCTGATGTC 4371
Qy LeuPheValLeuAlaSerLysAspGlyTrpValAspIleMetTyrAspGlyLeuAspAla 1498
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Qy ValGlyValAspGlnGlnProIleMetAsnHisAsnProTrpMetLeuLeuTyrPheIle 1518
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Qy SerPheLeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValValValGlu 1538
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Qy AsnPheHisLysCysArgGlnHisGlnGluGluAlaArgArgArgGluGluLys 1558
Db AACTTCATTAAGTCGACAGCAGCACCCAGGAGGAGGAGCGGCGGCTGAGGAAG 4611
Qy ArgLeuArgArgLeuGluLysLysArgArgLysAlaGlnCysLysProTyrTyrSerAsp 1578
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Qy TyrSerArgPheArgLeuLeuValHisHisLeuCysThrSerHisTyrLeuAspLeuPhe 1598
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Db 1621 ACTCCCTCTGGGGGCCCTCCGAGGGTGGGAGTCTGTACACAGCTTCTACACAGTCTGAC 1680
Qy 561 CysHisLeuGluProValArgCysGlnAlaProProProArgSerProSerGluAlaSer 580
Db 1681 TGCCACTTGGAGCAGTCCGTTGGCAGGACCCCTCCAGATGCCATCGGAGGCATCT 1740
Qy 581 GlyArgThrValGlySerGlyValTyProThrValHisThrSerProProGlu 600
Db 1741 GGTAGGACTTGGGTAGTGGGAAGGTGTACCCCACTGTGCATACAGCCCTCCACAGAG 1800
Qy 601 ThrLeuGlyGluLysAlaLeuValGluValAlaAlaSerSerGlyProProThrLeuThr 620
Db 1801 ATACTGAGGATTAAGCACTAGTGAGGTGGCCCCCAGCCCTGGGCCCCCCACCCCTAC 1860
Qy 621 SerLeuAsnIleProProGlyProTyProSerMetHisLysLeuLeuGluThrGlnSer 640
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Qy 641 ThrGlyAlaCysGlnSerSerCysLysIleSerSerProCysLeuLysAlaAspSerGly 660
Db 1921 ACGGAGCCTGCCATAGCTCTGCAAAATCTCCAGCCCTTGTCTCAAGGCAGACAGTGA 1980
Qy 661 AlaCysGlyProAspSerCysProTyProCysAlaArgAlaGlyAlaGlyGluValGluLeu 680
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Qy 681 AlaAspArgGluMetProAspSerAspSerGluAlaValTyGluPheThrGlnAspAla 700
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Qy 701 GlnHisSerAspLeuArgAspProHisSer---ArgArgGlnArgSerLeuGlyProAsp 719
Db 2101 CAGCACAGTACCTCCGGGATCCCAACAGCGCGGCGACAGCGAGCTCTGGGCCAGAT 2160
Qy 720 AlaGluProSerSerValLeuAlaPheThrArgLeuIleCysAspThrPheArgLysIle 739
Db 2161 GCAGAGCCTAGTCTGTCTGCTGCTTCTGGAGGCTGATCTGTGACACATTCGGAAGATC 2220
Qy 740 ValAspSerLysTyPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSer 759
Db 2221 GTAGATAGCAATACTTTGGCCGGGATCATGTCGCATCTCTGGTCAATACACTCAGC 2280
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Qy 780 IleValPheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuValTyGlyPro 799
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Qy 800 PheGlyTyIleLysAsnProTyAsnIlePheAspGlyValIleValIleSerVal 819
Db 2401 TTTGGCTACATTAAGATCCCTACACATCTTTGATGTTGTCATTTGTGTCATCAGTGTG 2460
Qy 820 TrpGluIleValGlyGlnGlnGlyGlyLeuSerValLeuArgThrPheArgLeuMet 839
Db 2461 TGGGAGATTGTGGCCAGCAGGAGTGGCCTGTGCTGCTGCGACCTTCGCGCTGATG 2520
Qy 840 ArgValLeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMet 859
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Qy 880 SerIleLeuGlyMetHisLeuPheGlyCysLysPheAlaSerGluArgAspGlyAspThr 899
Db 2641 AGCATCTCGGCATCATCTCTTTGGTTGCAAGTTCGCATCTGAAAGCGGATGGGACACG 2700
Qy 900 LeuProAspArgLysAsnPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIle 919
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Qy 920 LeuThrGlnGluAspTrpAsnLysValLeuTyPheGlyMetAlaSerThrSerSerTrp 939
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Qy 960 ValAlaIleLeuValGluGlyPheGlnAlaGluGluIleSerLysArgGluAspAlaSer 979
Db 2881 GTGGCCATTTCTGTGAAGGATTCAGGCAGAG----- 2913
Qy 980 GlyGlnLeuSerCysIleGlnLeuProValAspSerGlnGlyAspAlaAsnLysSer 999
Db 2914 -----GGAGATGCCACCAAGTCT 2931
Qy 1000 GluSerGluProAspPheSerProSerLeuAspGlyAspGlyAspArgLysLysCys 1019
Db 2932 GAGTCAGAGCCTGATTTCTTTCGCCAGTGTGATGGTGTATGGGACAGAAAGAGCGC 2991
Qy 1020 LeuAlaLeuValSerLeuGlyGluHisProGluLeuArgLysSerLeuLeuProLeu 1039
Db 2992 TTGGCCCTGTGTGGTGTGGGAGAACACGCGGAACCTACGAAAGAGCTTTTSCCACCCTC 3051
Qy 1040 IleIleHisThrAlaAlaThrProMetSerLeuProLysSerThrSerThrGlyLeuGly 1059
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Qy 1080 Ala---HisGluMetLysSerProProSerAlaArgSerSerProHisSerProTrpSer 1098
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QY 1339 GlnAlaTyrLeuArgSerSerTrpAsnValLeuAspGlyLeuLeuValLeuSerVal 1358
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QY 1379 ValLeuArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeu 1398
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QY 1419 CysCysAlaPhePheIleIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPhe 1438
DB 4192 TGCTGTGCTCTTCTCATATTTTGGAAATCTCGGGGTGAGCTCTTCAAGGGAAGTTC 4251
QY 1439 PheValCysGlnGlyGluAspThrArgAsnIleThrAsnLysSerAspCysAlaGluAla 1458
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QY 1459 SerTyrArgTrpValArgHisGlyTyrAsnPheAspAsnLeuGlyGlnAlaLeuMetSer 1478
DB 4312 AGCTACCGATGGTCCGGCACAGTACAACTTTGACAACTGGGCGAGGCTCTGATGTC 4371
QY 1479 LeuPheValLeuAlaSerLysAspGlyTrpValAspIleMetTyrAspGlyLeuAspAla 1498
DB 4372 CTGTTTGTGTGGCTTCAAGGATGGTGGGTGACATCATGTATGATGGCTCGATGCT 4431
QY 1499 ValGlyValAspGlnProIleMetAsnHisAsnProTrpMetLeuLeuTyrPheIle 1518
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DB 4552 AACTTCCATAAGTCAGACACACAGAGGAGGAGGCGGCGGTGAGAGAAG 4611
QY 1559 ArgLeuArgArgLeuGluLysLysArgArg-----LysAlaGln 1571
DB 4612 CGACTACGGAGCTGGAGAAAAGAGAGAGTGAAGGAGAGCAGATGGCCGAGCCAG 4671
QY 1572 CysLysProTyrTyrSerAspTyrSerArgPheArgLeuLeuValHisLeuCysThr 1591
DB 4672 TGCAAGCCCTACTACTCTGACTCTGAGATTCGGGCTCTTGTGTCCACCACTGTGTACC 4731
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DB 4792 ATGGACATTAACAGCAGCCCGATCTGCGAGGCTCTGAGAGTCTGCAATTACATC 4851
QY 1632 PheThrValIlePheValLeuGluSerValPheLysLeuValAlaPheGlyPheArgArg 1651

DB 4852 TTATCCGTCATCTTGTCTTGTGTCAGTCTTCAAACTTGTGCTTGTGCTTCCGCGT 4911
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QY 1672 IleThrLeuGluGluIleGluValAsnAlaSerLeuProIleAsnProThrIleIleArg 1691
DB 4972 ATCACACTGGAGGAGATTGAGTCAATCTGCTGCTGCCCATCAACCCACCATCATCGT 5031
QY 1692 IleMetArgValLeuArgIleAlaArgValLeuLysLeuLysMetAlaValGlyMet 1711
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QY 1892 HisProAlaAlaHisAlaArgSerAlaSerHisPheSerLeuGluHisProThrMetGln 1911
DB 5632 CACACACTGCCACATTTGGAGCAGCTCGGGCTTCTCCCTTGAGCACCCACCATGGTA 5691
QY 1912 ProHisProThrGluLeuPro-----GlyProAspLeuLeuThrValArgLysSer 1928
DB 5692 CCCCACCCCGAGGAGTGGCCAGTCCCTAGGACACAGACCTGTGCTGCTGAGGAAGTCT 5751
QY 1929 GlyValSerArgThrHisSerLeuProAsnAspSerTyrMetCysArgHisGlySerThr 1948
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QY 1969 LeuSerValHisSerGlnProAlaAspThrSerTyrIleLeuGlnLeuProLysAspAla 1988
DB 5872 TTGTCCCTTCACTCCCAACAGCAGACACAGCTGTCTTACAGCTTCCCAAGATGTG 5931
QY 1989 ProHisLeuLeuGlnProHisSerAlaProThrTrpGlyThrIleProLysLeuProPro 2008
DB 5931

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Qy 141 IlePheGlyLysLysCysTyrLeuGlyAspThrTrpAsnArgLeuAspPheIleVal 160
Db 534 ATCTTTGGGAAGAATGTTACCTGGGAGACACTTTGGAAACGGCTTGACTTTTTCATTGTGTC 593
Qy 161 IleAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArg 180
Db 594 ATTGACGGATGCTGGAGTATTCTGACCTGCAGAACAGTTCAGCTTCTCCGCAAGTCAGG 653
Qy 181 ThrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeu 200
Db 654 ACAGTCGGTGTGTCGCAACCGCTCAGGGCCATTAAACCGGGTGCACGACATGCGCATTTCTC 713
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Qy 221 ValPhePheIlePheGlyIleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArg 240
Db 774 GTCTTTTTCATCTTTGGCATCGTGGCGGTCAGCTGTGGCGAGGACTGCTTGGCAACCGG 833
Qy 241 CysPheLeuProGluAsnPheSerLeuProLeuSerValAspLeuGluArgTyrTyrGln 260
Db 834 TGCTTCTCTCCCGAAGACTTCAGGCTCCCCCTGAGCGTGGACCTGGAGCCTTATTACAG 893
Qy 261 ThrGluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArg 280
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Qy 281 SerCysArgSerValProThrLeuArgGlyAspGlyGlyGlyGlyProProCysGlyLeu 300
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Qy 301 AspTyrGluAlaTyrAsnSerSerSerAsnThrThrCysValAsnTrpAsnGlnTyrTyr 320
Db 1014 GACTATGAGCTTATACAGTTCAGCAACACCACTGTGTCAACTGGAAACCACTACTAT 1073
Qy 321 ThrAsnCysSerAlaGlyGluHisAsnProPheLysGlyAlaIleAsnPheAspAsnIle 340
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Qy 401 ThrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAla 420
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Qy 421 SerThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLeuLysTyrLeu 440
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Db 1434 GTGTACATCTCTCCGAAGACGCGGAGGCTGGCCCAAGGCTCTAGGGCTATAGGCGTG 1493
Qy 461 ArgValGlyLeuLeuSerSerProAlaProLeuGlyGlyGlnGluThrGlnProSerSer 480
Db 1494 CGGGTGGGCTGCTCAGCAGGCCAGTGCGCCGTAGTGGGCGAGGACCCCAAGCTGGC 1553
Qy 481 SerCysSerArgSerHisArgLeuSerValHisLeuValHisHisHisHisHis 500
Db 1554 AGCTGCACCTCGCTACACCGCTGCTGTCTGTCCACCACTTGGTCCACCACCATCACCC 1613

Qy 501 HisHisHisTyrHisLeuGlyAsnGlyThrLeuArgAlaProArgAlaSerProGlu 520
Db 1614 CACCATCACCACCTACCATCTGGGTAAATGGACGCTCAGAGTCTCCCGGGCGAGCCAGAG 1673
Qy 521 IleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProSerThrPro 540
Db 1674 ATCCAGACAGGATGCCAATGGGTCTCGCGGCTCATGTACACACCATCTCTACACCC 1733
Qy 541 AlaLeuSerGlyAlaProProGlyGlyAlaGluSerValHisSerPheTyrHisAlaAsp 560
Db 1734 ACTCCCTCTGGGGCCCTCCGAGGGTGGAGTCTGTACACAGCTTCTACCATGCTGAC 1793
Qy 561 CysHisLeuGluProValArgCysGlnAlaProProProArgSerProSerGluAlaSer 580
Db 1794 TGGCACTTGGAGCAGTCCGTTGCCAGGCACCCCTCCACAGATGCCCATCGAGGCATCT 1853
Qy 581 GlyArgThrValGlySerGlyLysValTyrProThrValHisThrSerProProGlu 600
Db 1854 GGTAGACTGTGGGTAGTGGGAAGGTGTACCCCACTGTGCATACCAAGCCCTCCACCAAG 1913
Qy 601 ThrLeuLysGluLysAlaLeuValGluValAlaAlaSerSerGlyProProThrLeuThr 620
Db 1914 ATACTGAGATTAAGCACTAGTGGAGTGGCCCCCAGCCCTGGGCCCTCCACCTCACC 1973
Qy 621 SerLeuAsnIleProProGlyProTyrSerSerMetHisLysLeuLeuGluThrGlnSer 640
Db 1974 AGCTTCAACATCCACCTGGGCCCTTCAGCTCCATGCACAAAGCTCTCTGGAGACACAGT 2033
Qy 641 ThrGlyAlaCysGlnSerSerCysLysIleSerSerProCysLeuLysAlaAspSerGly 660
Db 2034 ACCGGAGCTTGCATAGCTCTCCAAAATCTCCAGCCCTTGTCTCCAAAGGACAGTGGGA 2093
Qy 661 AlaCysGlyProAspSerCysProTyrCysAlaArgAlaGlyAlaGlyGluValGluLeu 680
Db 2094 GCCTGGCGGCGGACAGTGTCTCTACTGTGTCGGGACAGGACGAGGAGCCAGATCC 2153
Qy 681 AlaAspArgGluMetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAla 700
Db 2154 GCTGACCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2213
Qy 701 GlnHisSerAspLeuArgAspProHisSer--ArgArgGlnArgSerLeuGlyProAsp 719
Db 2214 CAGCACAGTACCTCCGGGATCCCCACAGCGCGGCGGACGAGGAGCCCTGGGCCCCAGAT 2273
Qy 720 AlaGluProSerValLeuAlaPheTrpArgLeuIleCysAspThrPheArgLysIle 739
Db 2274 GCAGAGCTTAGTCTGTGCTGGCTTCTGAGGCTGATCTGTGACACATTCGGAAGATC 2333
Qy 740 ValAspSerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSer 759
Db 2334 GTAGATAGCAAAATACTTTGGCCGGGAATCATGATGCCATCTCTGTGTCATACACTCAGC 2393
Qy 760 MetGlyIleGluTyrHisGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsn 779
Db 2394 ATGGGCATCCAGTACCAACGAGCAGCCGAGAGCTCACCAACGCGCTCGGAATCAGCAAC 2453
Qy 780 IleValPheThrSerLeuPheAlaLeuGluMetLeuLysLeuLeuValTyrGlyPro 799
Db 2454 ATCGTCTTACCAGCTCTTTCGCTTGGAGATGCTGCTGAAACTGCTGTCTACGGTCCC 2513
Qy 800 PheGlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleValIleSerVal 819
Db 2514 TTTGGCTACATTAAGAAATCCCTACACATCTTTGATGGTGTGTCATTTGGTGCATCAGTGTG 2573
Qy 820 TrpGluIleValGlyGlnGlnGlyGlyLeuSerValLeuArgThrPheArgLeuMet 839
Db 2574 TGGGAGATTGGGCCAGCAGGAGGTGGCTGTTCGGTGTGTCGGACCTTCCTCCGCTGATG 2633
Qy 840 ArgValLeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMet 859
Db 2634 CGGGTGTGAAGCTGGTGGCTTCTCTCGCGGCCCTTCGAGCGCCAGCTCGTGGTGTCTCATG 2693

Qy 860 LysThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePhe 879
Db 2694 AAGACATGGACACGTCGCCACCTTCCTGCATGCTCCCTCATGCTGTTCATCTTC 2753
Qy 880 SerIleLeuGlyMetHisLeuPheGlyCysLysPheAlaSerGluArgAspGlyAspThr 899
Db 2754 AGCATCTGGGCGATGATCTCTTTGGTTGCAAGTTCCGATCTGAACGGATGGGACACG 2813
Qy 900 LeuProAspArgLysAsnPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIle 919
Db 2814 TTGGCAGACCGGAGAAATTCGATCCCTGCTCGGCCATCGTCACTGTCTTCAGATT 2873
Qy 920 LeuThrGlnGluAspTrpAsnLysValLeuThrAsnGlyMetAlaSerThrSerSerTrp 939
Db 2874 CTGACTCAGGAAGACTGGAAATTAAGTCTCTACAAACGCATGGCTCCACATCGCTTGG 2933
Qy 940 AlaAlaLeuThrPheIleAlaLeuMetThrPheGlyAsnTrpValLeuPheAsnLeuLeu 959
Db 2934 GCTGCTCTTACTTCACTCGCCCTCATGACTTTTGGCAACTATGTGCTCTTTAACTGCTG 2993
Qy 960 ValAlaIleLeuValGluGlyPheGlnAlaGluIleSerLysArgGluAspAlaSer 979
Db 2994 GTGGCCATTCCTGTGAAGGATTCAGGCAGAG----- 3026
Qy 980 GlyGlnLeuSerCysIleGlnLeuProValAspSerGlnGlyGlyAspAlaAsnLysSer 999
Db 3027 -----GGAGATGCCACCAAGTCT 3044
Qy 1000 GluSerGluProAspPheSerProSerLeuAspGlyAspGlyAspArgLysCys 1019
Db 3045 GAGTCAGAGCCTGATTTCTTTCCGCCAGTGTGATGGTGGGACAGAAAGAGCGC 3104
Qy 1020 LeuAlaLeuValSerLeuGlyGluHisProGluLeuArgLysSerLeuLeuProProLeu 1039
Db 3105 TTGGCCCTGTGTGGTGGGAGAACACGCGGAACTACGAAAGAGCCTTTTGCACCCCTC 3164
Qy 1040 IleIleHisThrAlaAlaThrProMetSerLeuProLysSerThrSerThrGlyLeuGly 1059
Db 3165 ATCATCATACGGCTGGCGACACCAATGTCAACCCCAAGAGCTCCAGCACAGGTGTGGGG 3224
Qy 1060 GluAlaLeuGlyProAlaSerArgArgThrSerSerGlySerAlaGluProGlyAla 1079
Db 3225 GAAGCACTGGGCTCTGGCTCTCGACGTACAGTAGCAGTGGTCCGCTGAGCTGGAGCT 3284
Qy 1080 Ala---HisGluMetLysSerProProSerAlaArgSerSerProHisSerProTrpSer 1098
Db 3285 GCCCACCATGATGATAAATGTCCGCCAAGTCCCGCAGCTCCCGCAGCTCCCTGGAGT 3344
Qy 1099 AlaAlaSerSerTrpThrSerArgSerSerArgAsnSerLeuGlyArgAlaProSer 1118
Db 3345 CGCGCAAGCAGCTGGACAGCAGCGCTCCAGCAGGAACAGCCTGGGCGCGGCCCCAGC 3404
Qy 1119 LeuLysArgArgSerProSerGlyGluArgArgSerLeuLeuSerGlyGluGlnGlu 1138
Db 3405 CTAAGCGGAGAGCCCGAGCGGGAGCGGAGGTCCCTGCTGTCTGGAGAGGGCCAGGAG 3464
Qy 1139 SerGlnAspGluGluGluSerSerGluGluArgAlaSerProAlaGlySerAspHis 1158
Db 3465 AGTCAGGATGAGGAGGAAAGTTTCAGAGAGACCGCGGCAGCCCGCAGCGGAGTGCAT 3524
Qy 1159 ArgHisArgGlySerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeu 1178
Db 3525 CGCCACAGGGGTTCCTTGGAACTGTGAGCCCAAGAGTTCTTTTGAACCTGCCTGACACTCTG 3584
Qy 1179 GlnValProGlyLeuHisArgThrAlaSerGlyArgGlySerAlaSerGluHisGlnAsp 1198
Db 3585 CAGTGCCTGGGCTGTGACCGCAGCCAGCGCGCGAGCTCTGTGCTCTGACCAACCAAGAC 3644
Qy 1199 CysAsnGlyLysSerAlaSerGlyArgLeuAlaArgAlaLeuArgProAspAspPro 1218
Db 3645 TGTAATGGCAAGTCGGCTTCAGGCGGTTTGGCCCGCAGCCCTGAGGACTGATGATGCCCAA 3704
Qy 1219 LeuAspGlyAspAlaAspGluGlyAsnLeuSerLysGlyGluArgValArgAla 1238

Db 3705 CTGGATGGGATGATGATGATGAGGAAATCTGAGCAAAAGGGAACCGCATACAGCC 3764
Qy 1239 TrpIleArgAlaArgLeuProAlaCysTrpLeuGluArgAspSerTrpSerAlaTrpIle 1258
Db 3765 TGGGTACATCCCGGCTTCTGCTGTCGAGAGCGAGATTCCTGGTGGCCTATATATC 3824
Qy 1259 PheProGlnSerArgPheArgLeuLeuCysHisArgIleIleThrHisLysMetPhe 1278
Db 3825 TTTCTCTCTCAGTCAAGGTTTCGTCTCTGTGTCCCGGATCATCACCCACAAGATGTTT 3884
Qy 1279 AspHisValValLeuValIleIlePheLeuAsnCysIleThrIleAlaMetGluArgPro 1298
Db 3885 GACCATGTGCTCTGCTCATCATCTTCTCACTGTATCACCATCGCTATGGAGCGGCC 3944
Qy 1299 LysIleAspProHisSerAlaGluArgIlePheLeuThrLeuSerAsnTrpIlePheThr 1318
Db 3945 AAAATTGACCCACACGCGCTGAGCGCATCTTCTGACCCCTCTCCAACTACATCTTCAG 4004
Qy 1319 AlaValPheLeuAlaGluMetThrValLysValValAlaLeuGlyTrpCysPheGlyGlu 1338
Db 4005 GCAGTCTTTCTAGCTGAAATGACAGTGAAGTGTGGACCTGGGCTGGTCTTTGGGGAG 4064
Qy 1339 GlnAlaTrpLeuArgSerSerTrpAsnValLeuAspGlyLeuLeuValLeuIleSerVal 1358
Db 4065 CAGGCTTACCTGCGCAGCAGCTGGAAATGTGCTGAGCGGCTGTGCTGTCTCATCTCCGTC 4124
Qy 1359 IleAspIleLeuValSerMetValSerAspSerGlyThrLysIleLeuGlyMetLeuArg 1378
Db 4125 ATCGACATCTGCTGCTCCATGCTCTCGACAGCGGCACCAAGATCCTTGGCATCTGAGG 4184
Qy 1379 ValLeuArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeu 1398
Db 4185 GTGTGCGGCTGTGCGGACCCCTGCGTCCATCTCAGGCTCATCAGCGCGGCCAGGACTG 4244
Qy 1399 LysLeuValValGluThrLeuMetSerSerLeuLysProIleGlyAsnIleValValIle 1418
Db 4245 AGCTGTGTGTAGAGACTCTGATGTCTATCCCTCAACCCATTTGGCAACATTTGGTCAAT 4304
Qy 1419 CysCysAlaPhePheIleIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPhe 1438
Db 4305 TGCTGTGCTTCTTTCATCTTTTGGAAATCTCGGGGTGCAGCTCTTCAAAGGGAAGTTC 4364
Qy 1439 PheValCysGlnGlyGluAspThrArgAsnIleThrAsnLysSerAspCysAlaGluAla 1458
Db 4365 TTCTGTGTGAGGTGAGGACACCCAGGAACATCTAACAATCCGACTGCGCTGAGGCC 4424
Qy 1459 SerTrpArgTrpValArgHisLysTrpAsnPheAspAsnLeuGlyGlnAlaLeuMetSer 1478
Db 4425 AGCTACCGATGGGTCCCGGCACCAAGTACAACCTTTGACAACCTTGGGCGAGGCTCTGATGTCC 4484
Qy 1479 LeuPheValLeuAlaSerLysAspGlyTrpValAspIleMetTrpAspGlyLeuAspAla 1498
Db 4485 CTGTTTGTGCTGGCTCCAGGATGTTGGTTGCATCATGATGATGAGCTGGATGCT 4544
Qy 1499 ValGlyValAspGlnGlnProIleMetAsnHisAsnProTrpMetLeuLeuTrpPheIle 1518
Db 4545 GTGGGTGTGGATCAGCAGCCCATCATGAACCAACCCCTGGATGTCTATCTTCTATC 4604
Qy 1519 SerPheLeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValValGlu 1538
Db 4605 TCCCTCTCTCTCATCGTGGGCTTCTTTGTCTGAAACATGTTTGTGGGCGTGGTGGAG 4664
Qy 1539 AsnPheHisLysCysArgGlnHisGlnGluGluAlaArgArgArgGluGluLys 1558
Db 4665 AACTTCCATAAGTGCAGACAGCAGCAGGAGGAGGAGGAGCGCGCTGAGGAGAG 4724
Qy 1559 ArgLeuArgArgLeuGluLysLysArgArg-----LysAlaGln 1571
Db 4725 CGACTACGAGGCTGGAGAAAAAGAGAGAGGAGTAAGGAGACAGATGCGCGAGCCAG 4784
Qy 1572 CysLysProTrpTrpSerAspTrpSerArgPheArgLeuLeuValHisLysLeuCysThr 1591

4785 TCAGAGCCCTACTACTCTGACTACTCGAGATTCGGGCTCTCTGTCCACCACTGTGTACC 4844
1592 SerHisTyrLeuAspLeuPheIleThrGlyValIleGlyLeuAsnValValThrMetAla 1611
4845 AGCCACTACCTGGACCTCTTATCATCCTGGTGTATCGGGCTGACGCTGGTACCTATGGCC 4904
1612 MetGluHisTyrGlnGlnProGlnIleLeuAspGluAlaLeuIleCysAsnTyrIle 1631
4905 ATGGAACATTACCAAGAGCCAGATCCTGACGAGGCTCTGAAGATCTGCAATTACATC 4964
1632 PheThrValIlePheValLeuGluSerValPheIleValAlaPheGlyPheArgArg 1651
4965 TTTACCGTCATCTTTGTCTTGTAGTCACTTGAAGTCTGGGCTTGGCTTCCGCGCT 5024
1652 PhePheGlnAspArgTyrAsnGlnLeuAspLeuAlaIleValLeuLeuSerIleMetGly 1671
5025 TTTCTTCAGGACAGTGAACAGCTGACCTGGCTGATTTGTGCTTCTGTCTCATATGGCC 5084
1672 IleThrLeuGluGluIleGluValAsnAlaSerLeuProIleAsnProThrIleIleArg 1691
5085 ATCACACTGGAGGAGATTGAGTCAATCTGTCTGCTGCCATCAACCCACCATCATCGT 5144
1692 IleMetArgValLeuArgIleAlaArgValLeuIleValLeuIleValAlaValGlyMet 1711
5145 ATCATGAGGGTGTCTCCGATTTGCTCGAGTTCTGAAGCTGTGAAGATGGCTGTGGGCATG 5204
1712 ArgAlaLeuLeuAspThrValMetGlnAlaLeuProGlnValGlyAsnLeuGlyLeu 1731
5205 CGGCACTGTCTGCACAGGTGATGAGGCCCTGCCAGAGTGGGGAACCTTGGACTTCTC 5264
1732 PheMetLeuLeuPhePheIlePheAlaLeuGlyValGluLeuPheGlyAspLeuGlu 1751
5265 TTTATGTTATTTTTCATCTTTGACGCTCTGGGCTGGAGCTCTTTGGAGACCTGGAG 5324
1752 CysAspGluThrHisProCysGluGlyLeuClyArgHisAlaThrPheArgAsnPheGly 1771
5325 TGTGATGAGACACACCTTTGTGAGGGCTTGGGCTGGGCTGACCTTTAGGAACCTTTGGT 5384
1772 MetAlaPheLeuThrLeuPheArgValSerThrGlyAspAsnTyrAsnGlyIleMetLys 1791
5385 ATGGCTTTTCAGCCCTCTCCGAGTCTCCACTGGTGACACTGGAATGTTATATGAG 5444
1792 AspThrLeuArgAspCysAspGlnGluSerThrCysTyrAsnThrValIleSerProIle 1811
5445 GACACCTTCGGGACTGTGACAGAGTCCACCTGCTACAACTGTCTCATCTCCCTATC 5504
1812 TyrPheValSerPheValLeuThrAlaGlnPheValLeuValAsnValIleAlaVal 1831
5505 TACTTTGTCTCTGCTGCTGACGGCCAGTTTGTGCTGGTCAACGTTGTCATAGCTGTG 5564
1832 LeuMetLysHisLeuGluGluSerAsnLysGluAlaLysGluAlaGluLeuGluAla 1851
5565 CTGATGAGACCTCTGAAGAAAGCAACAAAGAGCCCAAGAGAGGCGGAGCTCGAGGCC 5624
1852 GluLeuGluLeuGluMetLysThrLeuSerProGlnProHisSerProLeuGlySerPro 1871
5625 GAGCTGGAGCTGGAGATGAAGACGCTCAGCCCGCAGCCCACTCCCTCCCTGGGAGCC 5684
1872 PheLeuTyrProGlyValGluClyProAspSerProAspSerProLysProGlyValLeu 1891
5685 TTCTCTGGCCGGGGTGGAGGTTCAACAGTACTGACGCCCTTAAGCCCTGGGGCTCCA 5744
1892 HisProAlaAlaHisAlaArgSerAlaSerHisPheSerLeuGluHisProThrMetGln 1911
5745 CACACCACTGCCCATTTGGAGAGCCTCGGGCTTCTCCCTTGAGCACCCCAACATGTA 5804
1912 ProHisProThrGluLeuPro-----GlyProAspLeuLeuThrValArgLysSer 1928
5805 CCCCACCCCGAGGAGTGCACAGTCCCTCCCTTAGCACCAGACCTGCTGACTGTGAGGAAGTCT 5864
1929 GlyValSerArgThrHisSerLeuProAsnAspSerTyrMetCysArgHisGlySerThr 1948
5865 GGTGTGACCCGACGACATCTCTGCCCCAATGACACTACATGTGCGCAATGGGAGCACT 5924

1949 AlaGluGlyProLeuGlyHisArgGlyTyrGlyLeuProLysAlaGlnSerGlySerVal 1968
5925 GCTGAGAGATCCCTAGACACAGGGGCTGGGGCTCCCCAAAGCCAGTCAGGCTCCATC 5984
1969 LeuSerValHisSerGlnProAlaAspThrSerTyrIleLeuGlnLeuProLysAspAla 1988
5985 TTTCTCGTTTCACTCCCAACAGCAGACACAGCTGCTACAGCTTCCCAAAGATGTG 6044
1989 ProHisLeuLeuGlnProHisSerAlaProThrTyrGlyThrIleProLysLeuProPro 2008
6045 CACTATCTGCTCCAGCTCATGGGGCTCCACCTGGGGGCCCATCTCTAACTACCCCA 6104
2009 ProGlyArgSerProLeuAlaGlnArgProLeuArgGlnAlaIleArgThrAsp 2028
6105 CTTGGCCGCTCCCTCTGCTCAGAGCCTCTCAGGCGCCAGCAGCAATAGGACTGAC 6164
2029 SerLeuAspValGlnGlyLeuGlySerArgGluAspLeuAlaGluValSerGlyPro 2048
6165 TCCCTGATGTGAGGGCTGGGTAGCCGGGAAGACCTGTGTGTCAGAGGTGAGTGGGCC 6224
2049 SerProProLeuAlaArgAlaTyrSerPheTyrGlyGlnSerSerThrGlnAlaGln 2068
6225 TCTGCTCTGACCCGGTCTCATCTTCTGGGGGGTTCGAGCATCCAGGTGCAGCAG 6284
2069 HisSerArgSerHisSerLysIleSerLysHisMetThrProProAlaProCysProGly 2088
6285 CGTTCCGGCATCCAGAGCAAGTCTCAAGCACATCCGCTGCAGGCCCTTGTCCCGAGC 6344
2089 ProGluProAsnTyrGlyLysGlyProGluThrArgSerSerLeuGluLeuAspThr 2108
6345 CTGGAACCCAGCTGGGCCAAGGACCTTCCAGAGACCAGAGAGCTTTAGAGCTGGACAG 6404
2109 GluLeuSerTyrIleSerGlyAspLeuLeuProProGlyGlyGlnGluProProSer 2128
6405 GAGCTGAGCTGGATTTTCAGAGACCTTCTT---CCAGCAGCCAGAGAACCCCTGTTT 6461
2129 ProArgAspLeuLysLysCysTyrSerValGluAlaGlnSerCysGlnArgArgProThr 2148
6462 CCAGCGGACCTGAAGAAGTCTACAGTGTAGAGACCCAGAGCTGCAGGCGCAGGCTGGG 6521
2149 SerTyrLeuAspGluGlnArgArgHisSerIleAlaValSerCysLeuAspSerGlySer 2168
6522 TTTCTGGCTAGATGAACAGCGGAGACACTCCATTTGCTGTCTGACCTGTCTGGACAGGCTCC 6581
2169 GlnProHisLeuGlyThrAspProSerAsnLeuGlyGlyGlnProLeuGlyGlyProGly 2188
6582 CAACCCGCTATGTCCAAGCCCTCAAGCTTCGGGGCCCAACCTCTTGGGGGTCTCTGGG 6641
2189 SerArgProLysLysLysLeuSerProProSerIleThrIleAspProProGluSerGln 2208
6642 AGCCGGCTTAAGAAAAAATCTAGCCCAACCCAGTATCTCTATAGACCCCGGAGAGCAG 6701
2209 GlyProArgThrProProSerProGlyIleCysLeuArgArgAlaProSerSerAsp 2228
6702 GGCTCTGGCCCCCATCGAGTCTTGGTGTCTGCTCTAGAGAGAGGGCGCCGCGCAGTGC 6761
2229 SerLysAspProLeuAlaSerGlyProProAspSerMetAlaAlaSerProSerProLys 2248
6762 TCTAAGGATCCCTCGGTCTCCAGCCCTTTCAGACGAGCGCTGCCTCACCTCCCAAG 6821
2249 LysAspValLeuSerLeuSerGlyLeuSerSerAspProAlaAspLeuAspPro 2266
6822 AAAGACACGCTGATCTCTCTGTTGTCTTCTTGTACCCCAACAGACATGGGACCC 6875

RESULT 14

RAX83486
ID RAX83486 standard; cDNA; 6795 BP.

XX AC RAX83486;

XX AC AC

DT 07-DEC-1999 (first entry)

XX

Rat T-type voltage-gated Ca channel alpha-1-G (rCavTib) cDNA.

Human; T-type voltage-gated calcium channel; membrane; pore; ion; activation; current; rat; screen; drug; cardiomyopathy; epilepsy; ds.

Rattus sp.

W09929847-A1.

17-JUN-1999.

30-OCT-1998; 98WO-US023161.

05-DEC-1997; 97US-00985809.

(LOYO) UNIV LOYOLA CHICAGO.

Perez-Reyes E, Cribbs LL;

WPI; 1999-394972/33.

P-PSDB; AAY14591.

New T-type voltage-gated calcium channels.

Disclosure; Page 76-85; 138pp; English.

This sequence represents the coding region for a rat T-type voltage-gated calcium (Ca) channel alpha-1-G designated rCavTib. Voltage gated channels are membrane bound glycosylated proteins formed of several subunits. The large alpha subunits form a pore in the membrane that is selective for a given ionic species. Each alpha subunit contains 4 domains (I, II, III, and IV) and each domain contains 6 putative transmembrane helical segments (SI-S6). T-type Ca channels are activated at a lower voltage than L- or N-type channels. Characteristics of T-type channels include short current time, slow activation kinetics near threshold, fast inactivation kinetics and slow tail current. The sequences AAX83481-X83492 represent novel T-type voltage-gated Ca channel genes from humans and rats. Each of the novel Ca-channels contains a putative IVS4 region comprising the amino acid sequence AAY14598. Cells expressing the T-type voltage-gated calcium channel proteins can be used to screen for drugs which affect calcium channels. Methods are also disclosed for treating a disease or disorder associated with a deficiency in a native T-type calcium channel nucleic acid, e.g. to treat cardiomyopathy, epilepsy, etc

SQ Sequence 6795 BP; 1366 A; 2055 C; 1923 G; 1451 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	0	Length:	6795
Score:	10939.50	Matches:	2107
Percent Similarity:	93.53%	Conservative:	34
Best Local Similarity:	92.05%	Mismatches:	101
Query Match:	91.90%	Indels:	47
DB:	2	Gaps:	6

US-09-611-257A-37 (1-2266) x AAX83486 (1-6795)

Qy	1	MetAspGluGluGluAspGlyAlaGlyAlaGluGluSerGlyGlnProArgSerPheMet	20
Db	1	ATGACGAGGAGGAGGATGGAGCGGGCGCGGAGGTCGGGACAGCCCGTAGCTTCACG	60
Qy	21	ArgLeuAsnAspLeuSerGlyAlaGlyGlyArgProGlyProGlySerAlaGluIysAsp	40
Db	61	CAGCTCAACACCTGTCTCCGGGGCGGGGGCGGGCGGGCGGGGTCGAGGAAAGGAC	120
Qy	41	ProGlySerAlaAspSerGluAlaGluGlyLeuProTyrProAlaLeuAlaProValVal	60
Db	121	CCGGGACGGGGGACTCCGAGCGGAGGGGGTGGCGTACCCGGGGCTAGCCCCGGTGGTT	180
Qy	61	PhePheTyrLeuSerGlnAspSerArgProArgSerTrpCysLeuArgThrValCysAsn	80
Db	181	TTCTTCTACTTGACCCAGGACAGCCCGCGGAGCTGGTGTCTCCGACCGGTCTGTAAAC	240
Qy	81	ProTrpPheGluArgIleSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMet	100

Db	241	CCGTGGTTCCAGCGAGTCAGTATGCTGTCATTCTTCTCAACTGTGTGACTCTGGGTATG	300
Qy	101	PheArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPhe	120
Db	301	TTCAGGCCGTGTGAGGACATTGCTGTGACTCCCGAGCGTCCCGGATCCTCGAGCCCTTC	360
Qy	121	AspAspPheIlePheAlaPhePheAlaValGluMetValValValValMetValAlaLeuGly	140
Db	361	GATGACTTCATCTTTTGGCTTCTTTGCTGTGAAATGGTGGTGAAGATGGTGGCTTGGGC	420
Qy	141	IlePheGlyIysIysCysTyrLeuGlyAspThrTrpAsnArgLeuAspPheIleVal	160
Db	421	ATCTTTGGGAGAAATGTTACCTGGGAGACACTTGGAAACCGGCTTGACTTTTTCATTGTC	480
Qy	161	IleAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArg	180
Db	481	ATTGACGGGATGCTGGAGTATTGCTGGACCTGCAGAACGTCAGCTTCTCCGAGTCAGG	540
Qy	181	ThrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeu	200
Db	541	ACAGTCCGTGTGTCGACCGCTCAGGGCCATTAAACCGGGTGCCAGCATGCGCATTCCTC	600
Qy	201	ValThrLeuLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePhe	220
Db	601	GTCACTATTCTGTGGACACTTGCCTATGCTGGGCAACGTCCTGCTGCTGCTGTTCTTC	660
Qy	221	ValPhePheIlePheGlyIleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArg	240
Db	661	GTCTTTTTCATCTTTGGCTGCTGGGCGTCAGCTGTGGGCGAGGACTGCTTCGCAACCGG	720
Qy	241	CysPheLeuProGluAsnPheSerLeuProLeuSerValAspLeuGluArgTyrTrpGln	260
Db	721	TGCTTCTCCCGAGAACTTTCAGCTCCCTCAGCTGAGCGTGGACCTGGAGCTTATATACCAG	780
Qy	261	ThrGluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArg	280
Db	781	ACAGAGAAATGAGGACGAGAGCCCTTCATCTGCTCTCAGCTTCGGGAGAAATGGCATGAGA	840
Qy	281	SerCysArgSerValProThrLeuArgGlyAspGlyGlyGlyGlyProProCysGlyLeu	300
Db	841	TCCTGACGAGGAGTGTGCCACACACACACACACACACACACACACACACACACACAC	900
Qy	301	AspTyrGluAlaTyrAsnSerSerAsnThrThrCysValAsnTrpAsnGlnTyrTyr	320
Db	901	GACTATGAGACCTATAACAGTTCAGCAACACACACCTGTGTCAACCTGGAACGAGTACTAT	960
Qy	321	ThrAsnCysSerAlaGlyGluHisAsnProPheIysGlyAlaIleAsnPheAspAsnIle	340
Db	961	ACCACTGCTCTGGGGCGAGCACACACCTTCAAGGGCGGCATCAACTTTGACACACTT	1020
Qy	341	GlyTyrAlaTrpIleAlaIlePheGlnValIleThrLeuGluGlyTrpValAspIleMet	360
Db	1021	GGCTATGCTGGATCGCCATCTTCCAGGTCAACACCTGAGGAGGCTGGTGGCATCATG	1080
Qy	361	TyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleIle	380
Db	1081	TACTTCGTAAATGGACGCTCACTCTCTACAACTTCACTTCACTTCTTCTCTCATCATC	1140
Qy	381	ValGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGlu	400
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Job time : 2872 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 16, 2005, 02:25:35 ; Search time 726 Seconds
(without alignments)
5107.167 Million cell updates/sec

Title: US-09-611-257A-37

Perfect score: 11904

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Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	11877.5	99.8	7741	3	US-09-426-998-4
3	11241	94.4	7405	4	US-09-949-016-3859
4	6315.5	53.1	3993	4	US-09-398-522-51
5	6214.5	52.2	7898	3	US-08-984-709A-49
6	5492.5	46.1	6816	3	US-09-404-650-1
7	5492.5	46.1	6816	4	US-09-935-541-1
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11	5418.5	45.5	6503	4	US-09-935-541-12
12	2237	18.8	70308	4	US-09-949-016-15601

13	1971.5	16.6	1669	3	US-08-984-709A-51	Sequence 51, Appl
14	1786.5	15.0	7376	1	US-08-288-163-3	Sequence 3, Appl
15	1784.5	15.0	7362	1	US-08-455-543A-7	Sequence 7, Appl
16	1784.5	15.0	7362	2	US-08-193-078B-7	Sequence 7, Appl
17	1784.5	15.0	7362	2	US-08-223-305C-7	Sequence 7, Appl
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24	1784.5	15.0	7266	3	US-08-713-118-1	Sequence 1, Appl
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41	1711.5	14.4	5975	1	US-08-884-599-1	Sequence 3, Appl
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43	1691	14.2	6112	4	US-09-495-714C-3	Sequence 25, Appl
44	1690	14.2	6114	4	US-09-495-714C-5	
45	1690	14.2	7089	3	US-08-949-386-25	

ALIGNMENTS

RESULT 1
US-09-426-998-3
; Sequence 3, Application US/09426998
; Patent No. 6358706
; GENERAL INFORMATION:
; APPLICANT: DUBIN, ADRIENNE E.
; APPLICANT: PYATI, JAYASHREE
; APPLICANT: ZHU, JESSICA Y
; APPLICANT: ERLANDER, MARK G
; APPLICANT: GALINDO, JOSE E
; TITLE OF INVENTION: DNA ENCODING HUMAN ALPHAIG T-TYPE CALCIUM
; TITLE OF INVENTION: CHANNEL (ALPHAIG-C)
; FILE REFERENCE: ORT-1057
; CURRENT APPLICATION NUMBER: US/09/426,998
; CURRENT FILING DATE: 1999-10-26
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PATENTIN VER. 2.0
; SEQ ID NO 3
; LENGTH: 6822
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
US-09-426-998-3

Alignment Scores:
Pred. No.: 0
Score: 11877.50
Percent Similarity: 99.65%
Best Local Similarity: 99.60%
Query Match: 99.78%
DB: 3
Length: 6822
Matches: 2264
Conservative: 1
Mismatch: 1
Indels: 7
Gaps: 1

US-09-611-257A-37 (1-2266) x US-09-426-998-3 (1-6822)

Qy 1 MetAspGluGluAspGlyAlaGlyAlaGluSerGlyGlnProArgSerPheMet 20
Db 1 ATGACGAGGAGGAGGATGGAGCGCGCCGAGGAGTCCGGACAGCCCGGAGCTTATG 60

Db 2221 ||||| GACAGCAAGTACTTTGGCGGGGATCATGATCGCCATCTTGTCACACACTCAGCATG 2280
Qy 761 GlyIleGluTyrHisGluGlnProGluGluLeuThrAenAlaLeuGluIleSerAsnIle 780
Db 2281 GGCATCGAATACCAAGCAGCGCGGAGGCTTACCAACGCGCTAGAAATCAGCAACATC 2340
Qy 781 ValPheThrSerLeuPheAlaLeuGluMetLeuLeuLeuValTyrGlyProPhe 800
Db 2341 GTCCTTACCAAGCCTTTTGGCCCTGGAGATGCTGTGAAGCTGTGTGTATGGTCCCTTT 2400
Qy 801 GlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleValIleSerValTyr 820
Db 2401 GGCTACATCAGAAATCCCTACAACTTCTCGATGGTGTCAATGTGCTCATCAGCGTGG 2460
Qy 821 GluIleValGlyGlnGlnGlyGlyLeuSerValLeuArgThrPheArgLeuMetArg 840
Db 2461 GAGATCGTGGCGCAGCAGCGGGGGCGCTGCGGTGTCGGAGCCTCCGCGCTGATGCGT 2520
Qy 841 ValLeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetLys 860
Db 2521 GTGCTGAAGCTGGTGGCGCTTCTGCCGCGCTGAGCGGCGAGCTGGTGGTCTCATGAAG 2580
Qy 861 ThrMetAspAenValAlaThrPheCysMetLeuLeuMetLeuPheIlePheSer 880
Db 2581 ACCATGGACAAGCTGGCCACCTTCTGCATGCTGCTTATGCTCTTCACTTCTTCAGC 2640
Qy 881 IleLeuGlyMetHisLeuPheGlyCysLysPheAlaSerGluArgAspGlyAspThrLeu 900
Db 2641 ATCCTGGGATGTCATCTCTCGGTGCAAGTTTGCCTCTGAGCGGAGTGGGACACCGCT 2700
Qy 901 ProAspArgLysAenPheAspSerLeuLeuTrrAlaIleValThrValPheGlnIleLeu 920
Db 2701 CCAGACGGAGAAATTTGACTCTCTGCTGGGCCCATCGTCACTGTCTTTCAGATCCTG 2760
Qy 921 ThrGlnGluAspTrrAsnLysValLeuTyrAsnGlyMetAlaSerThrSerTrrAla 940
Db 2761 ACCAGAGGAGTGGACAAAGTCTCTACAAATGATGGCTTACGCTCTCTGCGCG 2820
Qy 941 AlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuVal 960
Db 2821 GCCCTTTATTTCTTCCCTCATGACCTTCCGCAACTACGTGCTCTTCAATTTGCTGTC 2880
Qy 961 AlaIleLeuValGluGlyPheGlnAlaGluIleSerLysArgGluAspAlaSerGly 980
Db 2881 GCCATTCTGGTGGAGGCTTCCAGCGGAGGAAATCAGCAACCGGAGAGATGCGAGTGA 2940
Qy 981 GlnLeuSerCysIleGlnLeuProValAspSerGlnGlyGlyAspAlaAsnLysSerGlu 1000
Db 2941 CAGTTAAGCTGATTCAGCTGCTGCTGCTGCTGCCAGGGGGGAGATGCCAACAGTCCGAA 3000
Qy 1001 SerGluProAspPhePheSerProSerLeuAspGlyAspGlyArgLysLysCysLeu 1020
Db 3001 TCAGAGCCGATTTCTTCTCACCCAGCGCTGATGGTGGTGGGACAGGAAAGTGGCTTG 3060
Qy 1021 AlaLeuValSerLeuGlyGluHisProGluLeuArgLysSerLeuProProLeuIle 1040
Db 3061 GCCTTGGTGTCTTGGGAGACACCGGAGCTGGGAGAGCCTGCTGCCGCTCTCATC 3120
Qy 1041 IleHisThrAlaAlaThrProMetSerLeuProLysSerThrSerThrGlyLeuGlyGlu 1060
Db 3121 ATCCACACGGCGGCCACCCATGCTGCTGCCAAGAGCACAGCGGCTGGGCGAG 3180
Qy 1061 AlaLeuGlyProAlaSerArgThrSerSerSerGlySerAlaGluProGlyAlaAla 1080
Db 3181 CGCTGGGCCCTCGCTGCGCGCCAGCACAGCAGCGGCTGGCAGAGCCTGGGCGGCC 3240
Qy 1081 HisGluMetLysSerProProSerAlaArgSerSerProHisSerProTrrSerAlaAla 1100
Db 3241 CACGAGATGAAGTCAACCGCCAGCGCGCGAGCTCTCCGCAACAGCCCTGGAGCGCTGCA 3300
Qy 1101 SerSerTrrThrSerArgArgSerSerArgAsnSerLeuGlyArgAlaProSerLeuLys 1120
|||||

Db 3301 AGCAGCTGGACAGCGCGCTCCAGCGGGAACAGCCTCGCGCGTGCACCCAGCCTGAAG 3360
Qy 1121 ArgArgSerProSerGlyGluArgArgSerLeuLeuSerGlyGluGlyGlnGluSerGln 1140
Db 3361 CGGAGAAAGCCCAAGTGGAGAGCGCGGCTCCCTGTTGTCGGGAGAGGCGCAGAGAGCCAG 3420
Qy 1141 AspGluGluGluSerSerGluGluGluArgAlaSerProAlaGlySerAspHisArgHis 1160
Db 3421 GATGAAGAGGAGAGCTCAGAAGAGGAGCGGCCAGCCTCGCGGAGTGAGCATCGCCAC 3480
Qy 1161 ArgGlySerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeuGlnVal 1180
Db 3481 AGGGGGTCCCTGGAGCGGAGGCCCAAGAGTTCCTTTCAGCTGCCAGACACACTGCAGTG 3540
Qy 1181 ProGlyLeuHisArgThrAlaSerGlyArgGlySerAlaSerGluHisGlnAspCysAsn 1200
Db 3541 CCAGGGTGTGATCGCATCTGCCAGTGGCGAGGGTCTGCTTCTGAGCACACAGACTGCAAT 3600
Qy 1201 GlyLysSerAlaSerGlyArgLeuAlaArgAlaLeuArgProAspAspProProLeuAsp 1220
Db 3601 GGCAGGTGGCTTCAGGGCGCTTGGCCGCGCTTGGCGCTGATGACCCCCACTTGGAT 3660
Qy 1221 GlyAspAlaAspAspGluGlyAsnLeuSerLysGlyGluArgValArgAlaTrrIle 1240
Db 3661 GGGATGACGCCGATGACGAGGGCAACTGAGCAAGGGGAACGGGTCCGCGCTGGATC 3720
Qy 1241 ArgAlaArgLeuProAlaCysTyrLeuGluArgAspSerTrrSerAlaTyrIlePhePro 1260
Db 3721 CGAGCCGACTCCCTGCTGCTGCTGAGCGAGACTCTGCTGAGCCTACATCTTTCGCT 3780
Qy 1261 ProGlnSerArgPheArgLeuLeuCysHisArgIleIleThrHisLysMetPheAspHis 1280
Db 3781 CCTCAGTCCAGGTTCGCGCTCTGTGTCACCGGATCATCACCACAAAGATGTTTCAGCAC 3840
Qy 1281 ValValLeuValIleIlePheLeuAsnCysIleThrIleAlaMetGluArgProLysIle 1300
Db 3841 GTGCTCTTGTATCATCTTCTTAACTGATCATCACCATCGCATGGAGGCGCCCAAAAT 3900
Qy 1301 AspProHisSerAlaGluArgIlePheLeuThrLeuSerAsnTyrIlePheThrAlaVal 1320
Db 3901 GACCCACACAGCGCTGAACGATCTTCTGACCCCTTCCAAATTACATCTTTCACGCGAGTC 3960
Qy 1321 PheLeuAlaGluMetThrValLysValAlaLeuGlyTrrCysPheGlyGluGlnAla 1340
Db 3961 TTTCTGCTGCTAAATGACAGTGAAGTGGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4020
Qy 1341 TyrLeuArgSerSerTrrAsnValLeuAspGlyLeuLeuValLeuLysSerValIleAsp 1360
Db 4021 TACCTGGGAGCAGTGGAGAGCTGCTGAGCGGCTGTTGGTGTCTCATCTCCGTCATCGAC 4080
Qy 1361 IleLeuValSerMetValSerAspSerGlyThrLysIleLeuGlyMetLeuArgValLeu 1380
Db 4081 ATTCTGGTGTCCATGGTCTCTGACAGCGGACCAAGATCTCTGGGCTGCTGCTGCTGCTG 4140
Qy 1381 ArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeuLysLeu 1400
Db 4141 CGGCTGCTGGGAGCCCTGCGCCGCTCAGGGTGTATGACGCGGCGGAGGGGCTGAAGCTG 4200
Qy 1401 ValValGluThrLeuMetSerSerLeuLysProIleGlyAsnIleValIleCysCys 1420
Db 4201 GTGGTGGAGAGCGTGTATGCTCTCATGAAACCCATCGCAACATTTGATGATCTGCTGT 4260
Qy 1421 AlaPhePheIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPhePheVal 1440
Db 4261 GCCTTCTTCTCATTTTTCGCGCTCTTGGGGGTGCGAGCTCTTCAAAGGAGAGTCTTTCGTG 4320
Qy 1441 CysGlnGlyGluAspThrArgAsnIleThrAsnLysSerAspCysAlaGluAlaSerTyr 1460
Db 4321 TGCCAGGCGGAGGATACCAAGAACATCACCATAAATCGGACTGTGCGAGGCGCAGTTAC 4380
Qy 1461 ArgTrrValArgHisLysTyrAsnPheAspAsnLeuGlyGlnAlaLeuMetSerLeuPhe 1480
Db 4381 CGGTGGGTCCGGCAACAGTACACTTTTGACACACTTGGCCAGGCGCTGATGCTCTGCTTC 4440

QY	1481	ValLeuAlaSerLysAspGlyTrpValAspIleMetTyrAspGlyLeuAspAlaValGly	1500
DB	4441	GTTTTGGGCTCCAAAGATGGTGGGTGGACATCATGTACATGGGCTGGATGCTGTGGGC	4500
QY	1501	ValAspGlnGlnProIleMetAsnHisAsnProTrpMetLeuLeuTyrPheIleSerPhe	1520
DB	4501	GTGGACGAGCCCATCATGAACACACAAACCCCTGGATGCTGTACTTCATCTCGTTC	4560
QY	1521	LeuLeuIleValAlaPhePheValIleuAsnMetPheValGlyValValGluAsnPhe	1540
DB	4561	CTGCTCATTTGGCCCTCTTTGTCTGAACAATGTTTGGGTGTGGTGGTGGAGAACTTC	4620
QY	1541	HisLysCysArgGlnHisGlnGluGluAlaArgArgGluGluLysArgLeu	1560
DB	4621	CACAGTGTTCGGAGACACAGGAGGAAGAGAGCCCGGGCGGAGAGAAAGCCCTA	4680
QY	1561	ArgArgLeuGluLysLysArgArg-----LysAlaGlnCysLys	1573
DB	4681	CGAAGACTCGAGAAAAAGAGAGAGTAAAGAGAGCGATGGCTGAAGCCAGTCGAA	4740
QY	1574	ProTyrTyrSerAspTyrSerArgPheArgLeuLeuValHisHisLeuCysThrSerHis	1593
DB	4741	CCTTACTATCCGACTACTCCCGCTTCGGCTCTCGTCCACCACTTGTGCACGACAC	4800
QY	1594	TyrLeuAspLeuPheIleThrGlyValIleGlyLeuAsnValValThrMetAlaMetGlu	1613
DB	4801	TACCTGGACCTCTTCATCACAGGTGTCAATCGGGCTGAACGTGGTACCATGGCCATGGAG	4860
QY	1614	HisTyrGlnGlnProGlnIleLeuAspGluAlaLeuLysIleCysAsnTyrIlePheThr	1633
DB	4861	CATTCACGACGCCCCAGATTCTGGATGAGGCTCTGAAGATCTGCAACTATCATCTTCACT	4920
QY	1634	ValIlePheValLeuGluSerValPheLysLeuValAlaPheGlyPheArgArgPhePhe	1653
DB	4921	GTCACTCTTCTCTGGAGTCAGTCTTTCAAACTGTGGCCCTTTGGTTCCTCGTGGTCTTC	4980
QY	1654	GlnAspArgTrpAsnGlnLeuAspLeuAlaIleValLeuLeuSerIleMetGlyIleThr	1673
DB	4981	CAGACAGGTGGAAACAGCTGGACCTGGCCATGTGTCTCTCCATCATGGGCATCACG	5040
QY	1674	LeuGluGluIleGluValAsnAlaSerLeuProIleAsnProThrIleIleArgIleMet	1693
DB	5041	CTGGAGAAATCGAGGTCAACGGCTCGCTGCCCATCAACCCACCACCATATCCGCATCATG	5100
QY	1694	ArgValLeuArgIleAlaArgValIleLysLeuLeuLysMetAlaValGlyMetArgAla	1713
DB	5101	AGGGTGTGCGCCATTTGCCGAGTGTCTGAAGTCTCTGAAGATGGCTGTGGGCATCGGGCG	5160
QY	1714	LeuLeuAspThrValMetGlnAlaLeuProGlnValGlyAsnLeuGlyLeuLeuPheMet	1733
DB	5161	CTGCTGGACACGGTGATCGAGGCCCTGCCCCAGGTGGGAACCTTGGGATCTCTCTCATG	5220
QY	1734	LeuLeuPheIlePheAlaLeuGlyValGluLeuPheGlyAspLeuGluCysAsp	1753
DB	5221	TTGTGTGTTTTTCATCTTTGAGCTCTGGGCGTGGAGCTCTTTGGAGACCTTGGAGTGTGAC	5280
QY	1754	GluThrHisProCysGluGlyLeuGlyArgHisAlaThrPheArgAsnPheGlyMetAla	1773
DB	5281	GAGACACACCCCTGTGGGGCTGGGCCGTTCATGCCACCTTTCGAACTTGGCATGGCC	5340
QY	1774	PheLeuThrLeuPheArgValSerThrGlyAspAsnTrpAsnGlyIleMetLysAspThr	1793
DB	5341	TTCTTAACCCCTCTTCGAGTCTCCACAGGTGACAAATTGGAAATGGCATTAATGAAGGACAC	5400
QY	1794	LeuArgAspCysAspGlnGluSerThrCysTyrAsnThrValIleSerProIleTyrPhe	1813
DB	5401	CTCGGGACTGTGACAGAGTCCAACCTTCAGTGTACAAACACGGTCACTCGCCTACTACTTT	5460
QY	1814	ValSerPheValIleuThrAlaGlnPheValLeuValAsnValValIleAlaValLeuMet	1833
DB	5461	GTGTCTCTGTGTGACGGCCCGAGTCTGTGTAGTCAACGTGGTGTGATCGCGGTCTGATG	5520

QY	1834	LysHisLeuGluGluSerAsnLysGluAlaLysGluAlaGluLeuGluAlaGluLeu	1853
DB	5521	AAGCACCTTGGAGGAGAGACNACAGAGAGGCCAAGGAGGAGGCCGAGCTAGAGGCTGAGCTG	5580
QY	1854	GluLeuGluMetLysThrLeuSerProGlnProHisSerProLeuGlySerProPheLeu	1873
DB	5581	GAGCTGGAGAGTGAAGACCTCTCAGCCCCCAGCCACTCGCCACTGGCAGGCGCCCTTCCTC	5640
QY	1874	TrpProGlyValGluGlyProCaspSerProAspSerProLysProGlyAlaLeuHisPro	1893
DB	5641	TGGCCCTGGGGTCGAGGGGCCCGACAGACCCCGACAGCCCAAGCCTGGGGCTCTGCACCCCA	5700
QY	1894	AlaAlaHisAlaArgSerAlaSerHisPheSerLeuGluHisProThrMetClnProHis	1913
DB	5701	GGGGCCCCAGGAGATCAGCCTCCCACTTTTCCCTGGAGCACCCCAACATGAGGCCCAAC	5760
QY	1914	ProThrGluLeuProGlyProAspLeuLeuThrValArgLysSerGlyValSerArgThr	1933
DB	5761	CCACCGGAGCTGCCAGGACCACTTACTGTACTGTGGGAAGTCTGGGGTCTGAGCGAAGC	5820
QY	1934	HisSerLeuProAsnAspSerTyrMetCysArgHisGlySerThrAlaGluGlyProLeu	1953
DB	5821	CACTCTCTGCCCAATGACAGCTACATGTCTGGCATGGAGACACTGCCAGGGGGCCCTTG	5880
QY	1954	GlyHisArgGlyTTrpGlyLeuProLysAlaGlnSerGlySerValLeuSerValHisSer	1973
DB	5881	GGACACAGGGGCTGGGGGCTCCCCAAGACTCAGTCAGGCTCCGTCTTGTCCGTTCACCTCC	5940
QY	1974	GlnProAlaAspThrSerTyrIleLeuGlnLeuProLysAspAlaProHisIleLeuGln	1993
DB	5941	CAGCCAGCAGATACAGCTACATCTCTGCAGCTTCCCAAGATGCACCTCATCTGCTCCAG	6000
QY	1994	ProHisSerAlaProThrTrpGlyThrIleProLysLeuProProGlyArgSerPro	2013
DB	6001	CCCCACAGCGCCCCAACCTCTGGGACCAATCCCCAAGACTGCCCAACACTGCCCAACAGGACGCTCCCT	6060
QY	2014	LeuAlaGlnArgProLeuArgArgGlnAlaAlaIleArgThrAspSerLeuAspValGln	2033
DB	6061	TTGGCTCAGAGGCCACTCAGCGCCAGGACAGCAATAGGACTGACTCTCTTGGACGTTTCAG	6120
QY	2034	GlyLeuGlySerArgGluAspLeuLeuAlaGluValSerGlyProSerProProLeuAla	2053
DB	6121	GGTCTGGGGCAGCGGGAAGACCTGCTGGCAGAGGTGAGTGGGCCCTCTCCCGCCCTGGCC	6180
QY	2054	ArgAlaTyrSerPheTrpGlyGlnSerSerThrGlnAlaGlnGlnHisSerArgSerHis	2073
DB	6181	CGGCGCTACTCTTCTGGGGCCAGTCAAGTACCAGGCACAGCAGCAGCACTCCCGCAGCCAC	6240
QY	2074	SerLysIleSerLysHisMetThrProProAlaProCysProGlyProGluProAsnTrp	2093
DB	6241	AGCAAGATCTTCCAAAGCACATGACCCCGCCAGCCCTTGGCCAGGCCCAAGACCCCACTGG	6300
QY	2094	GlyLysGlyProProGluThrArgSerSerLeuLeuAspThrGluLeuSerTrpIle	2113
DB	6301	GGCAAGGGCCCTCCAGAGACCAGAAGCAGCTTAGAGTTGGACACGGAGCTCAGCTGGATT	6360
QY	2114	SerGlyAspLeuLeuProProGlyGlyGlnGluGluProProSerProArgAspLeuLys	2133
DB	6361	TCAGGAGACCTCTCTGCCCTCTGGCGCCAGAGGAGGCCCACTATCCCAAGGACCTGAAG	6420
QY	2134	LysCysTyrSerValGluAlaGlnSerCysGlnArgArgProThrSerTrpLeuAspGlu	2153
DB	6421	ANGTCTACAGCTGGAGGCCACAGAGCTGCCAGCGCGCGCTTACGCTCTCTGGCTGGATGAG	6480
QY	2154	GlnArgArgHisSerIleAlaValSerCysLeuAspSerGlySerGlnProHisLeuGly	2173
DB	6481	CAGAGGAGACACTCTATCGCGCTGAGCTGCCCTGGACAGCGGCTCCCAACCCCACTGGGC	6540
QY	2174	ThrAspProSerAsnLeuGlyGlyGlnProLeuGlyProGlySerArgProLysIle	2193
DB	6541	ACAGACCCCTCTAACTTGGGGGCCAGCCCTCTTGGGGGCCCGGAGCGCGGCCCAAGAA	6600
QY	2194	LysLeuSerProProSerIleThrLeuAspProProGluSerGlnGlyProArgThrPro	2213

Db 6601 AAACACGCGCGCTAGTATACCAATAGACCCCGGAGAGCAAGTCTCGGACCCCG 6660
Qy 2214 ProSerProGlyLeuArgArgAlaProSerSerAspSerLysAspProLeu 2233
Db 6661 CCCAGCCCTGCTATCTGCTCCGAGGAGGCTCGCTCCAGGACTCCCAAGGATCCCTTG 6720
Qy 2234 AlaSerGlyProProAspSerMetAlaAlaSerProSerProLysLysAspValLeuSer 2253
Db 6721 GCCTCTGGCCCCCTGACAGATGCTGCTGCGCCCTCCCAAGAAAGATGTGCTGAGT 6780
Qy 2254 LeuSerGlyLeuSerSerAspProAlaAspLeuAspPro 2266
Db 6781 CTCTCGGCTTATCTCTGACCCAGACACTGAGACCCC 6819

RESULT 2
US-09-426-998-4
; Sequence 4, Application US/09426998
; Patent No. 6358706
; GENERAL INFORMATION:
; APPLICANT: DUBIN, ADRIENNE E.
; APPLICANT: PYATI, JAYASHREE
; APPLICANT: ZHU, JESSICA Y
; APPLICANT: ERLANDER, MARK G
; APPLICANT: GALINDO, JOSE E
; TITLE OF INVENTION: DNA ENCODING HUMAN ALPHA1G T-TYPE CALCIUM
; TITLE OF INVENTION: CHANNEL (ALPHA1G-C)
; FILE REFERENCE: ORT-1057
; CURRENT APPLICATION NUMBER: US/09/426,998
; CURRENT FILING DATE: 1999-10-26
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PATENTIN VER. 2.0
; SEQ ID NO 4
; LENGTH: 7741
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
US-09-426-998-4

Alignment Scores:
Pred. No.: 0 Length: 7741
Score: 11877.50 Matches: 2264
Percent Similarity: 99.65% Conservativity: 1
Best Local Similarity: 99.60% Mismatches: 1
Query Match: 99.78% Indels: 7
DB: 3 Gaps: 1

US-09-611-257A-37 (1-2266) x US-09-426-998-4 (1-7741)

Qy 1 MetAspGluGluAspGlyAlaGlyAlaGluSerGlyGlnProArgSerPheMet 20
Db 523 ATGACGAGGAGGAGGATGGAGCGGCGCGGAGGATCGGAGACCGCGGAGCTTCATG 582
Qy 21 ArgLeuAsnAspLeuSerGlyAlaGlyGlyArgProGlyProGlySerAlaGluLysAsp 40
Db 583 CGGCTCAACGACCTGTGCGGGGCGGGGCGGCGGCGGGGCGGGGTGAGAGAAAGGAC 642
Qy 41 ProGlySerAlaAspSerGluAlaGluGlyLeuProTyrProAlaLeuAlaProValVal 60
Db 643 CCGGCGAGCGGCGACTCCAGCGGAGGCGGCTGCGGTACCGCGGCTGGCCCGCGTGT 702
Qy 61 PhePheTyrLeuSerGlnAspSerArgProArgSerTyrCysLeuArgThrValCysAsn 80
Db 703 TTCTTCTACTTGAACGACGAGGACGCGCGCGGAGCTGGTGTCTCCGACCGCTGTAAAC 762
Qy 81 ProTyrPheGluArgLeuSerMetLeuValLeuLeuAsnCysValThrLeuGlyMet 100
Db 763 CCCTGGTTGAGCGCATCAGCATGTGTGTCATCTTCTCAACTGCGTGACCTCGGGATG 822
Qy 101 PheArgProCysGluAspAlaCysAspSerGlnArgCysArgLeuGlnAlaPhe 120
Db 823 TTCCGGCCATCGGAGGACATCGCTGTGACTCCAGCGGCTCGCGGATCTCGAGGCTTT 882
Qy 121 AspAspPhePheAlaPhePheAlaValGluMetValValLysMetValAlaLeuGly 140

Db 883 GATGACTTCATCTTTGGCTTTTGGCGTGAGATGGTGGTGAAGATGGTGGCTTGGGC 942
Qy 141 IlePheGlyLysLysCysTyrLeuGlyAspThrTrpAsnArgLeuAspPhePheIleVal 160
Db 943 ATCTTTGGGAAAAAGTGTACCTGGGAGACACTTTGGAACCGGCTTGACTTTTTCATCGTC 1002
Qy 161 IleAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArg 180
Db 1003 ATCCAGGGATGCTGGAGTACTCGCTGACCTGCAGAACGTCAGCTTCTCAGCTGTTCAGG 1062
Qy 181 ThrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeu 200
Db 1063 ACAGTCCGTGCTGCGACCGCTCAGGCGCATTAACCGGGTCCGAGCATCGCATCTT 1122
Qy 201 ValThrLeuLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePhe 220
Db 1123 GTCAGGTTGCTGCTGGATAGCTGCTGCCCATGCTGGCAACGTCCTGCTGCTGCTTCTTC 1182
Qy 221 ValPhePhePheGlyIleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArg 240
Db 1183 GTCTTCTTTCATCTTTCGCGATCGTGGGCTCCAGCTGTGGGCGAGGCTGCTTCGGAACCGA 1242
Qy 241 CysPheLeuProGluAsnPheSerLeuProLeuSerValAspLeuGluArgTyrTrpGln 260
Db 1243 TGCTTCTTACCTGAGAAATTTTCAGCTCCCTGAGCGTGGACCTGGAGCGCTATTACCAG 1302
Qy 261 ThrGluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArg 280
Db 1303 ACAGAGAACGAGGATGAGAGCCCTTTCATCTGCTCCAGCCACGCGAGAACGCGCATGCGG 1362
Qy 281 SerCysArgSerValProThrLeuArgGlyAspGlyGlyGlyGlyProProCysGlyLeu 300
Db 1363 TCCTGCAAGACGTCGCCACGCTCGCGGGGACGGGGCGGTGGCCACCTTGGCGGTCTG 1422
Qy 301 AspTyrGluAlaTyrAsnSerSerSerAsnThrThrCysValAsnTrpAsnGluTyrTyr 320
Db 1423 GACTATGAGGCTTACAACAGCTCCAGCAACACCACTGTGTCAACTGGAACAGTACTAC 1482
Qy 321 ThrAsnCysSerAlaGlyGluHisAsnProPheLysGlyAlaIleAsnPheAspAsnIle 340
Db 1483 ACCAACTGCTCAGCGGGGAGCACAAACCTTCAAGGGCGGCATCACTTTGACAACATT 1542
Qy 341 GlyTyrAlaTrpIleAlaIlePheGlnValIleThrLeuGluGlyTrpValAspIleMet 360
Db 1543 GGCTATGCTGGATCGCCATCTTCCAGGTATCATCGCTGGAGGCTGGGTGCATCATG 1602
Qy 361 TyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIle 380
Db 1603 TACTTTGTGATGGATGCTCATCTTCTACAAATTCATCTACTCTCTCTCTCTCTCTCTCT 1662
Qy 381 ValGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGlu 400
Db 1663 GTGGCTCTCTTTCATGATCACTGCTGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1722
Qy 401 ThrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAla 420
Db 1723 ACCAAGCAGCGGAAAGCCAGCTGATCGGAGCAGCGGTGTGCGGTCTCTGTCACACGCC 1782
Qy 421 SerThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLeuLysTyrLeu 440
Db 1783 AGCACTTGGCTAGCTTCTCTGAGCCCGGAGCTGCTATGAGGAGCTGCTCAAGTACTCTG 1842
Qy 441 ValTyrIleLeuArgLysAlaAlaArgArgLeuAlaGlnValSerArgAlaAlaGlyVal 460
Db 1843 GTGTACATCTTCTGTAAGGAGCCCGCAGGCTGGCTCAGGTCTCTCGGGCAGCAGGTGTG 1902
Qy 461 ArgValGlyLeuLeuSerSerProAlaProLeuGlyGlyGlnGluThrGlnProSerSer 480
Db 1903 CGGTTGGCTGCTCAGCAGCCAGCACCCCTCGGGGGCGAGGAGCCAGCCAGCAGCAGC 1962
Qy 481 SerCysSerArgSerHisArgArgLeuSerValHisIleLeuValHisIleHisHis 500

Db 6343 CACTCTCTGCCAATGACACTACATGTGTCCGATCGGAGCACTGCCGAGGGGCCCTTG 6402
Qy 1954 GlyHisArgGlyTrpGlyLeuProLysAlaGlnSerGlySerValIleuSerValHisSer 1973
Db 6403 GGACACAGGGGCTGGGGGCTCCCAAGAGCTCAGTCAGGCTCCGTCTTGTCTCACTCC 6462
Qy 1974 GlnProAlaSerThrSerTyrlleLeuGlnLeuProLysAspAlaProHisIleuLeuGln 1993
Db 6463 CAGCAGCAGATACACAGCTACATCTCGAGCTTCCCAAGATGACCTCATCTGCTCCAG 6522
Qy 1994 ProHisSerAlaProThrTrpGlyThrIleProLysLeuProProGlyArgSerPro 2013
Db 6523 CCCCACAGCGCCCAACTGGGGACCATCCCCAACTGCCCAACACAGGAGCTCCCT 6582
Qy 2014 LeuAlaGlnArgProLeuArgGlnAlaAlaIleArgThrAspSerLeuAspValGln 2033
Db 6583 TTGGCTCAGAGCCACTCAGCGCCAGCGACATTAAGGACTGACTCTCTTGGAGCTTCAG 6642
Qy 2034 GlyLeuGlySerArgGluAspLeuAlaGluValSerGlyProSerProProLeuAla 2053
Db 6643 GGTCTGGGACGCCGGAGACTCTGTCAGAGGTGAGTGGGCCCTCCCGCCCTTGCC 6702
Qy 2054 ArgAlaTyrsrPheTrpGlyGlnSerThrGlnAlaGlnGlnHisSerArgSerHis 2073
Db 6703 CGGGCTACTCTTCTGGGGCCAGTCAAGTACCAGGACAGCAGCACTCCCGCAGCCAC 6762
Qy 2074 SerIleSerLysHisMetThrProAlaProCysProGlyProGluProAsnTrp 2093
Db 6763 AGCAAGATCTCAAGACATACCCCGCCAGCTTGGCCAGGCGCCAGAACCCACTGG 6822
Qy 2094 GlyLysGlyProProGluThrArgSerSerLeuGluLeuAspThrGluLeuSerTrpIle 2113
Db 6823 GCACAGGGCCCTCCAGACACCAAGACAGCTTAGAGTTGGACACGGAGCTGAGCTGATT 6882
Qy 2114 SerGlyAspLeuLeuProProGlyGlnGluProProSerProArgAspLeuLys 2133
Db 6883 TCAGAGAGCTCTCTGCCCTTGGGGCCAGGAGAGGCCCTCCCAACCCAGCTGAAG 6942
Qy 2134 LysCysTyrsrValGluAlaGlnSerCysGlnArgArgProThrSerTrpLeuAspGlu 2153
Db 6943 AAGTCTCAGAGGTGGAGGCCAGAGCTGCAGGCCCGGCTTACGTCCTGCTGGATGAG 7002
Qy 2154 GlnArgArgHisSerIleAlaValSerCysLeuAspSerGlySerGlnProHisLeuGly 2173
Db 7003 CAGAGAGACACTCTATCGCGTACGCTGGACAGCGGCTCCCAACCCAGCTGGGC 7062
Qy 2174 ThrAspProSerAsnLeuGlyGlnProLeuGlyGlyProGlySerArgProLysLys 2193
Db 7063 ACAGACCCCTTAACCTTGGGGGCCAGGCTCTTGGGGGCCCGGAGCGGCCCAAGAAA 7122
Qy 2194 LysLeuSerProProSerIleThrIleAspProProGluSerGlnGlyProArgThrPro 2213
Db 7123 AAACCTCAGCCCGCTAGTATACCATAGACCCCGGAGAGCAAGTCTCTCGACCCCG 7182
Qy 2214 ProSerProGlyIleCysLeuArgArgAlaProSerSerAspSerIleAspProLeu 2233
Db 7183 CCCAGCCCTGGTATCTGCTCCCGAGGAGGCTCCGTCAGCGCACTCCCAAGGATCCCTTG 7242
Qy 2234 AlaSerGlyProProAspSerMetAlaAlaSerProSerProLysIleAspValLeuSer 2253
Db 7243 GCCTCTGGCCCCCTGACAGCATGGCTGCTGCCCTCCCAAGAAAGATGCTGCTGAGT 7302
Qy 2254 LeuSerGlyLeuSerSerAspProAlaAspLeuAspPro 2266
Db 7303 CTCCTCGGTTTATCTCTGACCCAGCAGCACTGGACCCC 7341

RESULT 3

US-09-949-016-3859
; Sequence 3859, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3859
; LENGTH: 7405
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-3859

Alignment Scores:
Pred. No.: 0 Length: 7405
Score: 11241.00 Matches: 2162
Percent Similarity: 95.12% Conservative: 1
Best Local Similarity: 95.07% Mismatches: 1
Query Match: 94.43% Indels: 110
DB: 4 Gaps: 4

US-09-611-257A-37 (1-2266) x US-09-949-016-3859 (1-7405)

Qy 1 MetAspGluGluAspGlyAlaGlyAlaGluGluSerGlyGlnProArgSerPheMet 20
Db 373 ATGACGAGAGGAGGATGAGCGGCGCGGAGGAGTCCGGACAGCCCCGGAGTTCATG 432
Qy 21 ArgLeuAsnAspLeuSerGlyAlaGlyArgProGlyProGlySerAlaGluLysAsp 40
Db 433 CGSCTCAACGACCTGTCGGGGCGCGGGCGCGGGCGCGGGGTTCAGCAAGAAAGGAC 492
Qy 41 ProGlySerAlaAspSerGluAlaGlyLeuProTyProAlaLeuAlaProValVal 60
Db 493 CCGGGCAGCGCGACTCCGAGGGCGGAGGGCTGCCGTACCCGGCGCTGCCCGGTGGTT 552
Qy 61 PhePheTyrlleSerGlnAspSerArgProArgSerTrpCysLeuArgThrValCysAsn 80
Db 553 TTCTTCTACTTGAGCCAGGACAGCAGCCCGCGCGAGCTGGTGTCTCCGACGGTCTGTAAC 612
Qy 81 Pro---TrpPheGluArgIleSerMetLeuValIleLeuAsnCysValThrLeuGly 99
Db 613 CCTACCTGGTTTGAGCGCATCAGCATGTTGGTTCATCTTCTCAACTGCGTGACCCCTGGGC 672
Qy 100 MetPheArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAla 119
Db 673 ATGTTCCGGCCATCGCAGGACATCGCTGTGACTCCCGAGCGCTCCCGGATCCTGCAGGCC 732
Qy 120 PheAspAspPheIlePheAlaPhePheAlaValGluMetValValLysMetValAlaLeu 139
Db 733 TTTGATGACTTCATCTTTGCTTCTTTGCTTTCGCGAGATGGTGGTGAAGATGGTGGCCTTG 792
Qy 140 GlyIlePheGlyLysLysCysTyrlleGlyAspThrTrpAsnArgLeuAspPhePheIle 159
Db 793 GGCACTCTTGGGAAAAAGTGTATACCTCGGAGACACTTGGAAACCGGCTTGACTTTTTCATC 852
Qy 160 ValIleAlaGlyMetLeuGluTyrsrLeuAspLeuGlnAsnValSerPheSerAlaVal 179
Db 853 GTCATCCAGGGATGCTGGAGTACTCCGTGGAGTACTCCAGAACGTCAGCTTCTCAGCTGTC 912
Qy 180 ArgThrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIle 199
Db 913 AGGACAGTCCGTGTGCTGCGACCGCTCAGGGCCATTAAACCGGGTCCCGAGCATGCGCATC 972
Qy 200 LeuValThrIleLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhe 219
Db 973 CTTGTACAGTGTGCTGGATACCTGCCCATGCTGGGCAACGTCCTGCTGCTGCTGCTTC 1032
Qy 220 PheValPhePheIlePheGlyIleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsn 239

Db 1033 TCGCTCTTCTCATCTTCGCGCATCGTCGCGTCCAGCTGTGGCGAGGCTGCTTCGGAAAC 1092
Qy 240 ArgCysPheLeuProGluAsnPheSerLeuProLeuSerValAspLeuGluArgTyrTyr 259
Db 1093 CGATGCTTCTTACCTAGAAATTCAGCTCTCCCTGAGCGTGGACCTCGAGCGCTATTAC 1152
Qy 260 GlnThrGluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMet 279
Db 1153 CAGACAGAAACGAGGATGAGAGGCCCCCTTCATCTCTCCACGCCACGCGAAGCGGCATG 1212
Qy 280 ArgSerCysArgSerValProThrLeuArgGlyAspGlyGlyGlyGlyProProCysGly 299
Db 1213 CGGTCTGCAGAGCGTGCACCGCTGCGCGGAGCGGGCGGTGGCCACCTTTCGGGT 1272
Qy 300 LeuAspTyrGluAlaTyrAsnSerSerSerAsnThrThrCysValAsnTrpAsnGlnTyr 319
Db 1273 CTGGACTATGAGCGCTACACAGCTCCAGCAACACCACCTGTGTCAACTGGAAACCACTAC 1332
Qy 320 TyrThrAsnCysSerAlaGlyGluHisAsnProPheIleGlyAlaIleAsnPheAsn 339
Db 1333 TACACCAACTCTCAGCGGGGAGCACAAACCCCTTCAAGGGCGCCATCAACTTTGACAAAC 1392
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Qy 360 MetTyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIle 379
Db 1453 ATGTACTTTGTGTGATGCTCATTTCTTACAAATTTTCATCTACTTCTCTCTCATC 1512
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Db 1513 ATCTGGGCTCTTCTTTCATGATCAACCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1572
Qy 400 GluThrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsn 419
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Db 1633 GCCAGCACCTTGGCTAGCTTCTCTGAGCCCGCAGCTGCTATGAGGAGCTCTCAAGTAC 1692
Qy 440 LeuValTyrIleLeuArgLysAlaAlaArgArgLeuAlaGlnValSerArgAlaAlaGly 459
Db 1693 CTGTGTACATCTCTGTAAGCGACGCGCAGGCTGCTCAGGTCTCTCGGGCAGCAGGT 1752
Qy 460 ValArgValGlyLeuLeuSerSerProAlaProLeuGlyGlyGlnGluThrGlnProSer 479
Db 1753 GTGGGGTGTGGCTGCTCAGCAGCCCGACACCCCTCGGGGGCAGGAGACCCAGCCAGC 1812
Qy 480 SerSerCysSerArgSerHisArgArgLeuSerValHisHisLeuValHisHisHis 499
Db 1813 AGCAGCTGCTCTCGCTCCACCGCGCTATCCGTCCACACCACTGTGTGCACCAACCCAC 1872
Qy 500 HisHisHisHisHisTyrHisGlyAsnGlyThrLeuArgAlaProArgAlaSerPro 519
Db 1873 CACCATCACCACTACCATCTGGGCAATGGGACGCTCAGGGCCCCCGGGCGAGCCCG 1932
Qy 520 GluIleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProProSerThr 539
Db 1933 GAGATCCAGGACAGGATGCCAATGGGTCCCGCGGCTCATGCTGCCACCACTTCGACG 1992
Qy 540 ProAlaLeuSerGlyAlaProProGlyGlyAlaGluSerValHisSerPheTyrHisAla 559
Db 1993 CTGGCTCTCTCGGGGCCCCCTGGTGGCGCAGAGTCTGTGCACAGCTTCTACCATGCC 2052
Qy 560 AspCysHisLeuGluProValArgCysGlnAlaProProProArgSerProSerGluAla 579
Db 2053 GACTGCCACTTAGAGCAGTCCGCTGCCAGGCGCCCCCTCCAGGTCCCATCTCGAGGCA 2112
Qy 580 SerGlyArgThrValGlySerGlyLysValTyrProThrValHisThrSerProProPro 599

Db 2113 TCCGGCAGGACTGTGGCGAGCGGGAAGGTGTATCCACCGTGCAACACAGCCCTCCACGG 2172
Qy 600 GluThrLeuLysGlyLysAlaLeuValGluValAlaAlaSerSerGlyProProThrLeu 619
Db 2173 GAGACGCTGAAGGAGAAGGCACTAGTAGAGGTGGCTGCAGCTCTGGGCCCCCAACCTC 2232
Qy 620 ThrSerLeuAsnIleProProGlyProTyrSerSerMetHisLysLeuLeuGluThrGln 639
Db 2233 ACCAGCTTCAACATCCCAACCGGGCCCTACAGCTCCATGCACAAAGCTCTCGAGACAG 2292
Qy 640 SerThrGlyAlaCysGlnSerSerCysLysIleSerSerProCysLeuLysAlaAspSer 659
Db 2293 AGTACAGGTGCTGCCAAAGCTCTTGCAGATCTCCAGCCCTTGTCTTGAAGACAGCAGT 2352
Qy 660 GlyAlaCysGlyProAspSerCysProTyrCysAlaArgAlaGlyAlaGlyGluValGlu 679
Db 2353 GGAGCTGTGTCCAGACAGCTGCCCTTACTGTGCCGGCGGGCAGGAGGTGGAG 2412
Qy 680 LeuAlaAspArgGluMetProAspSerAspSerGluAlaValTyrGluPheThrGlnAsp 699
Db 2413 CTCGCCGACCGTGAATGCTCTGACTCAGACAGCGAGGAGTTATGAGTTCCACAGGAT 2472
Qy 700 AlaGlnHisSerAspLeuArgAspProHisSerArgArgGlnArgSerLeuGlyProAsp 719
Db 2473 GCCCAGCACAGCAGCTCCGGGACCCCAACAGCCGGCGGCAACGGAGCTTGGGCCAGAT 2532
Qy 720 AlaGluProSerSerValLeuAlaPheTrpArgLeuIleCysAspThrPheArgLysIle 739
Db 2533 GCAGAGCCAGCTCTGTGCTGGCTTCTGGAGGCTAATCTGTGACACCTTCGAAAGATT 2592
Qy 740 ValAspSerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSer 759
Db 2593 GTGGACACGAAGTACTTTGGCCGGGSAATCATGATGCCATCTCTGGTCAACACACTCAGC 2652
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Db 2653 ATGGGCATCGNATACCAAGCAGCAGCAGCCCGAGAGGCTTACCAACGCCCTAGAAATCAGCAAC 2712
Qy 780 IleValPheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuLeuValTyrGlyPro 799
Db 2713 ATCGTCTTACCAGCTCTTTGCCCTGGAGATGCTGTGTAAGCTGTGTGTATGGTCCC 2772
Qy 800 PheGlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleValIleSerVal 819
Db 2773 TTTGGCTACATCAAGAATCCCTACAACTTCTCATGTTGTGTGTTGTATCAGCGTG 2832
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Db 2893 CGTGTGTGAAGCTGT 2952
Qy 860 LysThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePheIlePhe 879
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Qy 900 LeuProAspArgLysAsnPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIle 919
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Qy 940 AlaAlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuLeu 959
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QY 960 ValAlaIleLeuValGluGlyPheGlnAlaGluGluIleSerLysArgGluAspAlaSer 979
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QY 980 GlyGlnLeuSerCysIleGlnLeuProValAspSerGlnGlyGlyAspAlaAenLysSer 999
Db 3286 -----GGAGATGCCAACAGTCC 3303
QY 1000 GluSerGluProAspPheSerProSerLeuAspGlyAspArgLysLysCys 1019
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QY 1020 LeuAlaIleValSerLeuGlyGluHisProGluLeuArgLysSerLeuLeuProLeu 1039
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QY 1080 AlaHisGluMetLysSerProProSerAlaArgSerSerProHisSerProTrpSerAla 1099
Db 3544 GCCCACGAGATGAAGTCAACCCGCCAGCCCGAGCTCTCCGACAGCCCTGGAGCGCT 3603
QY 1100 AlaSerSerTrpThrSerArgSerSerArgAenSerLeuGlyArgAlaProSerLeu 1119
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Db 3724 CAGGATGAAGAGAGAGCTCAGAGAGGAGCGGCGCCAGCCCTGGCGGCGAGTGCACATCGC 3783
QY 1160 HisArgGlySerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeuGln 1179
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Db 3844 GTGCCAGGGCTGCATCGCACTGCCAGTGGCCGAGGTTCTGCTTCTGAGCACACGAGACTGC 3903
QY 1200 AsnGlyLysSerAlaSerGlyArgLeuAlaArgAlaLeuArgProAspAspProLeu 1219
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QY 1220 AspGlyAspAlaAspAspGluGlyAsnLeuSerLysGlyGluArgValArgAlaTrp 1239
Db 3964 GATGGGATGACCGCATACAGAGGCAACCTGAGCAAGGGAACGGGTCCGCGCGTGG 4023
QY 1240 IleArgAlaArgLeuProAlaCysTyrLeuGluArgAspSerTrpSerAlaTyrIlePhe 1259
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Db 4504 CTGGTGGTGGAGACCGTGAATGCTCTCATGAAACCCATCGGCAACATTGTAGTCATCTGC 4563
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QY 1480 PheValLeuAlaSerLysAspGlyTrpValAspIleMetTyrAspGlyLeuAspAlaVal 1499
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QY 1633 ThrValIlePheValLeuGluSerValPheLysLeuValAlaPheGlyPheArgArgPhe 1652
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QY 1653 PheGlnAspArgTrpAsnGlnLeuAspLeuAlaIleValLeuLeuSerIleMetGlyIle 1672
Db 5284 TTCAGGACAGGTGGAGACCGAGCTGGCCATTTGTGCTGTGTGTCTCATCATGGCATC 5343
QY 1673 ThrLeuGluGluIleGluValAsnAlaSerLeuProIleAsnProThrIleIleArgIle 1692

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Qy MetLeuLeuPhePheIlePheAlaAlaLeuGlyValGluLeuPheGlyAspLeuGluCys 1752
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Db GCCTTCTTAAACCTCTCCAGAGTCTCCACAGGTGACAAATGGATGGCAATTATGAAGAC 5703
Qy ThrLeuArgAspCysAspGlnGluSerThrCysTyrAsnThrValIleSerProIleTyr 1812
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Qy LeuGlyHisArgGlyTTPGlyLeuProLysAlaGlnSerGlySerValLeuSerValHis 1972
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Qy GlnGlyLeuGlySerArgGluAspLeuAlaGluValSerGlyProSerProLeu 2052
|||||

Db 6424 CAGGCTGGGCAGCCCGGAAGACCTGCTGGCAGAG----- 6459
Qy 2053 AlaArgAlaTyrSerPheTrpGlyGlnSerSerThrGlnAlaGlnHisSerArgSer 2072
Db 6459 ----- 6459
Qy 2073 HisSerLysIleSerLysHisMetThrProProAlaProCysProGlyProGluProAsn 2092
Db 6459 ----- 6459
Qy 2093 TrpGlyLysGlyProProGluThrArgSerSerLeuGluLeuAspThrGluLeuSerTrp 2112
Db 6459 ----- 6459
Qy 2113 IleSerGlyAspLeuLeuProProGlyGlyGlnGluProProSerProArgAspLeu 2132
Db 6460 -----GAGGAGCCCCCATATCCCCACGGAGACCTG 6486
Qy 2133 LysLysCysTyrSerValGluAlaGlnSerCysGlnArgArgProThrSerTrpLeuAsp 2152
Db 6487 AAGAAGTGCTACAGCGTGGAGGCCAGAGCTGCCAGCGCCGCGCCACGCTCTGCTGGAT 6546
Qy 2153 GluGlnArgArgHisSerIleAlaValSerCysLeuAspSerGlySerGlnProHisLeu 2172
Db 6547 GAGCAGAGGAGACACTCTATCGCGCTCAGCTGCTGGACAGGGCTCCCAACCCACCTG 6606
Qy 2173 GlyThrAspProSerAsnLeuGlyGlnProLeuGlyGlyProGlySerArgProLys 2192
Db 6607 GGCAACAGCCCTTAACCTTGGGGGCGAGCTCTTGGGGGGCTGGAGCGGCCCAAG 6666
Qy 2193 LysLysLeuSerProProSerIleThrIleAspProProGluSerGlnGlyProArgThr 2212
Db 6667 AAAAACTCAGCCCGCTTAGTATCACCATAGACCCCGGAGAGCAAGGTCTCTGGACC 6726
Qy 2213 ProProSerProGlyIleCysLeuArgArgAlaProSerSerAspSerLysAspPro 2232
Db 6727 CCGCCAGCCCTGATATCTGCTCCGAGGAGGGCTCCGTCAGGACTCCAGGATCCC 6786
Qy 2233 LeuAlaSerGlyProProAspSerMetAlaAlaSerProSerProLysLysAspValLeu 2252
Db 6787 TTGGCTCTGGCCCGCCCTGACAGCATGCTGCTCGCCCTGCCCAAGAAAGATGTGCTG 6846
Qy 2253 SerLeuSerGlyLeuSerSerAspProAlaAspLeuAspPro 2266
Db 6847 AGTCTCTCGGTTTATCTCTGACCCAGACAGCTGGACCCC 6888

RESULT 4

US-09-398-522-51
; Sequence 51, Application US/09398522
; Patent No. 6783933
; GENERAL INFORMATION:
; APPLICANT: Issa, Jean-Pierre
; TITLE OF INVENTION: CAGNA1G POLYNUCLEOTIDE POLYPEPTIDE AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: JHU1590
; CURRENT APPLICATION NUMBER: US/09/398,522
; CURRENT FILING DATE: 1999-09-15
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 51
; LENGTH: 3993
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: CAGNA1G - a gene encoding a T-type calcium channel
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (373)....(3993)
US-09-398-522-51

Alignment Scores:
Pred. No.: 0 Length: 3993
Score: 6315.50 Matches: 1207

Percent Similarity:	98.13%	Conservative:	0
Best Local Similarity:	98.13%	Mismatches:	0
Query Match:	53.05%	Indels:	23
DB:	4	Gaps:	1
US-09-611-257A-37 (1-2266) x US-09-398-522-51 (1-3993)			
QY	1 MetAspGluGluAspGlyAlaGlyValaGluSerGlyGlnProArgSerPheMet	20	1333 ACCAACTGCTCAGCGGGGAGCACAACCCCTTCAAGGGCGCCATCAACTTTGACAACATT
DB	373 ATGGACGAGGAGGAGGATGAGCGGGCGCCGAGAGTCGGGACAGCCCGGAGCTTCATG	432	341 GlyTyrAlaTrpIleAlaIlePheGlnValIleThrLeuGluGlyTrpValAspIleMet
QY	21 ArgLeuAsnAspLeuSerGlyAlaGlyArgProGlyProGlySerAlaGluLysAsp	40	1393 GGCTATGCTGGATCGCCATCTTCCAGGTCTATCAGCTGGAGGGCTGGGTGACATCATG
DB	433 CGGCTCAACGACCTGTGCGGGCGCGGGCGCGGGCGGGGTCAGCAGAAAAGGAC	492	361 TyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleIle
QY	41 ProGlySerAlaAspSerGluAlaGluGlyLeuProTyrProAlaLeuAlaProValVal	60	1453 TACTTTGTGATGATGCTCATCTCTTCAATTTCACTTACTTCTCATCTCCTCATCATC
DB	493 CCGGCGAGCGGAGCTCCGAGCGGAGGGCTGCGTACCGGGGCTGGCCCGGGTGT	552	381 ValGlySerPhePheMetIleAsnLeuValIleAlaThrGlnPheSerGlu
QY	61 PhePheTyrLeuSerGlnAspSerArgProArgSerTrpCysLeuArgThrValCysAsn	80	1513 GTGGGCTCTCTTCTCATGATCAACCTGTGCTGGTGTGATGCCACGCGAGTCTTCAGAG
DB	553 TTCTTCTACTTGGAGCAGCAGCGCGCGGAGCTGTGTCTCCGACACGGTCTGTAAC	612	401 ThrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAla
QY	81 ProTrpPheGluArgIleSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMet	100	1573 ACCAAGCAGCGGAAAGCCAGCTGATGCGGGAGCAGCGTGTGCGTTCCTGTCTCAACGCC
DB	613 CCCTGGTTTGGCGCATCAGCATGTGTGTCATCTTCTCACTCGCTGACCTGGGCGATG	672	421 SerThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLysTyrLeu
QY	101 PheArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPhe	120	1633 AGCACCTTGGCTAGCTTCTGAGCCCGGAGCTGTATGAGGAGCTGTCTCAGTACTCTG
DB	673 TTCCGGCCATGCGAGGACATCGCTGTGACTCCCGAGCGCTCCGCGATCCTGCAAGCCTT	732	441 ValTyrIleLeuArgLysAlaAlaArgArgLeuAlaGlnValSerArgAlaAlaGlyVal
QY	121 AspAspPheIlePheAlaPhePheAlaValGluMetValLysMetValAlaLeuGly	140	1693 GTGTACATCTCTTCTGTAAGCGCAGCCCGAGCTGGCTCAGGTCTCTCTCGGCGAGCAGGTGTG
DB	733 GATGACTTTCATCTTGTCTTCTTCCGCTGGAGATGGTGGTGAAGATGGTGGCTTGGGC	792	461 ArgValGlyLeuLeuSerSerProAlaProLeuGlyGlyGlnGluThrGlnProSerSer
QY	141 IlePheGlyLysCysTyrLeuGlyAspThrTrpAsnArgLeuAspPheIleVal	160	1753 CGGTTGGCTCTCTCAGCAGCCAGCAGCCCTCGGGGCGCAGGAGACCCAGCCAGCAGC
DB	793 ATCTTTGGGAAAAGTGTACTCTGGAGACACTTGGAAACCGCTTGACTTTTCATGCTC	852	481 SerCysSerArgSerHisArgArgLeuSerValHisLeuValHisHisHisHis
QY	161 IleAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArg	180	1813 AGCTGCTCTCGCTCCACCGCGCTATCCGTTCCACCTCTGGTGTGACCCACCACCAC
DB	853 ATCGCAGGATGCTGGAGTACTCGCTGGACCTCGCAAGACGTTCAGCTTCTCAGCTGT	912	501 HisHisHisHisTyrHisLeuGlyAsnGlyThrLeuArgAlaProArgAlaSerProGlu
QY	181 ThrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeu	200	1873 CATCACCAACCATCACCTTGGCAATGGCGCTCAGGGCCCCCGGCGCCAGCCGCGAG
DB	913 ACAGTCCGTGTGTCGACGCTCAGGCGCATTAACCGGTGCCAGCATGCGCATCTT	972	521 IleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProProSerThrPro
QY	201 ValThrLeuLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePhe	220	1933 ATCCAGCAGAGGATGCCAATGGGTCCCGCGCTCATGCTGCCACCCCTCGAGCCT
DB	973 GTCACGTGCTGCTGGATAGCTGCCCATGCTGGGCAACGCTCTGCTGCTCTCTCTC	1032	541 AlaLeuSerGlyValAlaProProGlyGlyAlaGluSerValHisSerPheTyrHisAlaAsp
QY	221 ValPhePheIlePheGlyIleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArg	240	1993 GCCTCTCCGGGGCCCCCTTGGTGGCGCAGAGTCTGTGCACAGTCTTACCATGCGGAC
DB	1033 GTCTTCTTCATCTTCGCGCATCTGCGCGTCCAGCTGTGGCAGGCTGTCTCGAACCAG	1092	561 CysHisLeuGluProValArgCysGlnAlaProProProArgSerProSerGluAlaSer
QY	241 CysPheLeuProGluLeuPheSerLeuProLeuSerValAspLeuGluArgTyrTrpGln	260	2053 TGCCACTTAGAGCAGTCCGCTGCCAGGCGCCCCCTCCAGGGTCCCATCTGAGGCGATCC
DB	1093 TGCTTCTTACTGAGATTTACGCTCCCTCCCTCAGCGTGGACCTGGAGCGCTATTACCA	1152	581 GlyArgThrValGlySerGlyLysValTyrProThrValHisThrSerProProProGlu
QY	261 ThrGluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArg	280	2113 GGCAGGACTGTGGGCGAGGAGGAGTGTATCCACCGTGCACACCGAGCTCCACCGGAG
DB	1153 ACAGAGAACAGGATGAGAGCCCTTCATCTGCTCCAGCAGCCGAGAACGGCATGCGG	1212	601 ThrLeuLysGluLysAlaLeuValGluValAlaAlaSerSerGlyProProThrLeuThr
QY	281 SerCysArgSerValProThrLeuArgGlyAspGlyGlyGlyProCysGlyLeu	300	2173 ACCTGGAAGGAGGAGGAGCTAGTAGAGTGGCTGCCAGCTCTGGGCCCCCAACCTCACC
DB	1213 TCCTGCAAGACGTCGCCACGCTGCGGGGAGCGGGGCGGTGGCCACCTTCCGGTCTG	1272	621 SerLeuAsnIleProProGlyProTyrSerSerMetHisLysLeuLeuGluThrGlnSer
QY	301 AspTyrGluAlaIafTyrAsnSerSerAsnThrThrCysValAsnTrpAsnGlnTyrTyr	320	2233 AGCTCAACATCCACCCCGGCGCTACAGTCTCCATGCAAGCTGTGCTGGAGACACAGAT
DB	1273 GACTATGAGGCTCAACAGCTCCAGCAACACCACTGTGTCACTGGAAACCACTACTAC	1332	641 ThrGlyAlaCysGlnSerSerCysLysIleSerSerProCysLeuLysAlaAspSerGly
QY	321 ThrAsnCysSerAlaGlyGluHisAsnProPheLysGlyAlaIleAsnPheAspAsnIle	340	2293 ACAGGTGCTGCCAAAGCTCTTGCAGATCTCCAGCCCTTGTCTTGAAGCAGACAGTGA
			2352
			660
			2352
			680
			2412
			700
			2472

Qy 701 GlnHisSerAspLeuArgAspProHisSerArgGlnArgSerLeuGlyProAspAla 720
Db 2473 CAGCACAGCAGCCTCCGGGACCCACAGCGCGGCAACGAGAGCCTGGGCGCCAGATGCA 2532
Qy 721 GluProSerSerValLeuAlaPheTrpArgLeuIleCysAspThrPheArgLysIleVal 740
Db 2533 GAGCCCAAGCTCTGCTGGCCCTTCGGAGGCTAATCTGTGACACTTCGGAAGATTGTG 2592
Qy 741 AspSerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerMet 760
Db 2593 GACAGCAAGTACTTTGGCCGGGAATCATGATGCCATCTCTGGTCAACACACTCAGCATG 2652
Qy 761 GlyIleGlnTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnIle 780
Db 2653 GGCATCGAATACCAAGCAGCAGCGGAGGCTTACCAACGCCCTAGAAATCAGCAACATC 2712
Qy 781 ValPheThrSerLeuPheAlaLeuGluMetLeuLeuLeuValTyrGlyProPhe 800
Db 2713 GTCTTACCAAGCTCTTTGCCCTGGAGATGCTGTAAGCTGCTGTGTATGTGTCCTTT 2772
Qy 801 GlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleValIleSerValTrp 820
Db 2773 GGCTACATCAAGATCCTTACCAATCTTCGATGCTGTGTCATTCAGCGTGTGG 2832
Qy 821 GluIleValGlyGlnGlnGlyGlyLeuSerValLeuArgThrPheArgLeuMetArg 840
Db 2833 GAGATCGTGGGCCACAGCGGGGGCGCTGTCGGTGTCTCGGACCTTTCGCGCTGATCGT 2892
Qy 841 ValLeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetLys 860
Db 2893 GTGCTGAAGCTGGTGGCGCTTCTCCCGCGCTGCAGCGGCGAGCTGGTGGTGTCTCATGAG 2952
Qy 861 ThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePheSer 880
Db 2953 ACCATGACACAGTGGCCACCTTCTGCATGCTGCTTATGCTCTTCATCTTCATCTTCAGC 3012
Qy 881 IleLeuGlyMetHisLeuPheGlyCysLysPheAlaSerGluArgAspGlyAspThrLeu 900
Db 3013 ATCTTGGGCATGCATCTCTTGGCTGCAAGTTTGCCTCTGAGCGGGATGGGACACCCCTG 3072
Qy 901 ProAspArgLysAsnPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIleLeu 920
Db 3073 CCAGACCGAAGATTGTGACTCTCTGCTGGGCCATCGTCACTGCTTTCAGATCTCTG 3132
Qy 921 ThrGlnGluAspTrpAsnLysValLeuTyrAsnGlyMetAlaSerThrSerTrpAla 940
Db 3133 ACCCAGGAGGACTGGAACAAGTCTCTACAATGTATGGCTCCACGTCGTCCTGGGCG 3192
Qy 941 AlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuVal 960
Db 3193 GCCCTTTATTTCAATGCGCTCATGACCTTCGGCAACTACGTGCTCTTCAATTTGCTGTC 3252
Qy 961 AlaIleLeuValGluGlyPheGlnAlaGluIleSerLysArgGluAspAlaSerGly 980
Db 3253 GCCATTCTGGTGGAGGGCTTCAGCGGAG----- 3282
Qy 981 GlnLeuSerCysIleGlnLeuProValAspSerGlnGlyAspAlaAsnLysSerGlu 1000
Db 3283 -----GGAGATGCCAACAAGTCCGAA 3303
Qy 1001 SerGluProAspPhePheSerProSerLeuAspGlyAspGlyAspArgLysLysCysLeu 1020
Db 3304 TCAGAGCCGATTTCTTCTTCCACCCAGCCTGATGGTGTATGGGACAGAGAGTGTGTTG 3363
Qy 1021 AlaLeuValSerLeuGlyGluHisProGluLeuArgLysSerLeuLeuProProLeuIle 1040
Db 3364 GCCTTGGTGTCTTGGGAGACACCGGAGCTGGGAAGAGCCTGCTGCGCCCTCTCATC 3423
Qy 1041 IleHisThrAlaAlaThrProMetSerLeuProLysSerThrSerThrGlyLeuGlyGlu 1060
Db 3424 ATCCACAGCGCGCCACACCCATGCTGCTGCCAAGAGACACAGCAGCGGCTGGGCGAG 3483

Qy 1061 AlaLeuGlyProAlaSerArgArgThrSerSerSerGlySerAlaGluProGlyAlaAla 1080
Db 3484 GCGCTGGCGCTCGCTCGCGCCGCCACAGCAGCAGCGGTCTGGCAGAGCCTTGGGCGCGCC 3543
Qy 1081 HisGluMetLysSerProProSerAlaArgSerProHisSerProTrpSerAlaAla 1100
Db 3544 CACGAGATGAAGTCAACGCCCGCCGCGAGCTCTCCGACACAGCCCTTGAGGCGCTGCA 3603
Qy 1101 SerSerTrpThrSerArgSerSerArgAsnSerLeuGlyArgAlaProSerLeuLys 1120
Db 3604 AGCAGCTGGACAGCAGCGCTCCAGCGGGAACAGCCTCGGCCCTGCACCCAGCCTGAAG 3663
Qy 1121 ArgArgSerProSerGlyGluArgArgSerLeuLeuSerGlyGlyGlnGlnSerGln 1140
Db 3664 CGGAGAAGCCCAAGTGAGAGCGCGCTCCTGTGTGGGAGAAGGCCAGAGAGCCAG 3723
Qy 1141 AspGluGluGluSerSerGluGluArgAlaSerProAlaGlySerAspHisArgHis 1160
Db 3724 GATGAGAGGAGAGCTCAGAAAGAGAGCGGCGAGCCTTGGGGCAGTGACCATCGCCAC 3783
Qy 1161 ArgGlySerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeuGlnVal 1180
Db 3784 AGGGGCTCCCTGGAGCGGAGGCCAAGAGTTCTTTCACCTGCCAGACACACTGCAGGTG 3843
Qy 1181 ProGlyLeuHisArgThrAlaSerGlyArgGlySerAlaSerGluHisGlnAspCysAsn 1200
Db 3844 CCAGGGCTGTCATGCATCTGCCAGTGGCGGCGCTGCTCTTGAGCAGCAGGACTGCAAT 3903
Qy 1201 GlyLysSerAlaSerGlyArgLeuAlaArgAlaLeuArgProAspAspProLeuAsp 1220
Db 3904 GGCAGTCTGGCTTCAGGGCGCTGGCCCGGCGCTTGGGCTGATGATGATGATGATGAT 3963
Qy 1221 GlyAspAlaAspAspGluGlyAsnLeu 1230
Db 3964 GGGGATGACCGCATGACGAGGCAACCTG 3993

RESULT 5

US-08-984-709A-49
; Sequence 49, Application US/08984709A
; Patent No. 6320032
; GENERAL INFORMATION:
; APPLICANT: Williams, Mark E.
; APPLICANT: Stauderman, Kenneth A.
; APPLICANT: Harpold, Michael M.
; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
; TITLE OF INVENTION: METHODS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Heller Ehrman White & McAuliffe
; STREET: 4250 Executive Square, Suite 700
; CITY: La Jolla
; STATE: California
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/984,709A
; FILING DATE: 02-DEC-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L.
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 24735-9815 (formerly 6362-9815)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 450-8400
; TELEFAX: (619) 587-5360
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7898 base pairs

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; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 249...7307
; OTHER INFORMATION:
US-08-984-709A-49

Alignment Scores:
Pred. No.: 0 Length: 7898
Score: 6214.50 Matches: 1367
Percent Similarity: 65.17% Conservative: 212
Best Local Similarity: 56.42% Mismatches: 516
Query Match: 52.21% Indels: 328
DB: 59 Gaps: 59

US-09-611-257A-37 (1-2266) x US-08-984-709A-49 (1-7898)
QY 7 GlyAlaGlyAlaGluGluSerGlyClnProArgSerPheMetArgLeuAsnAspLeuSer 26
DB 317 GCGGTGGTGGGGGCGTCCCGGAGAGCCCGG----- 349
QY 27 GlyAlaGlyGlyArgProGlyPro-GlySer----- 36
DB 350 GCGCGCGGAGCGGAGCGGCGGCGGCGTCCGAGCTCGCGGTGCCTCCGAGAGCC 409
QY 37 -----AlaGluAspProGlySerAlaAspSerGluAlaGluGlyLeuProTyrProAl 55
DB 410 GCGCGCGGAGCGGCGGCGGAGCTCGGTCCGAGAGGAGGAGCGGCGGCGGCGGCGT 529
QY 55 AlaLeuProValValPhePheTyrLeuSerGlnAspSerArgProArgSerTyrCysLe 75
DB 470 CTTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 589
QY 75 uArgThrValCysAsnProTyrPheGluArgIleSerMetLeuValIleLeuLeuAsnCy 95
DB 530 CCGGCTGGTCTGCAACCCATGTTCCGAGCAGCTGAGCATGCTGGTAATCATGCTCACTG 589
QY 95 sValThrLeuGlyMetPheArgProCysGluAspIleAlaCysAspSerGlnArgCysAr 115
DB 590 CGTAGCCCTGGGCGATGTTCCGCGCCCTGTGAGAGCGTTGAGTGGCGCTCCGAGCGCTG 649
QY 115 gIleLeuGlnAlaPheAspPheIlePheAlaPhePheAlaValGluMetValVally 135
DB 650 CATCTGGAGGCTTTGACGCTTTCATTTTCGCTTTTTCGCTGAGATGCTCATCAA 709
QY 135 sMetValAlaLeuGlyIlePheGlyIleCysTyrLeuGlyAspThrTyrAsnArgIle 155
DB 710 GATGGTGGCTTGGGCGTGTCCGCGAGAGTGTACCTGGGTGACACGTGGAAAGAGCT 769
QY 155 uAspPhePheIleValIleAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnValse 175
DB 770 GGATTTCTTCATGCTGTCGCGGCGATGATGGAGTACTCGTTGACCGGACACAACTGAG 829
QY 175 rPheSerAlaValArgThrValArgValLeuArgProLeuArgAlaIleAsnArgValPr 195
DB 830 CCTCTCGCTATCAGGACCGTGGCGGTGCTGCGGCGCCCTCCGCGCCATCAACCGCTGCC 889
QY 195 oSerMetArgIleLeuValThrLeuLeuLeuAspThrLeuProMetLeuGlyAsnValle 215
DB 890 TAGCATGGGATCTCTGCTACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 949
QY 215 uLeuLeuCysPhePheValPhePheIleValIleValGlyValIleClnLeuTrpAlaGl 235
DB 950 TCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1009
QY 235 yLeuLeuArgAsnArgCysPheLeuProGluAsnPheSerLeuProLeuSerValAsp-- 254
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DB 1010 CCTCTCGGGAACCGCTGCTTCTCTGGACAGTGGCTTTGTGAGAACACACCTGACCTT 1069
QY 255 -LeuGluArgTyrTyrGlnThrGluAsnGluAspGluSerProPheIleCysSerGlnPr 274
DB 1070 CTTGGCGGCTTACTACGAGACGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1129
QY 274 oArgGluAsnGlyMetArgSerCysArgSerValPro-----ThrLeuArgGlyAs 291
DB 1130 CCGAGACACCGCATGCAAGAGTCTCGCACATCCCGCGCGCGCGAGCTGGCG----- 1184
QY 291 pGlyGlyGlyProProCysGlyLeuAspTyrGluAlaTyrAsn----- 306
DB 1185 -----ATGCCCTGCACCTTGGCTGGGAGGCTTACACGAGCGCGGAGCGGCGGA 1231
QY 307 -----SerSerSerAsnThrThrCysValAsnTyrAsnGlnTyrTyrThrAsnCys 324
DB 1232 GGGGTGGCGGCTGCACGCAACGCTGCATCACTGGAAACAGTACTACAACGTGTGCG 1291
QY 324 rAlaGlyGluHisAsnProPheLysGlyAlaIleAsnPheAspAsnIleGlyTyrAlaTr 344
DB 1292 CTCGGGTGACTCCAAACCCCAACACGTCGATCACTTCGACCAACATCGGCTACGCGCT 1351
QY 344 pIleAlaIlePheGlnValIleThrLeuGluGlyTyrValAspIleMetTyrPheValMe 364
DB 1352 GATTGCCATCTTCCAGGTGATCACGCTGGAAGCTGGGTGGACATCATGTACTACTGTCAT 1411
QY 364 tAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleValGlySerPh 384
DB 1412 GACGCGCCCATCTTCTACACTTCTATTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1471
QY 384 ePheMetIleAsnLeuCysLeuValIleAlaThrGlnPheSerGluThrLysGlnAr 404
DB 1472 CTTTCATGATCAACCTGTGCTGCTGATTCGACGAGCTTCTCGGAGACGAGACGCG 1531
QY 404 gGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAlaSerThrLeuAl 424
DB 1532 GAGAGTCTAGTGTGCTGCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1591
QY 424 aSerPheSerGluProGlySerCysTyrGluGluLeuLeuTyrLeuValTyrIleLe 444
DB 1592 CAGCTCTTCGAGCGCTTGGCAGCTGTCTACGAAAGCTGTGAAAGTACGTGGGCCACATAT 1651
QY 444 uArgLysAlaAlaArgArgLeuAlaGlnValSerArgAlaAlaGlyValArgValGlyLe 464
DB 1652 CCGCAGGTCTACGCGGCGGCGGCTTGGCGCTCTACGCGCGCTGGCAGCGCTGGCGCAA 1711
QY 464 uLeuSerSerProAlaProLeuGlyGlnGluThrGlnProSerSerSerCysSerAr 484
DB 1712 GAAGGTGACCCAGTCTGTGCAAGGCCAG-----GPTCCCGGCGGCGCGCGCGCGCG 1765
QY 484 gSerHisArgArg---LeuSerValHisLeuVal---HisHisHisHisHisHis 502
DB 1766 GCGAGGCGGCGACACGCTTGGTGGCACCTGCTGTACCAACCATCACCACCATCACCACCA 1825
QY 502 sHisHisTyrHisLeuGlyAsnGlyThrLeuA-gAlaProArgAlaSerProGluIleGl 522
DB 1826 CCACCACTACCATTTGACCATGCGAGCCCGCGGCGGCGGCGGCGGCGGCGGCGGCGCT 1885
QY 522 nAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProProSerThrProAlaLe 542
DB 1886 CGAC-----ACCAGGCTGGTCCGAGCTGGCGGCGGCGGCGGCGGCGGCGGCGGCT 1930
QY 542 uSerGlyAlaProProGlyGlyAlaGluSerValHisSerPheTyrHisAlaAspCysHi 562
DB 1931 CCCAGGCGGCGGACCCCGCGAGCGAGAGTCTGTGCACAGCATCTTACCATCCGACTGCCA 1990
QY 562 sLeuGlu-----ProValArgCysGlnAlaProProProArgSerProSerGluAlaSe 580
DB 1991 CATAGAGGCGGCGGAGGAGGCGGCGGCTGGCATGCGCGGCGGCGGCGGCGGCGGCGG 2050
QY 580 rGlyArg---ThrValGlySerGlyLysVal---TyrProThrVal----- 593
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2051 CCTCAGGCTGGCCACAGGGCTGGGCACCATGAACTACCCACGATCCTGCGCTCAGGGGT 2110
Qy
594 -----HisThrSerPro-----ProPr 599
2111 GGGCAGCGGCAAGAGCAGCAGCAGCGCCCGGCAAGGGGAAGTGGCGCGGTGACCGCC 2170
Db
599 oGluThrLeuLysGluLysAlaLeuValGluValAlaAlaSerSerGlyProProThrLe 619
Qy
2171 AGGCACC-----GGGGGGCAGCGCCGTTGAGCTT 2200
Db
619 uThrSerLeuAsnIleProProGlyProTySerSerMetHisLysLeuLeuGluThrGl 639
Qy
2201 GAACAGC-----CTGTATCCCTACGAGAAGATCCCGCATGTGGTGGCGGAGCA 2248
Db
639 nSerThrGlyAlaCysGlnSer-----SerCysLysIleSerSe 652
Qy
2249 TGGATGGCGCAGCGCCCTGGCCATCTGTGGGGCTCAGTGTGCCCTGCCCTGCCGAC 2308
Db
652 rProCysLeuLysAlaAspSerGlyAlaCysGlyProAspSerCysProTyCysAlaAr 672
Qy
2309 CCCC-----CCAGCGGCACACTGACCTGTGAGCTGAAGAGCTGCCCGTACTGCACCCG 2362
Db
672 gAla---GlyAlaGlyGluValGluLeuAlaAspArgGluMetProAspSerAspSerGl 691
Qy
2363 TGGCTGGAGGACCGGAGGGGTGAGCTCAGCGGCTCGGAAGTGGAGACTCAGATGGCCG 2422
Db
691 uAlaValTyGluPheThrGlnAspAlaGlnHisSerAspLeuArgAspPro----- 708
Qy
2423 TGGCGTCTATGAATTCACGAGGAGCGTCCGGCAGCGTGACCGCTGGGACCCCGCAGCC 2482
Db
709 -----HisSerArgArgGlnArgSe 715
Qy
2483 ACCCGTGGCAGGACACACAGCGCCAGGCGCCAGCGCGCGGCGGACAGCA 2542
Db
715 rLeuGlyProAspAlaGluProSerSerValLeuAlaPheTrpArgLeuLysCysAspTh 735
Qy
2543 GAGGGCAGCCCGGCGGAGCGCAGCTGATGGCGCGCTCTGGGTACCTTCACCGGCA 2602
Db
735 rPheArgLysIleValAspSerLysTyPheGlyArgGlyIleMetIleAlaLeuVa 755
Qy
2603 GCTCGCGCGCATCTGGGACAGCAAGTACTTCAGCGCTGGCATCATGATGGCCATCTTGT 2662
Db
755 lAsnThrLeuSerMetGlyIleGluTyHisGluGlnProGluGluLeuThrAsnAlaLe 775
Qy
2663 CAACACGCTGAGCATGGCGTGGAGTACCATGAGCAGCGCGGAGGAGCTGATAAGTCT 2722
Db
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795 uValTyGlyProPheGlyTyrlLysAsnProTyAsnIlePheAspGlyValIleVa 815
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2843 GGTATCAGCGCTCTGGGAGATCGGGGCGCAGCGGCGGTGGCTGTGTGTGTGGCGAC 2902
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2903 CTTCGGGCTGTGGTGTGTGAAGCTGGTGGCTTCTTCGACCGCTTCGCGCGCCAGCT 2962
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914 lThrValPheGlnIleLeuThrGlnGluAspTrpAsnLysValLeuTyAsnGlyMetAl 934
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974 sArgGluAspAlaSerGlyGlnLeuSerCysIleGlnLeuProValAspSerGlnGlyGl 994
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3312 -----GG 3313
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994 YAspAlaAsnLysSerGluSerGluProAspPhePheSerProSerLeuAspGlyAsp-- 1013
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1014 -----GlyAspArgLysLysCysLeuAlaLeuValSerLe 1025
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1025 uGlyGluHisProGluLeuArgLysSerLeuLeuProProLeuIleIleHisThrAlaAl 1045
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1212 uArgProAspAspProProLeuAspGlyAspAlaAspGluGlyAsnLeuSerLy 1232
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Db
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Qy	1252	pSerTrpSerAlaTrpIlePheProGlnSerArgPheArgLeuLeuCysHisArgIle	1272	Db	5138	CGTATCACCATGTCCTGAGGACCTATACCAACCAAGTCGTGAGGAGCCCTCAA	5197
Db	4058	GGCTGGGCGCTTACTCTCTCCACAGAACCGGTTCCGGCTCTCTCCGACAGAGGT	4117	Qy	1626	silCysAsnTrpIlePheThrValIlePheValLeuLeuGluSerValPheLysLeuValAl	1646
Qy	1272	eileThrHisLysMetPheAspHisValValLeuValIlePheLeuAsnCysIleTh	1292	Db	5198	GTACTGCAACTACGCTCTTCACCATCGGTGTTGCTTCGAGGCTGCACCTGAAGCTGGTAGC	5257
Db	4118	CATCACACACAGATGTTGATCAGCTGGTCTCGTCTTCATCTTCTCAACTGCGCTAC	4177	Qy	1646	apheGlyPheArgPhePheGlnAspArgTrpAsnGlnLeuAspLeuAlaIleValle	1666
Qy	1292	rileAlaMetGluArgProLysIleAspProHisSerAlaGluArgIlePheLeuThrLe	1312	Db	5258	ATTGGGTTCCGTCGGTCTTCAAGGACAGGTGGAACAGCTGCACCTGGCCATCTGCTGT	5317
Db	4178	CATCGCCCTGGAGAGGCTGACATTGACCCCGGACAGCACCAGGCGGTCTCTCCAGCCT	4237	Qy	1666	uLeuSerIleMetGlyIleThrLeuGluGluIleGluValAsnAlaSerLeuProIleAs	1686
Qy	1312	userAsnTrpIlePheThrAlaValPheLeuAlaGluMetThrValLysValValAlaLe	1332	Db	5318	GCTGTCACTCATGGGCATCGCTGAGGAGATAGATGAGCGCCCGCTGCCATCAA	5377
Db	4238	CTCCAAATTACATCTTCAGGCGCATCTTCGTGGCGAGATGATGTTGAAGGTGTGGCCCT	4297	Qy	1686	nProThrIleIleArgIleMetArgValLeuArgIleAlaArgValLeuLysLeuLeuLy	1706
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Qy	1392	sileLeuGlyMetLeuArgValLeuArgLeuLeuArgThrLeuArgProLeuArgValIl	1392	Db	5498	GAACCTGGGCGCTCTTTTCATGCTCTCTTTTATCTATCTGCTGGCTGGGAGTGAGCT	5557
Db	4418	GATCCTGGGTGTTCTCGCGCTGCTGCTGCTGCGGACCTGCGGCTCTTAAGGTTCAT	4477	Qy	1746	uPheGlyAspLeuGluCysAspGluThrHisProCysGluGlyLeuGlyArgHisAlaTh	1766
Qy	1392	eSerArgAlaGlnGlyLeuLysLeuValValGluThrLeuMetSerSerLeuLysProIl	1412	Db	5558	GTTTCGGGAGCTGGAGTGCAGTGAAGACAAACCCCTGCGAGGCGCTGAGCAGCGCAC	5617
Db	4478	CAGCGCGGCGCGCGCTCAAGCTGGTGGTGAGAGCGTGATATCTGCTCGCTCAGGCGCAT	4537	Qy	1786	rPheArgAsnPheGlyMetAlaPheIleuThrLeuPheArgValSerThrGlyVAspAsnTr	1786
Qy	1412	eGlyAsnIleValValIleCysCysAlaPhePheIleIlePheGlyIleLeuGlyValGl	1432	Db	5618	CTTCAGCAACTTCGGGCATGGCCCTTCTCAGCTGTTCGCGTGTCACGGGGGACCACTG	5677
Db	4538	TGGGAACATCGTCTCATCTGCTGGCGCTTCTTCATCATTTTGGCATCTTGGGTGTGCA	4597	Qy	1803	phangIleMetLysAspThrLeuArgAspCys-----AspGlnGluSerThrCy	1803
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Db	4598	GCTCTTCAAGGGAAGTCTTACTACTGCGAGGCGCCGACACACAGCAATCTCCACCAA	4657	Qy	1803	stYrAsnThrValIleSerProIleTyPheValSerPheValLeuThrAlaGlnPheVa	1823
Qy	1452	sSerAspCysAlaGluAlaSerTyArgTrpValArgHisLysTyAsnPheAspAsnLe	1472	Db	5738	CTACTGCGCGCCCTCGCCCGCTTCTTCTGACCTTCGTGCTGGTGGTGGCCAGTTCGT	5797
Db	4658	GGCACAGTCCGGCGCGCCCACTACCGCTGGGTGGGAGCAAGTACAACTTCGACAACT	4717	Qy	1823	lleuValAsnValIleAlaValLeuMetLysHisLeuGluGluSerAsnLysGluAl	1843
Qy	1472	uGlyGlnAlaLeuMetSerLeuPheValLeuAlaSerLysAspGlyTrpValAspIleMe	1492	Db	5798	GCTGGTGAACGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT	5857
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Qy	1552	aArgArgGluGluLysArgLeuArgLeuGluLysLysArgArg-----	1568	Db	5946	-----CCCTGCCCGCAGAGAGTCCGGGCGC	5971
Db	4958	GCGCGCGGAGAGGAGGAGGCGGCTGCGCGCGCTAGAGAGGAGGCGGAGGAGCTTCC	5017	Qy	1936	-----ProAspLeuLeuThrValArgLysSerGlyValSerArgThrHisSerLe	1936
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Qy 2025 eArgThrAspSerLeuaspValGlnGlyLeuGlySerArgGlnAspLeuLeu-----Al 2043
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RESULT 6

US-09-404-650-1
; Sequence 1, Application US/09404650
; Patent NO. 6309858

GENERAL INFORMATION:

; APPLICANT: Dietrich, Paul S.
; APPLICANT: McGovern, Joseph G.
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
; FILE REFERENCE: R0043B-REG sequence listing
; CURRENT APPLICATION NUMBER: US/09/404,650
; CURRENT FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1

; LENGTH: 6816

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (192)..(6716)

US-09-404-650-1

Alignment Scores:

Pred. No.:	0	Length:	6816
Score:	5492.50	Matches:	1236
Percent Similarity:	60.30%	Conservative:	213
Best Local Similarity:	51.44%	Mismatches:	506
Query Match:	46.14%	Indels:	449
DB:	3	Gaps:	55

US-09-611-257A-37 (1-2266) x US-09-404-650-1 (1-6816)

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Qy 87 SerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMetPheArgProCysGluAsp 106
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Db 3548 TCCCGAGAACAGGTTCCGGGTCTGTGTGCAGACCATATTATGCCCAACAACTTCTGCACT 3607
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Db 3728 CTTCTGGCGGAGATGACATTTGAAGTAGTCTCGCTGGGCTGTACTTCCGCGAGCAGGC 3787
Qy 1340 aTyrLeuArgSerSerTrpAsnValLeuAspGlyLeuLeuValLeuIleSerValIleAs 1360
Db 3788 GTACTAGCGAGCAGCTGGAACGCTGCTGGATGGCTTCTTGTCTTGTGCTGCATCATCGA 3847
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Qy 1400 uValValGluThrLeuMetSerSerLeuLysProIleGlyAsnIleValIleCysCy 1420
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Qy 1540 eHisLysCysArgGlnHisGlnGluGluAlaArgArgGluGluLysArgLe 1560
Db 4388 CCACAGTGGCGGAGCAGCAGGAGGCTGAAGAGCAGCGCGCGCTGAGGAGAGCGGCT 4447
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Qy 1600 rGlyValIleGlyLeuAsnValValThrMetAlaMetGluHisTyrGlnGlnProGlnIle 1620
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QY	1620	eLeuAspGluAlaIleuLeuValPheThrValIlePheValIleuGlu	1640	QY	1913	HisProThrGluLeuProGlyProAspLeuLeuThrValArgLysSerGly	1929
Db	4628	CCTGGAGACAGCCCTCAAGTACTGCACTATATGTTTACCACTGTCTTGTGTGGAGGC	4687	Db	5702	GGACAGCAAGGTGAGCTGGACCCACTGAGCCCATCGTGTGGAGACCTGGCGCAATG	5761
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Db	4688	TGTCTGAGCTGGTGGCAATTTGTCTGAGCGCTTCTTCAAGAGCCGATGGAACACGCT	4747	Db	5762	CTTCTCCCTTGTCTTACCGCGCTCTCGCGGATCCAGAGAACTTCTGTGTGAGAT	5821
QY	1660	uAspLeuAlaIleValLeuLeuSerIleMetGlyIleThrLeuGluIleGluValAs	1680	QY	1945	sGlySerThrAlaGluGlyProLeuGlyHisArgGlyTrpGlyLeuProLysAlaGlnSe	1965
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Db	4808	TGGCGCCCTGCCATCATCCACCATCATCCGATCATGAGGTTCTGGCATTCGCCG	4867	Db	5870	CAGTCAAGCACCCCAAGTCTCTCCCGGATGCTCCAGCCCTCTCTGCCCTGCC	5929
QY	1700	gValLeuLysLeuLeuLysMetAlaValGlyMetArgAlaIleuAspThrValMetG	1720	QY	1985	oLysAspAlaProHis---LeuLeuGlnProHisSerAlaProTh	1999
Db	4868	AGTCTGAAGCTGTGAAGATGGCCACAGGAATCGCGGCTGTGACACGGTGTGCA	4927	Db	5930	AGCCGAGTTCTTCCACCTCGAGTGTCTGCCAGCCAGAAAGGCCAGAAAGGSCACTGG	5989
QY	1720	nAlaLeuProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPheIlePheAl	1740	QY	1999	rTrpGlyThrIleProLysLeuProProGly---ArgSerProLe	2014
Db	4928	AGCTTTGCCAGGGGGCACTGGGCTCTCTTCTCATGCTCTTCTTCTCATATGC	4987	Db	5990	CACTGGAACCTTCCCAAGATTGGCTGAGGCTCTCTGGGCATCTCTGCGGTCAACAAG	6049
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QY	1760	yLeuGlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgVa	1780	QY	2034	yLeuGlySerArgGluAspLeuLeuAlaGluValSerGlyProSerProProLeuAlaAr	2054
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Db	5288	CGACAGCAACAGAGAGCGCAGGAGGACCGAGATGGATGGATGCGAGCTCGAGTGGAT	5347	QY	6255	---CGCGCGCGCGCGCTCTTCAG	6274
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RESULT 7
US-09-935-541-1
; Sequence 1, Application US/09935541
; Patent No. 6589787
; GENERAL INFORMATION:
; APPLICANT: Dietrich, Paul S.
; APPLICANT: McGovern, Joseph G.
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
; TITLE OF INVENTION: AND USES
; FILE REFERENCE: R0043B-REG sequence listing
; CURRENT APPLICATION NUMBER: US/09/935,541
; PRIORITY FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: 09/404,650
; PRIOR FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 1
; LENGTH: 6816
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (192)..(6716)
US-09-935-541-1

Alignment Scores:
Pred. No.: 0 Length: 6816
Score: 5492.50 Matches: 1236
Percent Similarity: 60.30% Conservative: 213
Best Local Similarity: 51.44% Mismatches: 506
Query Match: 46.14% Indels: 449
DB: 4 Gaps: 55

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Qy 67 AspSerArgProArgSerTyrCysLeuArgThrValCysAsnProTyrPheGluArgile 86
Db 384 ACCACGACCCCGGAACTGGTGATCAAGATGGTGTGCAACCCCGTGGTGGTGAATGTGC 443
Qy 87 SerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMetPheArgProCysGluAsp 106
Db 444 AGCATGCTGGTGATCTCTGCTGAACCTGGTGATGACACTTGGCATGTACACCGCTGGAGCAG 503
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3728 CTTCTGCGCGAGATGACATTAAGAGTAGTCTCGCTGGGCCCTGTACTTCGCGAGCAGC 3787
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3788 GTACTACGACGAGCTGGAACGTGTGATGGCTTTCTTCTCTGCTGCTCATCATCGA 3847
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3908 CGCGCTCTCGCACCTACGCCCTCGGTGTGCATCAGCCGGCGCGGCGCTGAAGCT 3967
Db
1400 uValValGluThrLeuMetSerLeuLysPheProIleGlyAsnIleValValIleCysCy 1420
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3968 GGTGTGTGAGACATCTCTCTCCCTCAAGCCCATCGCAACATCGTGTCTCATCTGCTG 4027
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1420 sAlaPhePheIleIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPhePheVa 1440
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4028 TGCCTCTTTCATCATCTTTGGATCTCTGGAGTGGAGCTCTTCAAGGCAAGTTCTACCA 4087
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Db
1892 -----HisProAlaAlaHisAla----- 1897
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 1901 r-----HisPheSerLeuGluHisProThrMetGlnPro----- 1912
 5642 CATCTGCTGGTGGTGGAGTGGTGGAGGAGGCTTCTCCCTGAATCAGACAGAGTCTCGTC 5701
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 5822 GGAGGAGATCCATTCACCTCTG-----CGGTCTCTGG-----CTGAACATGACAG 5869
 1965 rGlySerValLeuSerValHisSerGlnProAlaAspThrSerTyrIleLeuGlnLeuPr 1985
 5870 CAGTCAAGACACCCCAAGTCTCTCCCGATGCTCCAGGCTCTCTCTGCGCATGCC 5929
 1985 oLysAspAlaProHis-----LeuLeuGlnProHisSerAlaProTh 1999
 5930 AGCCGAGTCTCTCCACCTGTCAGTGTCTGCCAGCAGAAAGCCAGAAAGGCACTGG 5989
 1999 rTrpGlyThrIleProLysLeuProProGly-----ArgSerProLe 2014
 5990 CACTGGAACCTCTCCCAAGATTCGCTGCGGCTCTCTGCGATCTCTGCGTCAACCAAG 6049
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 6255 -----CGCGCGCGCGCTCTTCAG 6274
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 RESULT 8
 US-09-404-650-3
 ; Sequence 3, Application US/09404650
 ; Patent No. 6309858
 ; GENERAL INFORMATION:
 ; APPLICANT: Dietrich, Paul S.
 ; APPLICANT: McGiven, Joseph G.
 ; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
 ; TITLE OF INVENTION: AND USES
 ; FILE REFERENCE: R0043B-REG sequence listing
 ; CURRENT APPLICATION NUMBER: US/09/404,650
 ; CURRENT FILING DATE: 1999-09-23
 ; NUMBER OF SEQ ID NOS: 12
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 3
 ; LENGTH: 6855
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (192)..(6755)
 ; US-09-404-650-3
 Alignment Scores:
 Pred. No.: 0 Length: 6855
 Score: 5484.00 Matches: 1237
 Percent Similarity: 59.93% Conservative: 211
 Best Local Similarity: 51.20% Mismatches: 507
 Query Match: 46.07% Indels: 462
 Gaps: 56
 DB:
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 Db 324 GCTGATCTCTATGTCCTCCACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 383
 QY 67 AspSerArgProArgSerTrpCysLeuArgThrValCysAsnProTrpPheGluArgIle 86
 Db 384 ACCACCG 443
 QY 87 SerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMetPheArgProCysGluAsp 106
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 QY 127 PhePheAlaValGluMetValVallyMetValAlaLeuGlyIlePheGlyLysCys 146
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Qy 499 HisHisHisHisHisHisTyrHisLeuGlyAsnGlyThrLeuArgAlaProArgAlaSer 518

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Qy 1882 -----SerPro----- 1893

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Qy 1884 -----AspSerProLysProGlyAlaLeuHis----- 1892
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Qy 1893 -----ProAlaAla----- 1895
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Db 5822 GGCGCTCTCGCGGATCCAGAGAACTTCTGTGTGAGATGGAGGATCCCATTTCAACCC 5881
Qy 1952 oLeuGlyHisArgGlyTrpGlyLeuProLysAlaGlnSerGlySerValLeuSerValHi 1972
Db 5882 TGTG-----CGTCTCTGG-----CTGAAACATGACAGCAGTCAAGCACCACCAAGTCC 5929
Qy 1972 sSerGlnProAlaAspThrSerTyrIleLeuGlnLeuProLysAspAlaProHis----- 1990
Db 5930 CTTCTCCCGGATGCCCTCCAGCCCTCTCTGCCCATGCCAGCGAGTTCTTCCACCTGCG 5989
Qy 1991 -----LeuLeuGlnProHisSerAlaProThrTrpGlyThrIleProLysLe 2006
Db 5990 AGTGTCTGCCAGCAGCAAGAGCCAGAAAGGCGACATGGCACTGGACCTGGAACCTCCCAAGAT 6049
Qy 2006 uProProProGly-----ArgSerProLeuAlaGlnArgProLeuArgAr 2021
Db 6050 TGGCGCTCAGGCTCTCTGGGCGCATCTCTGCGGTCAACCAAGGCTCAACTGTACCTCTCCG 6109
Qy 2021 gGlnAlaAlaIleArgThrAspSerLeuAspValGlnGlyLeuGlySerArgGluAspLe 2041
Db 6110 GCAGGCCACCGCGGAGCGACAGCTGCTGGAC----- 6140
Qy 2041 uLeuAlaGluValSerGlyProSerProProLeuAlaArgAlaTyrSerPheTrpGlyGl 2061
Db 6141 -----GCCAGCCCGCAGCAGCTCCGCGGCGAGCTGCAGACCGCTCGAGGA 6187
Qy 2061 nSerSerThrGlnAlaGlnGlnHisSerArgSerHisSerLysIleSerLysHisMetTh 2081
Db 6188 CAGCTCAGCTCAGCGACAGACCCCGCGCTGCC-----CTGGG 6226
Qy 2081 rProProAlaProCysProGlyProGluProAsnTrpGlyLysGlyProProGluThrAr 2101
Db 6227 GCGCGCGCGCTCTCTCAGACCCCGCGCGCTGTCC-----CCGCGCGCTCG 6277
Qy 2101 gSerSerLeuGluLeuAspThrGluLeuSerTrpIleSerGlyAspLeuLeuProProGl 2121
Db 6278 CCGCGCGCTGAGCTG----- 6293
Qy 2121 yGlyGlnGluProProSerProArgAspLeuLysCysTyrSerValGluAlaGl 2141
Db 6294 -----CGCGCGCGGCTCTTTCAGCTGCGGGGCTGCGCGGCG-- 6332
Qy 2141 nSerCysGlnArgArgProThrSerTrpLeuAspGluGlnArgArgHisSerIleAlaVa 2161
Db 6333 -----CATCAGCGCAGCCACAGCAGCGGGG 6358
Qy 2161 lSerCysLeuAspSerGlySerGlnProHisLeuGlyThrAspProSerAsn----- 2178
Db 6359 CTCC---ACCAGCCCGGCTGCACCCACCGACTCCATGACCTCCATGACCTCGGAGGAGGG 6415

504 ATGGACTGCCTGTC CCGAGCCGCTC GCAAGATCTCTG CAGGTCTTTGA AGTACCTCATCTTTATC T 563
::: ||| ||| :::::::::::::::::::: |
127 PhePheAlaValGluMetValValLysMetValAlaLeuLeuGlyIlePheGlyLysLysCys 146
::: ||| :::::::::::::::::::: |
564 TTCTTTGGCATTGGAGATGGTGCTCAAGAATGGTGGCCCTGGGGAATTTTGGCAAGAAAGTGC 623
::: ||| :::::::::::::::::::: |
147 TyrLeuGlyAspThrTrpAsnArgLeuAspPhePheIleValIleAlaGlyMetLeuGlu 166
::: ||| :::::::::::::::::::: |
624 TACCCTCGGGACACATGGAACCCGCTGGATTTCTTCATCGTCATGGCAGGATGGTCGAG 683
::: ||| :::::::::::::::::::: |
167 TyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArgThrValArgValLeuArg 186
::: ||| :::::::::::::::::::: |
684 TACTCCTGGACCTTTCAGAACATCAAACCTGTGAGCCATCCGCCACCGTGGCGCTCCTGAGG 743
::: ||| :::::::::::::::::::: |
187 ProLeuArgAlaIleAsnArgValProSerMetArgIleLeuValThrLeuLeuLeuAsp 206
::: ||| :::::::::::::::::::: |
744 CCCTCTAAGAGCCATCAACCGGTGCCAGTA TGCGGATCTGCTGGAACTGCTGTAACCTGCTCCTGGAC 803
::: ||| :::::::::::::::::::: |
207 ThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePheValPhePheIlePheGly 226
::: ||| :::::::::::::::::::: |
804 ACACCTGCCATGCTGGGAAATGCTCTGCTCTGCTCTTTGTTCTTTTCACTTTTGGC 863
::: ||| :::::::::::::::::::: |
227 IleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArgCysPheLeuProGluAsn 246
::: ||| :::::::::::::::::::: |
864 ATCATAGGTGTGAGCTCTGGCGGGGCTGCTGCGTAA CGCTGTGCTTCTTGGAGGAGAAC 923
::: ||| :::::::::::::::::::: |
247 PheSerLeuProLeuSerValAspLeuGluArgTyrTyrGlnThrGluAsnGluAspGlu 266
::: ||| :::::::::::::::::::: |
924 TTCACATACAAGGGATGTGGCCTTGCCCCCATATTACACCGCGAGGAGATGATGAG 983
::: ||| :::::::::::::::::::: |
267 SerProPheIleCysSerGlnProArgGluAsnGlyMetArgSerCysArgSerValPro 286
::: ||| :::::::::::::::::::: |
984 ATGCCCTTCATCTGCTCCCTGFCGGGGCACAAATGGATAATGGGCTGCCATGAGATCCC 1043
::: ||| :::::::::::::::::::: |
287 ThrLeuArgGlyAspGlyGlyGlyGlyProProCysGlyLeu----- 300
::: ||| :::::::::::::::::::: |
1044 CCGTCTAAGAGCAG-----GGCCGTGAGTGTGCTGCTGCCAAGGACGACGCTCTPAC 1094
::: ||| :::::::::::::::::::: |
301 AspTyrGluAlaTyrAsnSerSerSerAsnThrThr-----CysValAsnTrpAsnGln 318
::: ||| :::::::::::::::::::: |
1095 GACTTTGGGGCGGGGCGCCAGGACCTCAATCCGAGCGGCTCTGTGTCACTGGAAACCGT 1154
::: ||| :::::::::::::::::::: |
319 TyrTyrThrAsnCysSerAlaGlyGluHisAsnProPheLysGlyAlaIleAsnPheAsp 338
::: ||| :::::::::::::::::::: |
1155 TACTACAAATGTGTCCGCGCGGGCGGCCAACCCCAAGGGTGCCATCAACTTGAC 1214
::: ||| :::::::::::::::::::: |
339 AsnIleGlyTyrAlaTrpIleAlaIlePheGlnValIleThrLeuGluGlyTrpValAsp 358
::: ||| :::::::::::::::::::: |
1215 AACATCGGTTATGTTGGATTGTCATCTTCCAGGTGATCACTCTGGAAGGCTGGGTGGAG 1274
::: ||| :::::::::::::::::::: |
359 IleMetTyrPheValMetAspAlaHiserPheTyrAsnPheIleTyrPheIleLeuLeu 378
::: ||| :::::::::::::::::::: |
1275 ATCATGTACTACGTATGGATGCTCACTCCTTTCACACTTCATCTACTTCACTCTGCTT 1334
::: ||| :::::::::::::::::::: |
379 IleIleValGlySerPhePheMetIleAsnLeuCysLeuValIleAlaThrGlnPhe 398
::: ||| :::::::::::::::::::: |
1335 ATCATAGTGGGCTCTCTTCTTCATGATCAACCTGTGCTCGTTCATAGGAGCCCAAGTTC 1394
::: ||| :::::::::::::::::::: |
399 SerGluThrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSer 418
::: ||| :::::::::::::::::::: |
1395 TCGGAGACCAAGCAACGGGAGCACCGGCTGTATGCTGGAGAGCGGCGAGCGCTACTGTCC 1454
::: ||| :::::::::::::::::::: |
419 AsnAlaSerThrLeuAlaSerPheSerGluProGlySerCysTyrGluLeuLeuLys 438
::: ||| :::::::::::::::::::: |
1455 ---TCCAGCACGGTGGCCAGCTACGCCGCGCTGGCGACTGCTACGAGGAGATCTCCGAC 1511
::: ||| :::::::::::::::::::: |
439 TyrLeuValTyrIleLeuArgLysAlaAlaArgArgLeuAlaGlnValSerArgAlaAla 458
::: ||| :::::::::::::::::::: |
1512 TATGTCTGCCACATCTCTCGCAAGGCCAAGCGC-----CGGCCCTG 1553
::: ||| :::::::::::::::::::: |
459 GlyValArgValGlyLeuLeuSerSerProAlaProLeuGlyGlyGlnThrGlnPro 478
::: ||| :::::::::::::::::::: |

[illegible]

[illegible]

QY	825	GlnGlnGlyGlyGlyLeuSerValLeuArgThrPheArgLeuMetArgValLeuLeuLysLeu	844
DB	2250	CAGCGCAGCGTGGGCTGTGCGTGTGCGGACCTTCGGCTGCTCGCGCGTGTGGAACATG	2309
QY	845	ValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetLysThrMetAspAsn	864
DB	2310	GTGGGCTTCATGCTGCGCTGCGGCGCCAGCTCGTGGTGCTCATGAAGACCATGGACAC	2369
QY	865	ValAlaThrPheCysMetLeuLeuMetLeuPheIlePheSerIleLeuGlyMet	884
DB	2370	GTGGCCACCTTCGCATGCTGCTCATGCTCTTCATCTTCAGCATCTCTTGGGATG	2429
QY	885	HisLeuPheGlyCysValysPheAlaSerGluArgAsp---	903
DB	2430	CATATTTTGGCTGCAGAGTTTTCCTCCGACCGACACTGGAGACAGGTGCCCGACAGG	2489
QY	904	LysAsnPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIleLeuThrGlnGlu	923
DB	2490	AAGAACTTCGACTCCCTGCTGTGGCGCATCGTCACTGTGTTCAGATCTCACCCAGGAG	2549
QY	924	AspTrpAsnLysValLeuTyrAsnGlyMetAlaSerThrSerSerTrpAlaAlaLeuTyr	943
DB	2550	GACTGGAACTCGTCTCTCAATAGCATGGCCCTCCACTTCTCCCTGGGCGCTCCCTCTAC	2609
QY	944	PheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuLeuValAlaIleLeu	963
DB	2610	TTTGTGCGCCCTCATGACTTCGCGCACTATGTGCTCTTCAACCTGTGTGGGCCATCTCTG	2669
QY	964	ValGluGlyPheGlnAlaGluIleSerLysArgGluAspAlaSerGlyGlnLeuSer	983
DB	2670	GTGAGGGCTTCCAGGCGGAG-----	2690
QY	984	CysIleGlnLeuProValAspSerGlnGlyValAspAlaAsnLysSerGluSerGluPro	1003
DB	2691	-----GGTGACGCCAATCGCTCTCTACTCGGACGAG	2720
QY	1004	AspPhePheSerProSer-----	1013
DB	2721	GACCAGAGCTCATCCAACATAGAAAGAGTTTGATAAGCTCCAGGAGGCGCTGGACGACG	2780
QY	1014	GlyAspArgLysCysLeuAlaLeuValSerLeuGlyHisProGluLeuArgLys	1033
DB	2781	GGAGATCCCAAGCTCTGCCCAATCCCATGACCCCAATGGGCGAC-----	2825
QY	1034	SerLeuLeuProProLeuIleIleHisThrAlaAlaThrProMetSerLeuProLysSer	1053
DB	2826	-----CTGACACCC-----AGTCTCCCACTGGGT	2849
QY	1054	ThrSerThrGlyLeuGlyGluAlaLeuGlyProAlaSerArgArgThr-----	1069
DB	2850	GGGCACCTAGGTCTGTGTGGGGCTGGGGACCTTGCCCGGACTCTCACTGCAGCCGGAC	2909
QY	1070	-----SerSerSerGlySerAlaGluProGlyAlaAla	1080
DB	2910	CCCATGCTGTGGCTGGGCTCCGGAAGACAGATGTCTGTCTATGGAGGATGAGC	2969
QY	1081	HisGluMetLysSerProProSerAlaArgSerSerProHisSerProTrpSerAlaAla	1100
DB	2970	TATGACACCGCTCCCTGTCCAGCTCCCGGAGCTCTACTACGGGCGCATGGGCGCGCAG	3029
QY	1101	SerSerTrpThrSerArgArgSerArgAsnSerLeuGlyArgAlaProSerLeuLys	1120
DB	3030	CGCGCTTGGGCCAGCGCTCGCTCCAGTGGAAC-----AGCTTCAAG	3071
QY	1121	ArgArgSerProSerGlyGluArgArgSerLeuSerGlyGlu---	1139
DB	3072	CACAAGCCCGTTCGGCGAGCATGAGTCTCTCTCTCGGAGCGCGCGCGCGCGCC	3131
QY	1140	GlnAspGluGluSerSerGluGlu-----	1157
DB	3132	CGGCTCTGCGAGTGTTCGGCGACAGAGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCC	3191

QY 1158 His-----ArgHisArgGly 1162
 Db 3192 CACGCCACCATTCATACGGGCCCCATCTGGCGCACCGCCACCGCCACCGCCG 3251
 QY 1163 SerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeuGlnValProGly 1182
 Db 3252 ACGTGTCCTCGACAAACAGGACTCGGTGGACTGGCGGAGTGGTCCCGCGGTGGGC 3311
 QY 1183 LeuHisArgThrAlaSerGlyArg-----GlySerAlaSerGluHisGlnAspCysAsn 1200
 Db 3312 GCCACCCCGGGCGCTGGAGGGCGGAGCGCCGCGCGCGGATGAGGACTGCAAT 3371
 QY 1201 GlyLysSerAlaSerGlyArgLeuAlaArgAlaLeuArgProAspAspProProLeu-As 1220
 Db 3372 GGCAGGAT-GCCAGCATCGC--CAAGAGCGTCTTCACCAAGATGGCGACCGCGGGA 3427
 QY 1220 pGlyAspAlaAspAspGluGlyAsnLeuSerLysGlyGluArgValAlaAlaTrpI 1240
 Db 3428 TCGCGGGAGGATGAGGAGGAATGCACTACACCTGTGCTTCGCGTCCGCAAGATGAT 3487
 QY 1240 eArgAlaArgLeuProAlaCysTyrLeuGluArgAspSerTrpSerAlaTyrIlePhePr 1260
 Db 3488 CGACGTCTATAAGCCGACTCGTGGAGGTCCGGAAGACTGGTCTGTCTACCTCTTCTC 3547
 QY 1260 oProGlnSerArgPheArgLeuLeuCysHisArgIleIleThrHisLysMetPheAspHi 1280
 Db 3548 TCCGAGAACAGGTTCGGGTCCTGTGTGACAGCATATTGCCCAAACTCTTCGACTA 3607
 QY 1280 sValValLeuValIlePheLeuAsnCysIleThrIleAlaMetGluArgProLysI 1300
 Db 3608 GGTGCTCTGGCTTCATCTTCTCACTGCATCACCCTGCGCGGCGGCTCAGAT 3667
 QY 1300 eAspProHisSerAlaGluArgIlePheLeuThrLeuSerAsnTyrIlePheThrAlaVa 1320
 Db 3668 CGAGCCGCGACACCGAACGATCTTCTCACCGTGTCCAACACTACATCTTCAGGCGAT 3727
 QY 1320 lPheLeuAlaGluMetThrValLysValAlaLeuGlyTrpCysPheGlyGluGlnAl 1340
 Db 3728 CTTCGTGGCGAGATGACATTGAAGTAGTCTCGTGGCGCTGTACTTCGGCGAGCGGC 3787
 QY 1340 aTyrLeuArgSerSerTrpAsnValLeuAspGlyLeuLeuValLeuIleSerValIleAs 1360
 Db 3788 GTACCTACGACGACGCTGCTGGATGGCTTCTTCTCTCTGCTGCATCATCGA 3847
 QY 1360 pIleLeuValSerMetValSerAspSerClyThrLysIleLeuGlyMetLeuArgValLe 1380
 Db 3848 CATCGTGTGTCCTCGGCTCAGCCGGGAGCCAGGATCTTGGGGGTCTTCCGAGCTT 3907
 QY 1380 uArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeuLysLe 1400
 Db 3908 GCGGCTCTGCGACCCCTACGCCCTCGGTGTGTCATCAGCGGGCGCGGCGCTGAAGCT 3967
 QY 1400 uValValGluThrLeuMetSerSerLeuLysProIleGlyAsnIleValIleCysCy 1420
 Db 3968 GGTGTGGAGACACTCATCTCTCCCTCAAGCCCATCGGCAACATCGTGTCTCATCTGTG 4027
 QY 1420 sAlaPhePheIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPhePheVa 1440
 Db 4028 TGCTCTTCTCATCATCTTGGGATCTCTGGAGTGGAGCTTCTCAAGGCGAGTCTTACCA 4087
 QY 1440 lCysGlnGlyGluAspThrArgAsnIleThrAsnLysSerAspCysAlaGluAlaSerTy 1460
 Db 4088 CTGTCTGGGCGTGGACACCGCAACATCACCAACCGCTCGGACTGTGATGGCGGCAACTA 4147
 QY 1460 rArgTrpValArgHisLysTyrAsnPheAspLeuGlyGlnAlaLeuMetSerLeuPh 1480
 Db 4148 CCGCTGGGTCCATCAAAATACAACTTCGACAACTTGGGCCAGGCTCTGATGCTCTTCT 4207
 QY 1480 eValLeuAlaSerLysAspGlyTrpValAspIleMetTyrAspGlyLeuAspAlaValGl 1500
 Db 4208 TGTCTTGGCATCAAGAGTGTGGGTGAACATCATGATCAATGGAGTGGATGCTGTTC 4267
 QY 1500 yValAspGlnGlnProIleMetAsnHisAsnProTrpMetLeuLeuTyrPheIleSerPh 1520

Db 4268 TGTGACGACGAGCTGTGACCAACCAACCCCTGGATGCTGTACTTTCATCTCTT 4327
 QY 1520 eLeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValValValGluAsnPh 1540
 Db 4328 CTTGCTCATCGTCAGCTCTTTTGTGCTCAACATGTTTGTGGGTGTGTTGGTGAACATT 4387
 QY 1540 eHisLysCysArgGlnHisGlnGluGluGluAlaArgArgGluGluLysArgLe 1560
 Db 4388 CCACAAAGTGGCGGACGACACGAGGCTGAAGAGCAGCGCGGCTGAGAGAGAGCGCT 4447
 QY 1560 uArgArgLeuGluLysLysArgLysAlaGlnCysLysProTyrTyrSerAspTyrSe 1580
 Db 4448 GCGGCGCTGGAGAAAGAGCGCGGAGCGCGCTGCTACTATATGCCACTATG 4507
 QY 1580 rArgPheArgLeuValHisHisLeuCysThrSerHisTyrLeuAspLeuPheIleTh 1600
 Db 4508 TCACACCCCGGCTGCTATCCACTCCATGTGTGACACGACCTACTCTGGACATCTTCATC 4567
 QY 1600 rGlyValIleGlyLeuAsnValValThrMetAlaMetGluHisTyrGlnGlnProGlnI 1620
 Db 4568 CTTTCATCTCTGCTCAAGCTGTTCACCATGTATGTTCACCACTGTCTTGTCTGGAGC 4627
 QY 1620 eLeuAspGluAlaLeuLysIleCysAsnTyrIlePheThrValIlePheValLeuLysE 1640
 Db 4628 CTTGAGAGCAGCGCTCAAGTACTGCAACTATATGTTCACCACTGTCTTGTCTGGAGC 4687
 QY 1640 rValPheLysLeuValAlaPheGlyPheArgArgPhePheGlnAspArgTrpAsnGlnLe 1660
 Db 4688 TGTGCTGAAGCTGTGGGCACTTGTCTGAGGCGCTTCTCAAGGACCGATGAACAGCT 4747
 QY 1660 uAspLeuAlaIleValLeuLeuSerIleMetGlyIleThrLeuGluGluIleGluValAs 1680
 Db 4748 GGACCTGGCCATTGTCTACTGTCTGTCATGAGGATGCGGCGCTGTCGAGACAGATCAA 4807
 QY 1680 nAlaSerLeuProIleAsnProThrIleArgIleMetArgValLeuArgIleAlaAr 1700
 Db 4808 TGGCGGCTTGGCCCATCAATCCCACTCATCGCATCATGAGGGTCTGCGCATTTGCCG 4867
 QY 1700 gValLeuLysLeuLeuLysMetAlaValGlyMetArgAlaLeuLeuAspThrValMetGl 1720
 Db 4868 AGTGCTGAAGCTGTGAAGATGCGCAACAGGATGCGGCGCTGTCGAGACAGCGTGA 4927
 QY 1720 nAlaLeuProGlnValGlyAsnLeuGlyLeuPheMetLeuLeuPhePheIlePheAl 1740
 Db 4928 AGCTTTCGCGGCTGGGCAACCTGCGGCTCTCTTCATGCTGCTCTTCTTCTATCTATGC 4987
 QY 1740 aAlaLeuGlyValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGluGl 1760
 Db 4988 TGCTCTCGGGGTGAGCTCTTTCGGAAGCTGGTCTGCAACGACGAGAACCCGTCGAGGG 5047
 QY 1760 yLeuGlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgVa 1780
 Db 5048 CATGAGCGCGCATGCCACCTTCGAGAACTTCGCGCATGGCTCTCTCCTCTTCTTCAGGT 5107
 QY 1780 lSerThrGlyAspAsnTrpAsnGlyIleMetLysAspThrLeuArgAspCys---AspGl 1799
 Db 5108 CTCCACGGGTGACAACTGGAAACGGGATCATGAAGACACGCTGCGGAGCTGCACCCACGA 5167
 QY 1799 nGluSerThrCysTyrAsnThrVal-----IleSerProIleTyrPheValSerPheVa 1817
 Db 5168 CGAGCGGAGCTGCTGAGCAGCTGTCAGTTTGTGTCGCGCTGTACTCTGCTGAGCTTCGT 5227
 QY 1817 lLeuThrAlaGlnPheValLeuValAsnValValIleAlaValLeuMetLysHisLeuGl 1837
 Db 5228 GCTCAGCGCGAGTTCGTGCTCATCAACGCTGGTGGTGTGCTGTCTATGAAGCACTTGA 5287
 QY 1837 uGluSerAsnLysGluAlaLysGluAlaGluLeuGluAlaGluLeuGluLeuGluMe 1857
 Db 5288 CGACGACAAAGAGGCGGACGAGGAGCGCGAGATGATGATGATGATGATGATGATGAT 5347
 QY 1857 t---LysThrLeuSerProGlnProHisSerProLeuGlySerProPheLeuTrpProGl 1876

Db 500 TTCAGTGTGTGAGCATGCTGGTTATTCTCTGAACTGTGTGACCTGGGCATGTACCAG 559
 QY 103 ProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPheAspAsp 122
 Db 560 CCATGTGATGACATGGAGTGCCTGTGGACCGTTCGAAGATCTCTGAGGTCTTCGATGAC 619
 QY 123 PheIlePheAlaPhePheAlaValGluMetValValValMetValAlaLeuGlyIlePhe 142
 Db 620 TTCATCTTCATCTCTCTTGGCATGGAGATGGTCTTAAGATGTGGCCCTGGGCATTTTT 679
 QY 143 GlyIleCysCysTyrLeuGlyAspThrTyrAsnArgLeuAspPhePheIleValIleAla 162
 Db 680 GGCAGAGAGTCTACCTCGGAGACACATGACCGCTGGATTCITCATTTGTCATGGCA 739
 QY 163 GlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArgThrVal 182
 Db 740 GGGATGGTGTGATCTCTCTGACCTACAGAACATCAACCTGTCCAGCCATCCGACCTGTG 799
 QY 183 ArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeuValThr 202
 Db 800 CGTGTCTGAGGCTCTCAAGAGCCATCAACCGTGTACCCAGCATCGGATCCTGGTGAAC 859
 QY 203 LeuLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPheValPhe 222
 Db 860 CTGCTGTCTGACACGCTGCCATGCTGGGAACTGCTCTCTGCTCTCTCTCTCTCTCTC 919
 QY 223 PheIlePheGlyIleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArgCysPhe 242
 Db 920 TTCATCTTCGGCATCATTTGGGTGTCAGCTCTGGGACGCTGTACCGAACCGCTGCTTC 979
 QY 243 LeuProGluLeuAsnPheSerLeuProLeuSerValAspLeuGluArgTyrTyrGlnThrGlu 262
 Db 980 CTGGAGAGAACTTCACCTATCAAGGGGATGTGGCCCTGCCCTTATTACCAACCCAGAG 1039
 QY 263 AsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArgSerCys 282
 Db 1040 GAGGATGACGAGATGCCCTTTATCTCTCTGCTGCTGAGTGGGACAAATGGCATCATGGGTGC 1099
 QY 283 ArgSerValProThrLeuArgGlyAspGlyGlyGlyProProCysGlyLeu----- 300
 Db 1100 CACGAGATCCCCCACTGAAGGAGCAG-----GGCCGGGAATGCTGCTGTCCAAA 1150
 QY 301 -----AspTyrGluAlaTyrAsnSerSerAsnThrThr-----CysVal 314
 Db 1151 GATGATGTGTATGATCTCGGGCGGGCGCCGAGGACCTCAACGCGCGGTCTGTGGCTC 1210
 QY 315 AsnTrpAsnGlnTyrTyrThrAsnCysSerAlaGlyGluHisAsnProPheIleGlyAla 334
 Db 1211 AACTGGAAACCGCTACTACAACGCTCTGCCGACGCGGCAACGCCAACCCCTCAAGGGCGCC 1270
 QY 335 IleAsnPheAspAsnIleGlyTyrAlaTrpIleAlaIlePheGlnValIleThrLeuGlu 354
 Db 1271 ATCAACTTGGACAACTGGCTATGCGGGATGTGATTTTCCAGGTGATCATCTGGAA 1330
 QY 355 GlyTrpValAspIleMetTyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyr 374
 Db 1331 GGCTGGGTGGAGATCATGTACTATGTATGTAGGACGACATCTCTTCTACAACTTCATCTAC 1390
 QY 375 PheIleLeuLeuIleValGlySerPhePheMetIleAsnLeuCysLeuValIle 394
 Db 1391 TTCATTTCTCTCATCATAGTGGGTCTCTTTCATGATCAACTTGTGCTCTGTGTGATA 1450
 QY 395 AlaThrGlnPheSerGluThrLysGlnArgGluSerGlnLeuMetArgGluGlnArgVal 414
 Db 1451 GCNACCCAGTTCTGTAGACCAAGCAACCGGAGCACCGGCTGATGCTGGAGCAACGCCAG 1510
 QY 415 ArgPheLeuSerAsnAlaSerThrLeuAlaSerPheSerGluProGlySerCysTyrGlu 434
 Db 1511 CGTACCTGTGCC---TCCAGCAGGTGGCGCAGTTAGCTGAGCCCGGTGATTGCTATGAG 1567
 QY 435 GluLeuLeuIleTyrLeuValTyrIleLeuArgLysAlaAlaArgLeuAlaGlnVal 454
 Db 1568 GAGATCTTCCATATGTGTGTACATCTCTTCGCAAGCCAGGCGCGTCCCTAGGCCTC 1627

QY 455 SerArgAlaAlaGlyValArgValGlyLeuLeuSerSerProAlaProLeuGlyGlyGln 474
 Db 1628 TACCAGGCCCTGCACAAACCG----- 1648
 QY 475 GluThrGlnProSerSerCysSerArgSerHisArgArgLeuSerValHisIleLeu 494
 Db 1648 ----- 1648
 QY 495 ValHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHis 514
 Db 1648 ----- 1648
 QY 515 ProArgAlaSerProGluIleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeu 534
 Db 1649 -----CGCCAGGCCATGGGC----- 1663
 QY 535 ProProProSerThrProAlaLeuSerGlyAlaProProGlyGlyAlaGluSerValHis 554
 Db 1664 -----CCGGGACACACAGCC-----CCTGCCAAGCTTGGGCC----- 1696
 QY 555 SerPheTyrHisAlaAspCysHisLeuGluProValArgCysGlnAlaProProArg 574
 Db 1697 -----CATGCCAAG-----GAGCCCGCCACTGCAAGCTGTGCCACGACAC 1738
 QY 575 SerProSerGluAlaSerGlyArgThrValGlySerGlyLysValTyrProThrValHis 594
 Db 1739 AGCCCTCTGCAC----- 1762
 QY 595 ThrSerProProGluThrLeuLysGluLysAlaLeuValGluValAlaAlaSerSer 614
 Db 1763 ACATGCTGCACGCC----- 1777
 QY 615 GlyProProThrThrSerLeuAsnIleProProGlyProTyrSerSerMetHisLys 634
 Db 1777 ----- 1777
 QY 635 LeuLeuGluThrGlnSerThrGlyAlaCysGlnSerSerCysLysIleSerSerProCys 654
 Db 1778 -----ATCTCTGCCATT 1789
 QY 655 LeuLysAlaAspSerGlyAlaCysGlyProAspSerCysProTyrCysAlaArg----- 672
 Db 1790 CTGGCTCTGCAC-----CCGACGAGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1834
 QY 673 -----AlaGlyAlaGlyGluValGluLeuAlaAspArgGluMetProAspSer 688
 Db 1835 GGCAGCGCGCCCTCTGGCTGGGCGACACTGAC---TCAGGCCAGGAAGCTCAGGTCT 1891
 QY 689 AspSerGluAlaValTyrGluPheThrGlnAspAla---GlnHisSerAsp-LeuArgAs 707
 Db 1892 GGTGGCTCTGCAGAGCCGGAAGCAATGGGATGGAGCTCCAGAGAGTGGATGGGTC 1951
 QY 707 pProHisSer-----ArgArgGlnArgSerLeuGlyProAspAlaGluProSerSe 724
 Db 1952 TCCTCGACCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2002
 QY 724 rValLeuAlaPheTrpArgLeuIleCysAspThrPheArgLysIleValAspSerLysTyr 744
 Db 2003 TGTGGG-GATGTGTGGCGCGAGACACGAAAAAAGCTGCGGGGATCTGTGACAGCAAGTA 2061
 QY 744 rPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerMetGlyIleGluTyr 764
 Db 2062 CTTCAACAGAGGATCATGATGGCTATCTCTGGTGAACACAGTCAAGCATGGCATCGAGCA 2121
 QY 764 rHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnIleValPheThrSe 784
 Db 2122 CCACGACAGCCCGGAGGAGCTGACCAACATCTGGAGATCTGCAATGTGTCTTCCACAG 2181
 QY 784 rLeuPheAlaLeuGluMetLeuLeuLysLeuLeuValTyrGlyProPheGlyTyrIleLys 804
 Db 2182 TATGTTTGGCTGGAGATGATCTCTGAAACCTGGCCCGCTTTGGGGCTCTTCGACTACCTGCG 2241

Db	4237	CCTGGCCACGCGATTGATGTCCTCTTTGTCTCTGGCCCTCCAGAGCAGCGCTGGGTGAACAT	4296
Qy	1491	eMetTyAspGlyLeuAspAlaValGlyValAspGlnGlnProileMetAsnHisAsnPr	1511
Db	4297	CATGTATATGGATTAGATGCTGTGGTGTGGACAGCAGCGAGTGAAGAACCAACCC	4356
Qy	1511	oTrpMetLeuLeuTyPheIleSerPheLeuLeuIleValAlaPhePheValLeuAsnMe	1531
Db	4357	CTGGATGCTACTGTACTTCAATTTCGTCTCATCTGCTCAGCTTCTTTGTGCTCAACAT	4416
Qy	1531	tPheValGlyValValValGluAsnPheHisCysCysArgGlnHisGlnGluGluGluGl	1551
Db	4417	GTTTGTGGGGCGTGGTGGTGAGAACTTCCACAAGTGCCTGGAGAGGCTGTGGA	4476
Qy	1551	uAlaArgArgArgGluGluLysArgLeuArgLeuGluLysLysArgArgLysAlaGl	1571
Db	4477	GGCGCGAGCGGTGAGAGAAACGGCTGGCGGCGCTGGAAAAGAGCGCGTAAAGCTCA	4536
Qy	1571	nCysLysProTyrTyrSerAspTyrSerArgPheArgLeuLeuValHisLeuCysTh	1591
Db	4537	GAGCTTCCCTACTATGCTACTTACTTCCACAGGCTGCTCTATCCACTCCATGTGCAC	4596
Qy	1591	rSerHisTyrLeuAspLeuPheIleThrGlyValIleGlyLeuAsnValValrMetAl	1611
Db	4597	CAGCCACTACTGGACATCTTACTTACCTTCATCATCTGCCTCAATGTGTCCACTGTC	4656
Qy	1611	aMetGluHisTyrGlnGlnProGlnIleLeuAspGluAlaLeuLysIleCysAsnTyrIl	1631
Db	4657	CCTGGAGCACTTACAAACAGGCTACATCCCTAGAGCAGAGCCCTTAAGTACTGCACTACAT	4716
Qy	1631	ePheThrValIlePheValLeuGluSerValPheLysLeuValAlaPheGlyPheArgAr	1651
Db	4717	GTTCACCACTGCTCTTTGTGTGGAGGCTGTGCTGAAGCTGGTGGCATTTGGCTGAGCG	4776
Qy	1651	gPhePheGlnAspArgTrpAsnGlnLeuAspLeuAlaIleValLeuLeuSerIleMetGl	1671
Db	4777	TTTCTTCAAGCAGCGATGGAAACCAAGCTGGAACCTGGCCATTTGCTGCTGCTGATGG	4836
Qy	1671	ylleThrLeuGluGluIleGluValAsnAlaSerLeuProIleAsnProThrIleIleAr	1691
Db	4837	CATCACTGGAGGAGATCGAGATCAATCGCGCCCTTCCCATCAACCCACCATCATCG	4896
Qy	1691	gIleMetArgValLeuArgIleAlaArgValLeuLysLeuLeuLysMetAlaValGlyMe	1711
Db	4897	TATCATGCGTGTCTTCGTATATCGCCGGGTGTGGAAGCTATTGAAGATGGCCACAGAAAT	4956
Qy	1711	tArgAlaLeuLeuAspThrValMetGlnAlaLeuProGlnValGlyAsnLeuGlyLeuLe	1731
Db	4957	GGGGCGCTTGTGGACAGTGTGTACAGGCTCTGCCCCAGGTGGCAACCTGGGCTGCT	5016
Qy	1731	uPheMetLeuLeuPhePheIlePheAlaLeuGlyValGluLeuPheGlyAspLeuGl	1751
Db	5017	CTTCATGCTGCTCTTCTTCTCATCTATGCTGCTCTGGAGTGGAGCTCTTCGGAAGCTGGT	5076
Qy	1751	uCysAspGluThrHisProCysGluGlyLeuGlyArgHisAlaThrPheArgAsnPheGl	1771
Db	5077	CTGCAATCAGAGAACCCCGTGTGAGGATCATGAGCGGCACGCCACCTTTGAAAACTTCGG	5136
Qy	1771	yMetAlaPheLeuThrLeuPheArgValSerThrGlyAspAsnTrpAsnGlyIleMetLy	1791
Db	5137	CATGGCTTCTCTCCAGCTCTTCCAGGTCTCCACAGCGCATTAACCTGGAATTATGAA	5196
Qy	1791	sAspThrLeuArgAspCys---AspGlnGluSerThrCysTyrAsnThrVal-----Il	1808
Db	5197	GGACACCTTCGAGACTGTATCCCATGATGAGCGCACGTGCTCATGACGCTGCAGTTTGT	5256
Qy	1808	eSerProIleTyrPheValSerPheValLeuThrAlaGlnPheValLeuValAsnValVa	1828
Db	5257	GTCAACCGCTACTTTGTGTGAGTCTGTGTCTCAACAGCTCAGTTCGTGCTCATCAACG	5316
Qy	1828	lIleAlaValLeuMetLysHisLeuGluGluSerAsnLysGluAlaLysGluGluAlaGl	1848
Db	5317	GGTGGCGCTGCTGATGAAACATCTGATGACAGCAACAGGAGGCGCCAGAGAGATGACGA	5376

1848	QY	uLeuGluAlaGluLeuGluLeuMet---	LysThrIleuSerProGlnProHisSerPr	1867
5377	DB			5428
		GATGGATGCTGAGATCGAGCTGGAGTGGCCATGGCTCGGCCCTCGCCCT		
1867	QY	oLeuGlySerProPheLeuTrrProGlyValGluGlyProAspSerProAspSerProLy	1897	
5429	DB			5436
		GGCCCTCG		
1887	QY	sProGlyAlaLeuHisProAlaAlaHisAlaArgSerAlaSerHisPheSerLeuGluHi	1907	
5437	DB			5443
		CCCTGGT		
1907	QY	sProThrMetGlnProHisProThrGluLeuProGlyProAspLeuLeuThrVal	1925	
5444	DB			5502
		CCCTGCCCTGCCCTGCCCTGCCCTGCTGCTGCCCGAGGCTGCCACTAGTTCCACC		
1926	QY	-----ArgLysSerGlyValSerArgThrHisSerLeuProAsnAspSerTy	1941	
5503	DB	TGGGGCTCCGGGCGGAGGATCGGAGGGCAGGTGCTGGAGGC---	5559	
		GACACCGAGTCA		
1941	QY	rMetCysArgHisGlySerThrAlaGluGlyProLeuGlyHisArgGlyTrrGlyLeuPr	1961	
5560	DB			5569
		CCTGTGCCG		
1961	QY	oLysAlaGlnSerGlySerValLeuSerValHisSerGlnProAlaAspThrSerTyI	1981	
5569	DB			5569
1981	QY	eLeuGlnLeuProLysAspAlaProHisIleuLeuGlnProHisSerAlaProThrTrrPgl	2001	
5570	DB			5602
		CACTGCTATTCTCCAGCCCGAGGACCCCTGTGG		
2001	QY	yThrIleProLysLeuProProGlyArgSerProLeuAlaGlnArgProLeuArgAr	2021	
5603	DB			5610
		CTGGACAG		
2021	QY	gGlnAlaAlaIleArgThrAspSerIleuAspValGlnGlyLeuGlySerArgGluAspLe	2041	
5611	DB			5655
		CGTCTCTTAAATCATCAAGGACTCCTTGGAG		
2041	QY	uLeuAlaGluValSer-GlyProSer-ProProLeuAlaArgAlaTrrSerPheTrrPgly	2060	
5656	DB			5715
		CATTGACCAACCTGTCTGGTCCGCTTCCACCTACCTACCTGCGGTGTGGCAA		
2061	QY	GlnSerSerThrGlnAlaGlnGlnHisSerArgSer-----HisSerLysIleSer	2077	
5716	DB			5775
		GTGTCCACCATGACAAGACAGACAGCTTTCATCATCTGCTGGGGATGACCTGAGT		
2078	QY	LysHisMetThrProAlaProCysProGlyProGluProAsnTrrPglyLysGlyPro	2097	
5776	DB			5808
		CTTGAGGACCCACCGCTGTGCCA		
2098	QY	ProGluThrArgSerSerLeuGluLeuAspThrGluLeuSerTrrIleSerGlyAspLeu	2117	
5809	DB			5829
		AGGAGAGCAG		
2118	QY	LeuProProGlyGlyGlnGluProProSerProArgAspLeuLysCysTrr	2136	
5830	DB			5877
		GAGCCTCCG		
2137	QY	-----SerVal-----	2138	
5878	DB	CCCTTTGCCAAGGAGCCAGTGTCCACAGGCCACGAGAGCCTGCTGTGCGAGATGGGGC	5937	
2139	QY	---GluAlaGlnSerCys-GlnArgArgProThrSerTrrLeuAspGluGlnArgGHi	2157	
5938	DB			5985
		CATTCCATTCAACCCCTGTCCAG-----TCCTGGCTCAACACGAGAGCAGCCCA		
2157	QY	sSerIleAlaValSerCysLeuAspSerGlySerGlnPro-----	2170	
5986	DB			6045
		AGCACCCCGAGGCCCTTTCTCCCGGATGGCTCCAGCCCTCTCTCTGTAGATGCCCTGTGTA		

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Qy 2171 -----HisLeuGlyThrAspProSerAsnLeuGlyGlnProLeuGlyGlyProG1 2188
Db 6046 GTTCTTCACCTGCTGTCTGCAGCCAGAGCGGACCAACCGGCATGATGTCAGG 6105
Qy 2188 ySerArgProLysLysLysLeuSerProProSerIleThrIleAspProGluSerG1 2208
Db 6106 AACCTGCCCAAGATTGCACCTTCAG-----GGGTCTG 6138
Qy 2208 nGlyProArgThrProProSerProGlyIleCysLeuArgArgAlaProSerSerAs 2228
Db 6139 GGCATCGCTGAGGTCAACGAGTGTCACTGCACCTCTTGGCCAGGCTACTGTGAGTGA 6198
Qy 2228 pSerLysAspProLeuAlaSerGlyProProAspSerMetAlaAlaSerProSerProLy 2248
Db 6199 CACGTCC-----TTGAGTCCAGTCTTAGCAGCTCAGCGGGCAGCTTACAGACCACT 6252
Qy 2248 sLysAspValLeuSerLeuSer 2255
Db 6253 GGAAGACAGTCTGACTGTGAGT 6274

RESULT 11
US-09-935-541-12
; Sequence 12, Application US/09935541
; Patent No. 6589787
; GENERAL INFORMATION:
; APPLICANT: Dietrich, Paul S.
; APPLICANT: McGivern, Joseph G.
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
; TITLE OF INVENTION: AND USES
; FILE REFERENCE: R0043B-REG sequence listing
; CURRENT APPLICATION NUMBER: US/09/935,541
; CURRENT FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: 09/404,650
; PRIOR FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 6503
; TYPE: DNA
; ORGANISM: Rattus sp.
US-09-935-541-12

Alignment Scores:
Pred. No.: 0 Length: 6503
Score: 5418.50 Matches: 1212
Percent Similarity: 60.47% Conservative: 209
Best Local Similarity: 51.57% Mismatches: 446
Query Match: 45.52% Indels: 484
DB: 4 Gaps: 53

US-09-611-257A-37 (1-2266) x US-09-935-541-12 (1-6503)

Qy 27 GlyAlaGlyArgProGlyProGlySerAlaGluLysAspProGlySerAlaAspSer 46
Db 320 GGATCATCTAGCAGCGGGCCCGGAGTCCCTCCATCCCTCCAGGCTCGAGAG 379
Qy 47 GluAlaGluGly-----LeuProTyrProAlaLeuAlaProValValPhePhe 62
Db 380 CCATTGGAAGAACCAACCTCGACGTCCACATCCAGACCTGGCTCTGTTGTTCTTC 439
Qy 63 TyrLeuSerGlnAspSerArgProArgSerTyrCysLeuArgThrValCysAsnProTyr 82
Db 440 TGCCTGCGCCAGACCCAGCAGCGAAGTGTGTCATCAAGATGGTTGTGAACCCGTGG 499
Qy 83 PheGluArgIleSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMetPheArg 102
Db 500 TTCAGGTGTGACATGCTGTTATCTGCTGAACTGTGTGACCTCTGGGATGTACAG 559
Qy 103 ProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPheAspAsp 122
Db 560 CCATGTGATGATGAGGTGCTGTGCGACCGTTTGAAGATCCTGTCAGGTCTTCGATGAC 619
Qy 123 PheIlePheAlaPheAlaValGluMetValValLysMetValAlaLeuGlyIlePhe 142
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Db 620 TTCACTTTCATCTTCTTTGGCATGGAGATGGTCTTAAGATGGTGGCCCTGGGCATTTT 679
Qy 143 GlyLysLysCysTyrLeuGlyAspThrTyrAsnArgLeuAspPhePheIleValIleAla 162
Db 680 GGCAAGAAGTGTACCTCGGAGACACATGGAACCGCTGGATTCTTTCATTTGTATGCA 739
Qy 163 GlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArgThrVal 182
Db 740 GGGATGTTGTAGTACTCTCTGGACCTACAGAACATCAACCTGTGAGCCATCCGCACTG 799
Qy 183 ArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeuValThr 202
Db 800 CGTGTCTGAGGCTCTCAAGAGCCATCAACCGTGTACCAGCATGCGGATCTGTGTGAAC 859
Qy 203 LeuLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPheValPhe 222
Db 860 CTGCTGCTCGACACGCTGCCCATGCTGGGAACGTCCTCTGCTCTGTTTCTTCGTCTTC 919
Qy 223 PheIlePheGlyIleValGlyValGlnLeuTyrAlaGlyLeuLeuArgAsnArgCysPhe 242
Db 920 TTCATCTTCGGCATCATTTGGCGTGCAGCTCTGGGCGAGGCTGTACGGAACCGCTGCTTC 979
Qy 243 LeuProGluAsnPheSerLeuProLeuSerValAspLeuGluArgTyrTyrGlnThrGlu 262
Db 980 CTGGAAGAGAACTTCACCATACAGGGGATGTGGCCCTGCCCTTATTACCAACCCAGAG 1039
Qy 263 AsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArgSerCys 282
Db 1040 GAGGATGACGAGATGCTCTTATCTGCTCCCTGAGTGGGACATGTCATCATGGCTGC 1099
Qy 283 ArgSerValProThrLeuArgGlyAspGlyGlyProProCysGlyLeu----- 300
Db 1100 CACGAGATCCCCCACTGAAGAGGAGCAG-----GGCCGGGAATGCTGCTCTCCAAA 1150
Qy 301 -----AspTyrGluAlaTyrAsnSerSerSerSerSerSerSerSerSerSer 314
Db 1151 GATGATGTGTATGACTTCGGGGCGGGCGGCGGACCTCAACGCCAGCGGTCTGTGCGTC 1210
Qy 315 AsnTrpAsnGlnTyrTyrThrAsnCysSerAlaGlyGluHisAsnProPheLysGlyAla 334
Db 1211 AACTGGAACCGCTACTACACGCTCGCGGAGGGAACGCCAACCCCTCACAGGGGCGCC 1270
Qy 335 IleAsnPheAspAsnIleGlyTyrAlaTrpIleAlaIlePheGlnValIleThrLeuGlu 354
Db 1271 ATCAACTTTGACAAACATTGGCTATGCGCGGATTTGTGATTTTCCAGGTGATCACTCTG 1330
Qy 355 GlyTrpValAspIleMetTyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyr 374
Db 1331 GGTGGGTGGAGATCATGTACTATGTGATGACGCACATTTCTTTCACACTTCATCTAC 1390
Qy 375 PheIleLeuLeuIleValGlySerPhePheMetIleAsnLeuCysLeuValValIle 394
Db 1391 TTCATCTGCTCATATAGTGGGCTCTTCTTCATGATCAACTTGTGCTCTGTTGTGTCATA 1450
Qy 395 AlaThrGlnPheSerGluThrLysGlnArgGluSerGlnLeuMetArgGluGlnArgVal 414
Db 1451 GCAACCCAGTTCTCTGAGACCAAGCAACGGGAGCACCGGCTGTGCTGGAGCAACGCCAG 1510
Qy 415 ArgPheLeuSerAsnAlaSerThrLeuAlaSerPheSerGluProGlySerCysTyrGlu 434
Db 1511 CGTACTCTGTCC---TCCAGCACGGTGGCCAGTTACGCTGAGCCCGGTGATTGCTATGAG 1567
Qy 435 GluLeuLeuLysTyrLeuValTyrIleLeuArgLysAlaAlaArgArgLeuAlaGlnVal 454
Db 1568 GAGATCTTCCAAATATGCTGTGCATCTCTTCGAAAGCAACGCCCGCTGGCCCTAGGCCCTC 1627
Qy 455 SerArgAlaAlaGlyValArgValGlyLeuLeuSerSerProAlaProLeuGlyGlyGln 474
Db 1628 TACCAGGCTTCGAGAACCCG----- 1648
Qy 475 GluThrGlnProSerSerSerCysSerArgSerHisArgArgLeuSerValHisLeu 494
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Db 5429 -----GGCCCTCG 5436
Qy 1887 sProGlyAlaLeuHisProAlaAlaHisAlaArgSerAlaSerHisPheSerLeuGluHi 1907
Db 5437 CCCTGGT----- 5443
Qy 1907 sProThrMetGlnProHisProThrGluLeuProGlyProAspLeuLeuThrVal----- 1925
Db 5444 -CCCTGCCCTCGCCCTCGCCCTCGCCCTCGCTGTGGCCCGAGCTGCCACTAGTTCACC 5502
Qy 1926 -----ArgLysSerGlyValSerArgThrHisSerLeuProAsnAspSerTy 1941
Db 5503 TGGGGCTCCGGGGCGAGATCGGAGGGCGAGCTGTGGAGGC---GACACCCGAGAGTCA 5559
Qy 1941 rMetCysArgHisGlySerThrAlaGluGlyProLeuGlyHisArgGlyTrpGlyLeuPr 1961
Db 5560 CCTGTGCGG----- 5569
Qy 1961 oLysAlaGlnSerGlySerValLeuSerValHisSerGlnProAlaAspThrSeryrIl 1981
Db 5569 ----- 5569
Qy 1981 eLeuGlnLeuProLysAspAlaProHisLeuGlnProHisSerAlaProThrTrpGl 2001
Db 5570 -----CACTGCTATTCTCCAGCCCGAGGAGCCCTGTGG-- 5602
Qy 2001 yThrIleProLysLeuProProGlyArgSerProLeuAlaGlnArgProLeuArgAr 2021
Db 5603 -----CTGGACAG 5610
Qy 2021 gGlnAlaAlaIleArgThrAspSerLeuAspValGlnGlyLeuGlySerArgGluAspLe 2041
Db 5611 CTTCTTTTATCATCAGAGACTCTCTGAG-----GGGAGCTGACCAT 5655
Qy 2041 uLeuAlaGluValSer-GlyProSer-ProProLeuAlaArgAlaTySerPheTrpGly 2060
Db 5656 CATTCACAACCTGTCTGGGTCTCGTCTCCACCATACGCTCACCTGACGCTGTGGCAA 5715
Qy 2061 GlnSerSerThrGlnAlaGlnHisSerArgSer-----HisSerLysIleSer 2077
Db 5716 GTGTCAACATGACAGACAGACAGAGTCTTCATCCATCTGCTGGGGATGACCTGAGT 5775
Qy 2078 LysHisMetThrProAlaProCysProGlyProGluProAsnTrpGlyLysGlyPro 2097
Db 5776 -----CTTGAGGACCCACGCGCTGCCCA-----CAGGGCCCC 5808
Qy 2098 ProGluThrArgSerSerLeuGluLeuAspThrGluLeuSerTrpIleSerGlyAspLeu 2117
Db 5809 AAGGAGAGCAAG-----GGTGAACATA 5829
Qy 2118 LeuProProGlyGlyGlnGluProProSerProArgAspLeuLysCysTyr--- 2136
Db 5830 GAGCCTCCG-----GAGCCCATGCGGCTGGAGACTGGATGATGCTTTGG 5877
Qy 2137 -----SerVal----- 2138
Db 5878 CCCTTTTCCAAAGCGAGCCAGTGTCCACAGGCCCGAGAGCCCTGCTGTGCGAGATGGGGC 5937
Qy 2139 ---GluAlaGlnSerCys-GlnArgArgProThrSerTrpLeuAspGluGlnArgHis 2157
Db 5938 CATTCATTCAACCTGTCTCCAG-----TCTGGCTCAACACAGCAGCAGCACA 5985
Qy 2157 sSerIleAlaValSerCysLeuAspSerGlySerGlnPro----- 2170
Db 5986 AGCACCCAGAGCCCTTCTCCCGGATGGCTCCAGCCCTCTCTCTAGATGCTGCTGA 6045
Qy 2171 -----HisLeuGlyThrAspProSerAsnLeuGlyGlnProLeuGlyGlyProGl 2188
Db 6046 GTTCTTCCACCTGCTGTGTCTGCCAGCAGAGAGGGGAGAACCCGGGATGATGCCAG 6105
Qy 2188 ySerArgProLysLysLysLeuSerProProSerIleThrIleAspProProGluSerGl 2208
Db 6106 AACCTGCCCAAGATTGCACTTCAG-----GGGTCTCTG 6138

Qy 2208 nGlyProArgThrProProSerProGlyIleCysLeuArgArgAlaProSerSerAs 2228
Db 6139 GGCATCGTGGAGTCAACCGAGTGTCACTGCACCCCTCTTGGCCAGGCTACTGTGAGTGA 6198
Qy 2228 pSerLysAspProLeuAlaSerGlyProProAspSerMetAlaAlaSerProSerProLy 2248
Db 6199 CACGTCC-----TTGGATGTCAGTCTTACAGCTCAGCGGGCAGCTTACAGACCACT 6252
Qy 2248 sLysAspValLeuSerLeuSer 2255
Db 6253 GGAACACAGTCTGACTCTGAGT 6274

RESULT 12

US-09-949-016-15601
; Sequence 15601, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 15601
; LENGTH: 70308
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15601

Alignment Scores: 2,33e-127 Length: 70308
Pred. No.: 2237.00 Matches: 730
Score: 2237.00
Percent Similarity: 21.93% Conservative: 25
Best Local Similarity: 21.20% Mismatches: 64
Query Match: 18.79% Indels: 2626
Gaps: 19

US-09-611-257A-37 (1-2266) x US-09-949-016-15601 (1-70308)

Qy 2 AspGluGluGluAspGlyAlaGlyAlaGluGluSerGlyGlnProArg----- 17
Db 9554 GATGAGAA-----GCTGGTCCAGAGAGGTGAGATGACCAAGGTGGGACTCCCT 9604
Qy 18 SerPheMetArgLeuAsnAspLeuSerGlyAlaGlyGlyArg-----ProGlyProGly 35
Db 9605 TCTCTGATGAGGATCTCGGGCTG-----GGGGCTGGTCTGTATGTATGTCAGGGCCCTGGC 9661
Qy 36 SerAla-----GluLysAspProGly----- 42
Db 9662 ACCACACTGTTAGCTTACCTCAGATGAGCAGAGGTAACAGAGGAGGAGTGTAGGGCG 9721
Qy 43 SerAlaAspSerGluAlaGluGlyLeuProTyrProAlaLeuAlaProValPhePhe 62
Db 9722 GGGTCGGGGCGCGCGCTCAGCTCCAGCTTGGCCAGCTGTTTCC----- 9766
Qy 63 TyrLeuSerGlnAspSerArgProArgSerTrpCysLeuArgThrValCysAsnProTrp 82
Db 9767 -----TTGACTGCCAGTACCTGG 9784
Qy 83 PheGluArgIleSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMetPheArg 102
Db 9785 TTTGAGCCATCAGATGTTGGTTCATCTCACTGCGTGACCTGGGATGTTCCGG 9844
Qy 103 ProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeu----- 117

QY	196	-----	196	QY	249	-----	249
Db	12064	GTGTAAATTGATGGACTTCTGAGAGACAGTATTGTATCTCTTCAGGTCCTGATTGGG	12123	Db	13144	CTGGTGCCACCTCCAGAGATTCTGATTTCATTGCTCTGGGGCTCAGCTTGGATGTAAG	13203
QY	196	-----	196	QY	249	-----	249
Db	12124	GATCTGCACCAAGCAGGGAATAGTTTCAGGAAAGCAGGGCTCAGAGCCATAGTGAAGCAC	12183	Db	13204	ATTTTTTCAGCCCTCCAGTGATCTTAACCTTGCAGTGAAATTTGAAAATCACTATTCCAG	13263
QY	196	-----	196	QY	249	-----	249
Db	12184	AGGCATCTTGGCCCCCTGCCTAGGAGCTGGCTCTCAAAATGAGATTTCCTGCTGCTCA	12243	Db	13264	GATGTGACCTTCCAACTCTGAGTCTGGAGTTTCCCACTCAGGCCTCATGCTCTGGT	13323
QY	196	-----	196	QY	249	-----	249
Db	12244	TTCCTCTGGAGTTGCTGCTCAGTTTCCCTAATGACTCTGGTGGTGATAACTTAGAA	12303	Db	13324	GCCCAAAATCCCTGCCCTGCCAGTCCCTTCCCAATTCTTGGTTCTGCCCTGTCTACCC	13383
QY	196	-----	196	QY	249	-----	249
Db	12304	GGTCAAGTGAAGTGTGCTGTGAGAGAAAGTAGTAGGAGTGTGCTGTGAATGTG	12363	Db	13384	TATATGCTCGAGCACTCGTGCCATCTCTCCCTTCTGGGCCCTCTCCCTGGAGAGCCCA	13443
QY	196	-----	196	QY	250	-----	256
Db	12364	TGCGGTGTGGTGTGTGAGAGGAGTTTCGGAAGCCTCGGTTCCAGTTCGG	12423	Db	13444	CTCCCACTCTCACCCCTGTTCCCTTCCCATCTCTGAGCCCTCTGAGCTGGACCTGGA	13503
QY	196	-----	196	QY	256	uArgTyrGlnThrGluAsnGluSerProPheIleCysSerGlnProArgI	276
Db	12424	GCACCTACACTTAGCAGCTGTGTGATCTGGGTGAGTCAAGTCAATTTCTCAAGCCTCAG	12483	Db	13504	GCCTATTACACAGACAGAGATGAGAGCCCTTCATCTCTCCAGCCACGGGA	13563
QY	196	-----	196	QY	276	uAsnGlyMetArgSerCysArgSerValProThrLeuArgGlyAspGlyGlyGlyPyr	296
Db	12484	ACTTCTCATCTGTGAATTGGAGTGATATTATCCATGTGATGATGTTGGAGAGTTAG	12543	Db	13564	GAACGCAATGCGGTCTCTGAGAAGCGTCCCAAGCTGCGGGGAGCGGGGGGGTGGCC	13623
QY	196	-----	196	QY	296	oProCysGlyLeuAspTyrGluAlaTyrAsnSerSerSerAsnThrThrCysValAsnTr	316
Db	12544	GAGGGGCCACAGTTTCCCAAGCTCACTGTGTGTGTAAGTGTGAGATACCGTGGCAAG	12603	Db	13624	ACCTTCCGCTCTGACTATGAGCCCTTACAAAGCTCCAGCAACACACCTGTGTCAACTG	13683
QY	196	-----	196	QY	316	pAsnGlnTyrTyrThrAsnCysSerAlaGlyGluHisAsnProPheLeuGlyValAlaLeas	336
Db	12604	CCACAAGGGGAAGTGGTGGGGGCAAGGGGTCGAGAGGCTATCTGGGGAGTCAGAGTG	12663	Db	13684	GAACCACTACTACCAACTGCTCAGCGGGGAGACAAACCCCTTCAAGGGGCGCCATCAA	13743
QY	196	-----	196	QY	336	nPheAspAsnIleGlyTyrAlaTyrIleAlaIlePheGln	349
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QY	197	-----	208	QY	349	-----	349
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QY	208	uProMetLeuGlyAsnValLeuLeuLeuCysPhePheValPhePheIlePheGlyIleVa	228	QY	350	-----	361
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Db	12904	CGCGCTCCAGCTGTGGGCAAGGCTGCTTCGGAACCGATGCTTCTTCTTCTTCTTCTTCT	12963	Db	13984	ACTTTGTGATGGATGCTCATTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT	14042
QY	248	rLeu	249	QY	380	-----	380
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Db	13024	CCCCAAGTTCTCACTTCCGGTTGCTACTGACATATCTGTTCTTAACATCTGAGACATATC	13083	Db	14103	TCCAGAGGGGATAGTTTGTCTGTCTGAAAGTTTTTAGCTCTCAGGACAAAGTCTGTAG	14162
QY	249	-----	249	QY	380	-----	380
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				QY	380	-----	380

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Db	16503	TGGTGGTGAATGCCACGCGAGTTCTCAGAGACCAAGCAGCGGAAAGCAGCTAGTGGGG	16562	Db	17583	TGGATCCTCTCTACCCATTAAAGTAGAGGCTTCTTAGCATCCCCATTGTGTGGATGAGA	17642
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Db	16623	GCTGCTATGAGAGCTGCTCAAGTACCTGGTGTATACCTTCGTAAAGCAGCCCGCAGG	16682	Db	17703	ACTCGGGGCCCGCAGCTCGGAGCTCTTGTGTGAGGCTCAGAGAGAAATGGTGTGTGAC	17762
Qy	451	euAlaGlnValSerArgAlaAlaGlyValArgValGlyLeuLeuSerSerProAlaProL	471	Qy	641	-----	641
Db	16683	TGGTCTCAGGCTCTCTCGGGCAGCAGGTGTGGGGTTGGGCTGCTCAGCAGCCAGCACCC	16742	Db	17763	TGTGCCAGGTTTCATGCCCCCACTGGGCTAAACCTGAGTCTCATTTGCCCTCCGCACAGGAGA	17822
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Qy	531	rgLeuMetLeuProProSerThrProAlaLeuSerGlyValaProGlyGlyValaG	551	Qy	641	-----	641
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Qy	611	laAlaSerSerGlyProProThrLeuThrSerLeuAsnIleProProGlyProTyrSerS	631	Qy	641	-----	641
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Db	17283	GTGCCCTCGTCTGGGGAATGGGTGGCTCCAGAGGGGACTAGGGGGTCTGGAGTCAGAG	17342	Db	18363	TGTGCGCACGAGTCATCTAGTATGCGTGTATGCGTCTATGCTATGCTCCATGAAGGGTCCAGTG	18422
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Db	17403	TCCCTGTATGAGCTCGAAATTTTCTATCTGCTAAAGTGAACCTCATTAATTCCTACATTG	17462	Db	18483	GCTTGATGTGTAGGTGCATGTGCGATGTGAGCTCTTTCTTCTTGGTGTGTGTGCATGTG	18542
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Db	17463	TAATAGCAGTAACATATGTAATAAGCACCTGCTTCTGTGTTTGTGCAATGATGCTCTAG	17522	Db	18543	TGCATATGTCTGCGCATATGTCCGCTGTGTGAATGTGTGTGTGTGCACACATGTGTGTGGTATG	18602
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Db 19443 ATCGGCATCTCTGGTCAACACACTCAGCATGGGCATCGAATACACAGCAGCAGGTAGGAG 19502
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Qy 811 AspGlyValIleValValIleSer-ValTyrGluLysValGlnGlnGlyGlyLe 830
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Qy 857 1 857
Db 19761 G 19761
RESULT 13
US-08-984-709A-51
; Sequence 51, Application US/08984709A
; Patent No. 6320032
; GENERAL INFORMATION:
; APPLICANT: Williams, Mark E.
; APPLICANT: Stauderman, Kenneth A.
; APPLICANT: Harpold, Michael M.
; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
; TITLE OF INVENTION: METHODS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Heller Ehrman White & McAuliffe
; STREET: 4250 Executive Square, Suite 700
; CITY: La Jolla
; STATE: California
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/984,709A
; FILING DATE: 02-DEC-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L.
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 24735-9815 (formerly 6362-9815)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 450-8400
; TELEFAX: (619) 587-5360
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1669 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
US-08-984-709A-51
Alignment Scores:
Pred. No.: 3.36e-113 Length: 1669
Score: 1971.50 Matches: 423
Percent Similarity: 57.77% Conservative: 38
Best Local Similarity: 53.01% Mismatches: 83
Query Match: 16.56% Indels: 255
DB: 3 Gaps: 8
US-09-611-257A-37 (1-2266) x US-08-984-709A-51 (1-1669)
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Qy 129 AlaValGluMetValValLysMetValAlaLeuGlyLysPheGlyLysCysTyrLeu 148
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RESULT 14

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RES001 14
US-09-268-163-3
; Sequence 3, Application US/09268163B
; Patent No. 6353091
; GENERAL INFORMATION:
; APPLICANT: Lipscombe, Diane
; APPLICANT: Schorge, Stephanie
; TITLE OF INVENTION: HUMAN N-TYPE CALCIUM CHANNEL ISOFORM AND USES THEREOF
; FILE REFERENCE: B1055/7000
; CURRENT APPLICATION NUMBER: US/09/268,163B
; CURRENT FILING DATE: 1999-03-12
; EARLIER APPLICATION NUMBER: US 60/077,901
; EARLIER FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 7376
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 146..7174
US-09-268-163-3

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1929 -----ArgGlyTrpGlyLeuPro-LysAla 1963
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2011 ArgSerProLeuAlaGlnArgProLeuArgGlnAlaAlaIleArg----- 2026
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6274 GAGCGCCCGCCAGGAGCGGTCTGCGGAGCGGTCTGCGGAGCGGCGGCGGCGGCGG 6318
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6319 CCG-----CTG 6324
2118 LeuProProGlyGlyGlnGlu-----GluProProSerProArgAspLeuLysLysCysTyr 2136
6325 CCACCGCCCGCAGGAGCAGGAGCGGTCTGAGAGAGGCGGCGGCGGCGGCGGCGGCGG 6381
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6382 -----CGATATGATGGCGCACCAGCAG----- 6405
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6507 CCT-----CATCTCTCTCGGAGAGCAGCGCTTCTACTCTCTGCGACC 6551
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RESULT 15

US-08-455-543A-7
Sequence 7, Application US/08455543A
Patent No. 5792846

GENERAL INFORMATION:

APPLICANT: Harpold, Michael
APPLICANT: Ellis, Steven
APPLICANT: Williams, Mark
APPLICANT: Feldman, Daniel
APPLICANT: McCue, Ann
APPLICANT: Bremer, Robert
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
METHODS
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:

ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92101-2926

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5

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GenCore version 5.1.6
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Searched: 5622541 seqs, 303335566 residues
Total number of hits satisfying chosen parameters: 11245082

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	11815.5	99.3	7648	18	US-10-377-139-10 Sequence 10, Appl
2	11815.5	99.3	7648	18	US-10-757-262-15 Sequence 15, Appl
3	11353	95.4	8116	17	US-10-062-674-2011 Sequence 2011, Ap
4	11111	93.3	7129	10	US-09-383-894-1 Sequence 1, Appli
5	11111	93.3	7285	10	US-09-383-894-3 Sequence 3, Appli
6	10945	91.9	6942	18	US-10-377-139-7 Sequence 7, Appli
7	6315.5	53.1	3993	19	US-10-930-301-51 Sequence 51, Appli
8	5496.5	46.2	6990	18	US-10-377-139-8 Sequence 8, Appli
9	5492.5	46.1	6816	9	US-09-935-541-1 Sequence 1, Appli
10	5492.5	46.1	6816	16	US-10-425-800-1 Sequence 1, Appli
11	5484	46.1	6855	9	US-09-935-541-3 Sequence 3, Appli
12	5484	46.1	6855	16	US-10-425-800-3 Sequence 3, Appli
13	5418.5	45.5	6503	9	US-09-935-541-12 Sequence 12, Appl
14	5418.5	45.5	6503	16	US-10-425-800-12 Sequence 12, Appl
15	3959.5	33.3	5562	9	US-09-030-482B-18 Sequence 18, Appl
16	3867	32.5	6073	18	US-10-377-139-11 Sequence 11, Appl
17	1786.5	15.0	7376	13	US-10-033-026-3 Sequence 3, Appli
18	1784.5	15.0	7362	17	US-10-375-253-11 Sequence 11, Appl
19	1782.5	15.0	7364	9	US-09-954-456-1179 Sequence 1179, Ap
20	1782.5	15.0	7364	13	US-10-033-026-5 Sequence 5, Appli
21	1782.5	15.0	7364	18	US-10-736-883-31 Sequence 31, Appl
22	1782.5	15.0	7364	19	US-10-843-641A-4206 Sequence 4206, Ap
23	1778	14.9	7175	17	US-10-375-253-13 Sequence 13, Appl
24	1776	14.9	7177	13	US-10-033-026-7 Sequence 7, Appli
25	1776	14.9	7177	18	US-10-736-883-33 Sequence 33, Appl
26	1773.5	14.9	6792	17	US-10-627-370-1 Sequence 1, Appli
27	1757.5	14.8	7121	18	US-10-736-883-43 Sequence 43, Appl
28	1755.5	14.7	6984	18	US-10-736-883-37 Sequence 37, Appl
29	1752	14.7	7185	18	US-10-736-883-39 Sequence 39, Appl
30	1751.5	14.7	7713	18	US-10-736-883-41 Sequence 41, Appl
31	1751.5	14.7	9695	18	US-10-736-883-27 Sequence 27, Appl
32	1751.5	14.7	9695	19	US-10-486-706-207 Sequence 207, App
33	1738.5	14.6	7363	18	US-10-723-860-5192 Sequence 5192, Ap
34	1728.5	14.5	7011	13	US-10-033-026-9 Sequence 9, Appli
35	1728.5	14.5	7011	18	US-10-736-883-29 Sequence 29, Appl
36	1725.5	14.5	6503	13	US-10-377-139-16 Sequence 16, Appl
37	1717	14.4	6083	13	US-10-029-413A-21 Sequence 21, Appl
38	1708	14.3	7477	18	US-10-322-696-177 Sequence 177, App
39	1704	14.3	8490	15	US-10-101-510-617 Sequence 617, App
40	1693.5	14.2	7348	18	US-10-322-696-175 Sequence 175, App
41	1693	14.2	7089	17	US-10-375-253-39 Sequence 39, Appl
42	1693	14.2	7291	18	US-10-322-696-83 Sequence 83, Appl
43	1692.5	14.2	8491	17	US-10-333-191-1 Sequence 1, Appli
44	1692	14.2	9704	18	US-10-322-696-80 Sequence 80, Appl
45	1690.5	14.2	8491	17	US-10-333-191-3 Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-10-377-139-10
; Sequence 10, Application US/10377139
; Publication No. US20040175761A1
; GENERAL INFORMATION:
; APPLICANT: MacKinnon, Roderick
; APPLICANT: Jiang, Youxing
; APPLICANT: Lee MacKinnon, Alice
; APPLICANT: Ruta, Vanessa
; TITLE OF INVENTION: Voltage Sensor Domains of Voltage-Dependent Ion Channel Proteins
; FILE REFERENCE: Seq. Nos. 1-21 for 1119-9
; CURRENT APPLICATION NUMBER: US/10/377,139
; CURRENT FILING DATE: 2003-03-01
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 7648
; TYPE: DNA
; ORGANISM: Homo sapiens

US-10-377-139-10									
Alignment Scores:									
Pred. No.:	0	Length:	7648						
Score:	11815.50	Matches:	2264						
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Qy 721 GluProSerSerValLeuAlaPheTrpArgLeuIleCysAspThrPheArgLysIleVal 740
Db 2161 GAGCCAGCTCTGTGCTGCCCTCTCGAGGCTAATCTGTGACACCTTCGGAAGATTGTG 2220
Qy 741 AspSerLysTyrPheGlyArgGlyIleMetIleAlaLeuValAsnThrLeuSerMet 760
Db 2221 GACAGCAAGTACTTTGGCGGGGAATCATGATCGCCATCTCTGGTCAACACACTCAGCATG 2280
Qy 761 GlyIleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnIle 780
Db 2281 GGCAATCGAATACACAGAGACCCGAGAGCTTACCACGCCCTTAGAAATCAGCAACATC 2340
Qy 781 ValPheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuValTyrGlyProPhe 800
Db 2341 GTCTTACCAGCTCTTTGCCCTGGAGATGCTGCTGAAGCTGCTTGTGATGTTCCCTTT 2400
Qy 801 GlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleValIleSerValTrp 820
Db 2401 GGCTACATCAAGATCCCTACACATCTTCGATGGTGTCTTGTGGTTCATCAGCGTGTGG 2460
Qy 821 GluIleValGlyGlnGlnGlyGlyLeuSerValLeuArgThrPheArgLeuMetArg 840
Db 2461 GAGATCGTGGGCCAGCAGGGGGCGGCTGTCGTGCTCGGAGCTTCCGCGCTGATCGGT 2520
Qy 841 ValLeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetLys 860
Db 2521 GTGCTGAAGCTGTGTGCGCTTCTCGCGGCTGAGCGGAGCTGTGTGTCTCATGAG 2580
Qy 861 ThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePheSer 880
Db 2581 ACCATGACACAGTGGGCACCTTCTGCGTGTGCTTATGCTTCTTCTCATCTTCAGC 2640
Qy 881 IleLeuGlyMetHisLeuPheGlyCysLysPheAlaSerGluArgAspGlyAspThrLeu 900
Db 2641 ATCTCGGCGATGCAATCTTCCGCTGCAAGTTTCCCTCTGAGCGGAGTGGGACACCCCTG 2700
Qy 901 ProAspArgLysAsnPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIleLeu 920
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Qy 921 ThrGlnGluAspTrpAsnLysValLeuTyrAsnGlyMetAlaSerThrSerTrpAla 940
Db 2761 ACCCAGGAGGACTGGAAACAAAGTCTCTACAAATGGTATGGCTCCACGTCGTGGGCG 2820
Qy 941 AlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuVal 960
Db 2821 GCCCTTTATTTCAATGTCCTCATGACCTTCGGCAACTACGTCCTTTCAAATTTGCTGGTC 2880
Qy 961 AlaIleLeuValGluGlyPheGlnAlaGluGluIleSerLysArgGluAspAlaSerGly 980
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Qy 981 GlnLeuSerCysIleGlnLeuProValAspSerGlnGlyAspAlaAsnLysSerGlu 1000
Db 2941 CAGTTAAGCTGATTTACGTGCTGCTGCTCCAGGGGGGAGATGCCAACAGTCCGAA 3000
Qy 1001 SerGluProAspPhePheSerProSerLeuAspGlyAspArgLysLysCysLeu 1020
Db 3001 TCAGAGCCCGATTTCTTCTCAACCGAGCTGGATGGTGGGACAGGAAGTGTCTG 3060
Qy 1021 AlaLeuValSerLeuGlyGluHisProGluLeuArgLysSerLeuLeuProLeuIle 1040
Db 3061 GCCTTGTGTCCTTGGGAGAGACACCCGAGCTGCGGAAGAGCCCTGCTGCCCTCTCATC 3120

Qy 1041 IleHisThrAlaAlaThrProMetSerLeuProLysSerThrSerThrGlyLeuGlyGlu 1060
Db 3121 ATCCACACGGCGGCACACCATGTGCTGCCAAGAGCACAGCACGGGCTTGGCGAG 3180
Qy 1061 AlaLeuGlyProAlaSerArgTrpSerSerGlySerAlaGluProGlyValAla 1080
Db 3181 CGCTGGGGCTGCTGGTCCGCCCGCACAGCAGCGGTCCGGAGAGCCTTGGGGCGGCC 3240
Qy 1081 HisGluMetLysSerProSerAlaArgSerSerProHisSerProTrpSerAlaAla 1100
Db 3241 CACGAGATGAAGTCAACGCCCGCGCGCTCTCCGACACAGCCCTCGAGCGCTGCA 3300
Qy 1101 SerSerTrpThrSerArgArgSerSerArgAsnSerLeuGlyArgAlaProSerLeuLys 1120
Db 3301 AGCAGCTGGAGCCAGCAGCGCTCCAGCGGAACAGCCTCGGCCGTGCACCCAGCTGAAG 3360
Qy 1121 ArgArgSerProSerGlyGluArgArgSerLeuLeuSerGlyGlyGlnGlnSerGln 1140
Db 3361 CGGAAGAAGCCCAAGTGAGAGCGCGGTCTCTGTGTCGGGAAGAGCCAGAGAGCCAG 3420
Qy 1141 AspGluGluGluSerSerGluGluArgAlaSerProAlaGlySerAspHisArgHis 1160
Db 3421 GATGAAGAGGAGAGCTCAGAAAGAGAGCGGGCCAGCCCTCGGGCAGTGCACATCGCCAC 3480
Qy 1161 ArgGlySerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeuGlnVal 1180
Db 3481 AGGGGGTCCCTGGAGCGGAGGCGCAAGAGTTCTTTGACCTGCCAGACACACTGCAGGTG 3540
Qy 1181 ProGlyLeuHisArgThrAlaSerGlyArgGlySerAlaSerGluHisGlnAspCysAsn 1200
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Qy 1201 GlyLysSerAlaSerGlyArgLeuAlaArgAlaLeuArgProAspAspProProLeuAsp 1220
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Qy 1221 GlyAspAspAlaAspAspGluGlyAsnLeuSerLysGlyGluArgValArgAlaTrpIle 1240
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Qy 1241 ArgAlaArgLeuProAlaCysTyrLeuGluArgAspSerTrpSerAlaTyrIlePhePro 1260
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Qy 1281 ValValLeuValIleIlePheLeuAsnCysIleThrIleAlaMetGluArgProLysIle 1300
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Db 4021 TACTGCGGAGCAGTGGAACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4080
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Db 4081 ATTCTGT 4140
Qy 1381 ArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeuLysLeu 1400
Db 4141 CGGCTGT 4200

Qy 1401 ValValGluThrLeuMetSerSerLeuLysProIleGlyAsnIleValValIleCysCys 1420
 Db 4201 GTGTGGAGACGGTGTGCTCTCACTGAAACCCATCGCAACATTGTAGTCACTGCTGT 4260
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 Db 4261 GCCTTCTTCATCTTTTCGGCATCTTTGGGGGTGACCTCTTCAAGGGAAGTTTTCGGT 4320
 Qy 1441 CysGlnGlyGluAspThrArgAsnIleThrAsnLysSerAspCysAlaGluAlaSerTyr 1460
 Db 4321 TGCCAGGCGCAGGATACAGAAACATCCCAATAATCGGACTGTGCCGAGGCCAGTTAC 4380
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 Db 4501 GTGGACCGAGCCCATCATGACCAACACCCCTGGATGCTGTGTACTTCACTCGCTTC 4560
 Qy 1521 LeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValValValGluAsnPhe 1540
 Db 4561 CTGCTCAITTTGGCCTTCTTTGCTGAACATGTTTGGGTGGTGGTGGTGGTGGTGGTGG 4620
 Qy 1541 HisLysCysArgGlnHisGlnGluGluAlaArgArgGluGluGluLysArgLeu 1560
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 Qy 1561 ArgArgLeuGluLysLysArgArg 1568
 Db 4681 CGAAGACTGGAGAAAAGAGAGAGGAACTAATGTCTGGACGATGTAATGTCTCGGCGAGC 4740
 Qy 1569 -----LysAlaGlnCysLysProTyrTyrSerAspTyrSerArgPhe 1582
 Db 4741 TCAGCCAGCGCTGGTGCAGAGCCCGACGTCGAAACCTTACTACTCGGACTACTCGCGCTTC 4800
 Qy 1583 ArgLeuLeuValHisHisLysCysThrSerHisTyrLeuAspLeuPheIleThrGlyVal 1602
 Db 4801 CGGCTCTCTGTCACCATTTGTGCACAGCCACTACTGGACCTCTTCAACAGGTTGTC 4860
 Qy 1603 IleGlyLeuAsnValValThrMetAlaMetGluHisTyrGlnGlnProGlnIleLeuAsp 1622
 Db 4861 ATCGGGCTGAACGTGTGTCACCATGGCCATGGAGCACTACAGAGCCCGCCAGATTCTGGAT 4920
 Qy 1623 GluAlaLeuLysIleCysAsnTyrIlePheThrValIlePheValLeuGluSerValPhe 1642
 Db 4921 GAGGCTCTGAAGATCTGCAACTACATCTTCACTGTCTATCTTGTCTTGGAGTCACTTTTC 4980
 Qy 1643 LysLeuValAlaPheGlyPheArgPhePheGlnAspArgTirpAsnGlnLeuAspLeu 1662
 Db 4981 AAACCTTGCGCTTTGGTTTTCGTCGGTCTTCCAGGACAGGTGGAAACAGCTGGACCTG 5040
 Qy 1663 AlaIleValLeuLeuSerIleMetGlyIleThrLeuGluGluIleGluValAsnAlaSer 1682
 Db 5041 GCCATTGTGCTGTCTTCATCATGGGCATCACCTCGAGGAAATCGAGGTCAACGCTCG 5100
 Qy 1683 LeuProIleAsnProThrIleArgIleMetArgValLeuArgIleAlaArgValLeu 1702
 Db 5101 CTGCCCCATCAACCCACCATCATCCGCATCATGAGGGTGTGCGCATTCGCCGAGTGTCTG 5160
 Qy 1703 LysLeuLysMetAlaValGlyMetArgAlaLeuLeuAspThrValMetGlnAlaLeu 1722
 Db 5161 AAGCTGTGTAAGATGGCTGTGGCATTCGGGGCGCTGTGGACACGGTGTATGTCAGGCCCTG 5220
 Qy 1723 ProGlnValGlyAsnLeuGlyLeuPheMetLeuLeuPhePheIlePheAlaLeu 1742
 Db 5221 CCCCAGGTGGGAACTTGGGACTTCTCTTCAATGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5280
 Qy 1743 GlyValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGluGlyLeuGly 1762

Db 5281 GCGGTGGAGCTCTTTGGAGACCTGGAGTGTGACGACACACACCCCTGTGAGGCGCTGGGC 5340
 Qy 1763 ArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgValSerThr 1782
 Db 5341 CGTCATGCCACCTTTGGAACTTTGGCATGGCCCTTCTTAACCCCTCTTCCGAGTCTCCACA 5400
 Qy 1783 GlyAspAsnTirpAsnGlyIleMetLysAspThrLeuArgAspCysAspGlnGluSerThr 1802
 Db 5401 GGTGACAACTTGGATGCAATATGAGGACACCTCCGGGACTGTGACCGAGGAGTCCACC 5460
 Qy 1803 CysTyrAsnThrValIleSerProIleTyrPheValSerPheValLeuThrAlaGlnPhe 1822
 Db 5461 TGCTACAACACGGTCATCTCGCCTATCTTGTGTGCTTCTGTGCTGACGCGCCAGTTC 5520
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 Db 5521 GTGCTAGTCAACGTTGGTGTGCTGCTGATGAAGCACCTGGAGGAGAGCAACAGGAG 5580
 Qy 1843 AlaLysGluGluAlaGluLeuGluAlaGluLeuGluMetLysThrLeuSerPro 1862
 Db 5581 GCCAAGGAGGAGGCGAGCTAGAGGCTGAGCTGGAGTGGAGATGAAGACCTCAGCCCC 5640
 Qy 1863 GlnProHisSerProLeuGlySerProPheLeuTirpProGlyValGluGlyProAspSer 1882
 Db 5641 CAGCCCCACTCGCCACTGGGCGAGCCCTTCTCTGGCTGGGGTCGAGGGCCCCGACAGC 5700
 Qy 1883 ProAspSerProLysProGlyValAlaLeuHisProAlaAlaHisAlaArgSerAlaSerHis 1902
 Db 5701 CCCGACAGCCCCAACCTGGGGCTTCGACCCAGCGGCCACGCGAGATGACGCTCCAC 5760
 Qy 1903 PheSerLeuGluHisProThr----- 1909
 Db 5761 TTTTCCCTGGAGCACCCACCGACGAGCAGGCGAGCTGTTTGACACCATATCCCTGCTGATCCAG 5820
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 Db 5941 ATGGAGGCTCTGCTCTGACGTCAGAGATTGTGTCTGAACCGCTGCTGCTCTCTAGCTCTG 6000
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 Db 6061 ATGACGCCCCCACCACCGAGCTGCCAGGACGAGCTTACTGACTGTGGGAAGTCTGGG 6120
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 Db 6121 GTACAGCGAAGCGACTCTCTGCCAATGACAGCTACATGTGTGCGCATGGAGACTGCC 6180
 Qy 1950 GluGlyProLeuGlyHisArgGlyTirpGlyLeuProLysAlaGlnSerGlySerValLeu 1969
 Db 6181 GAGGGGCGCTGGGACACAGGGGCTGGGGCTCCCCNAAGCTCAGTCAGGCTCCGCTCTG 6240
 Qy 1970 SerValHisSerGlnProAlaAspThrSerTyrIleLeuGlnLeuProLysAspAlaPro 1989
 Db 6241 TCCGTTTACTCCAGCCAGCAGATACAGCTATCATCTGCGAGCTTCCCAAAGATGCACCT 6300
 Qy 1990 HisLeuLeuGlnProHisSerAlaProThrTirpGlyThrIleProLysLeuProProPro 2009
 Db 6301 CATCTGCTCCAGCCCCACAGCGCCCACTGGGGGACCATCCCAAACTGCCCCCCACCA 6360
 Qy 2010 GlyArgSerProLeuAlaGlnArgProLeuArgArgGlnAlaAlaIleArgThrAspSer 2029

Db 6361 GGACGCTCCCTTTGGCTCAGAGGCCACTCAGGCGCCAGGCGAGCAATAAGGACTGACTCC 6420
Qy 2030 LeuaspValGlnGlyLeuGlySerArgGluaspLeuAlaGluValSerGlyProSer 2049
Db 6421 TTGGACGTTACGGGCTCTGGGAGCGGGAACACCTCTGTCGAGAGGAGTGGTGGGCGCTCC 6480
Qy 2050 ProProLeuAlaArgAlaTySerPheTrpGlyGlnSerSerThrGlnAlaGlnHis 2069
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Qy 2070 SerArgSerHisSerLysHisSerLysHisMetThrProProAlaProCysProGlyPro 2089
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Qy 2090 GluProLanTrpGlyLysGlyProProGluThrArgSerSerLeuGluLeuAspThrGlu 2109
Db 6601 GAACCCAACTGGGCAAGGCGCTCCAGAGACCAAGACAGCTTAGAGTTGGACACGGAG 6660
Qy 2110 LeuSerTrpLeuSerGlyAspLeuProProGlyGlnGluProProSerPro 2129
Db 6661 CTGAGCTGGATTTTCAAGAGACTCTCTGCGGCTGGCGGCGAGGAGGCCCTCCCA 6720
Qy 2130 ArgAspLeuLysCysTySerValGluAlaGlnSerCysGlnArgProThrSer 2149
Db 6721 CGGACCTGAAGAGTGTACAGCGTGGAGGCCAGAGCTGCCAGCGCGGCTACGCTCC 6780
Qy 2150 TrpLeuaspGluGlnArgArgHisSerIleAlaValSerCysLeuAspSerGlySerGln 2169
Db 6781 TGGCTGGATGACGAGAGGAGACTCTATCGCGCTCAGCTGCTGGAGCAGCGGCTCCAA 6840
Qy 2170 ProHisLeuGlyThrAspProSerAsnLeuGlyGlnProLeuGlyGlyProGlySer 2189
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Db 6901 CGGCCCCAAGAAAACCTCAGCGCGCTAGTATCACCATAGACCCCGCCGAGCCAGCT 6960
Qy 2210 ProArgThrProProSerProGlyLysCysLeuArgArgAlaProSerSerAspSer 2229
Db 6961 CCTCGACCCCGCCAGCGCTTGGTATCTGCTCGGAGGAGGCTCGCTCCAGCGACTCC 7020
Qy 2230 LysAspProLeuAlaSerGlyProProAspSerMetAlaAlaSerProSerProLys 2249
Db 7021 AAGATCCCTTGGGCTCTGGGCGGCTTACAGCATGCTGCTCGGCGGAGGCTCGCTCC 7080
Qy 2250 AspValLeuSerLeuSerGlyLeuSerSerAspProAlaAspLeuAspPro 2266
Db 7081 GATGTGCTGAGTCTCTCGGTTTATCTCTCAGCCAGCAGACTGGACCC 7131

RESULT 2

US-10-757-262-15
; Sequence 15, Application US/1075262
; Publication No. US20040197825A1
; GENERAL INFORMATION:
; APPLICANT: Karicheti, Venkateswarlu
; APPLICANT: Silos-Santiago, Inmaculada
; APPLICANT: Eliasof, Scott D.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: UROLOGICAL DISORDERS USING 44390, 54181, 211, 5687, 884,
; TITLE OF INVENTION: 1405, 636, 4421, 5410, 30905, 2045, 15405, 18560, 2047,
; TITLE OF INVENTION: 33751, 52872, 14063, 20739, 32544, 43239, 44373, 51164,
; TITLE OF INVENTION: 53010, 16852, 1587, 2207, 22245, 2387, 52908, 69112, 14990,
; TITLE OF INVENTION: 18547, 115, 579, 15985, 15625, 760, 18603, 2395, 2554, 8675,
; TITLE OF INVENTION: 32720, 4809, 14303, 16816, 17827, 32620, 577, 619, 1423,
; TITLE OF INVENTION: 2158, 8263, 15402, 16209, 16386, 21165, 30911, 41897, 1643,
; TITLE OF INVENTION: 2543, 9626, 13231, 32409, 84260, 2882, 8203, 32678 OR
; TITLE OF INVENTION: 55053
; FILE REFERENCE: MPI03-007P1RNMNM
; CURRENT APPLICATION NUMBER: US/10/757,262
; CURRENT FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: US 60/440,318
; PRIOR FILING DATE: 2003-01-15

; PRIOR APPLICATION NUMBER: US 60/444,783
; PRIOR FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: US 60/457,901
; PRIOR FILING DATE: 2003-03-27
; PRIOR APPLICATION NUMBER: US 60/468,775
; PRIOR FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: US 60/471,614
; PRIOR FILING DATE: 2003-05-19
; PRIOR APPLICATION NUMBER: US 60/478,742
; PRIOR FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: US 60/488,529
; PRIOR FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 60/491,156
; PRIOR FILING DATE: 2003-07-30
; PRIOR APPLICATION NUMBER: US 60/499,594
; PRIOR FILING DATE: 2003-09-02
; PRIOR APPLICATION NUMBER: US 60/506,332
; PRIOR FILING DATE: 2003-09-26
; NUMBER OF SEQ ID NOS: 136
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 7648
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(7134)
US-10-757-262-15
Alignment Scores:
Pred. No.: 0 Length: 7648
Score: 11815.50 Matches: 2264
Percent Similarity: 95.29% Conservative: 1
Best Local Similarity: 95.25% Mismatches: 1
Query Match: 99.26% Indels: 111
DB: 18 Gaps: 2
US-09-611-257A-37 (1-2266) x US-10-757-262-15 (1-7648)

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Qy 21 ArgLeuAsnAspLeuSerGlyAlaGlyGlyArgProGlyProGlySerAlaGluLysAsp 40
Db 61 CGGCTCAACGACCTGTCTGGGGCGCGGGCGCGGGCGGGGTCAGCAGAAAAGGAC 120
Qy 41 ProGlySerAlaAspSerGluAlaGluGlyLeuProTyProAlaLeuAlaProValVal 60
Db 121 CCGGGCAGCGCGACTCCGAGCGGAGGGGCTCGGTACCCCGGCTGGCCCGGTGGTT 180
Qy 61 PhePheTyLeuSerGlnAspSerArgProArgSerTrpCysLeuArgThrValCysAsn 80
Db 181 TTCTTCTACTTGAACGAGGACAGCGCGCGGAGCTGGTGTCTCCGACACGGTCTGTAAAC 240
Qy 81 ProTrpPheGluArgIleSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMet 100
Db 241 CCCTGGTTTGAAGCGCATCAGCATGTGGTCTATCTCTCAACTCGCTGACCCCTGGGCATG 300
Qy 101 PheArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPhe 120
Db 301 TTCCGGCGATCGAGGACATCGCTGTGACTCCAGCGGCTCGCGGATCTCTGAGGCCCTTT 360
Qy 121 AspAspPheIlePheAlaPhePheAlaValGluMetValValLysMetValAlaLeuGly 140
Db 361 GATGACTTCTCTTTGCTCTCTTTGCGCGTGGAGATGGTGGTGAAGATGTTGGCCTTGGC 420
Qy 141 IlePheGlyLysLysCysTyLeuGlyAspThrTrpAsnArgLeuAspPheIleVal 160
Db 421 ATCTTTGGGAAAAAGTGTGTACTCTGGAGACACTTTGGAAACCGGCTTTGATCTTTTCATC 480
Qy 161 IleAlaGlyMetLeuGluTySerLeuAspLeuGlnAsnValSerPheSerAlaValArg 180

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181 ThrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeu 200 Qy
541 ACAGTCCGTGTGTCCAGCGCTCAGGCGCATTAACCGGGTCCAGCATGCGCATCCTT 600 Db
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601 GTCAAGT 660 Db
221 ValPhePheIlePheGlyIleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArg 240 Qy
661 GTCTTCTTCACTTCGGCATCGTCCGCTGAGCTGTGGCAGGGCTGTCTGGAAACCGA 720 Db
241 CysPheLeuProGluAsnPheSerLeuProLeuSerValAspLeuGluArgTyrTyrGln 260 Qy
721 TGTCTTCTACCTGAGAAATTCAGCCTCCCTGAGCGTGGACCTGGAGCGCTATTACCAG 780 Db
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781 ACAGAGAACGAGGATGAGAGCGCTTCACTGTCTCCAGCCACCGCAGAACGGCATGCGG 840 Db
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841 TCCTGCAGAGCTGCCACGCTGCGGGGACGGGGCGGTGGCCCACTTGGGTCTG 900 Db
301 AspyrGluAlaTyrAsnSerSerSerAsnThrThrCysValAsnTrpAsnGlnTyrTyr 320 Qy
901 GACTATGAGCGCTACACAGCTCCAGCAACACCACTGTGTCACTGGAAACGATCTAC 960 Db
321 ThrAsnCysSerAlaGlyGluHisAsnProPheIleGlyAlaIleAsnPheAspAsnIle 340 Qy
961 ACCAACTGTCTACGGGGGAGCACAACCCCTTCAAGGGCGCATCACTTGGACCAATT 1020 Db
341 GlyTyrAlaTrpIleAlaIlePheGlnValIleThrLeuGluGlyTrpValAspIleMet 360 Qy
1021 GGCTATGCTGATGCCATCTTCCAGGTCACTACGCTGGAGGGGTGGGTGCATCATG 1080 Db
361 TyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuIleIle 380 Qy
1081 TACTTTGTGATGGATGCTCATTTCTTCTACAAATTCATCTACTTCACTTCTCTCATCATC 1140 Db
381 ValGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGlu 400 Qy
1141 GTGGGCTCTCTTTCATGATCAACCTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGT 1200 Db
401 ThrLysGluArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAla 420 Qy
1201 ACCAAGCAGCGGAAAGCCAGCTGATGCGGGAGCAGCGTGTGCGGTTCCTGTCCAAAGCC 1260 Db
421 SerThrLeuAlaSerPheSerGluProGlySerCysTyrGluLeuLeuLysTyrLeu 440 Qy
1261 AGCACCTGTGGTAGCTTCTCTGAGCCCGCAGCTGTGTATGAGAGCTGTCAAGTACCTG 1320 Db
441 ValTyrIleLeuArgLysAlaAlaArgArgLeuAlaGlnValSerArgAlaIleGlyVal 460 Qy
1321 GTGTACATCTTCTGTAAAGCAGCCCGCAGGCTGGCTCAGGTCTCTGCGGCAGCAGGTGTG 1380 Db
461 ArgValGlyLeuLeuSerSerProAlaProLeuGlyGlyGlnGluThrGlnProSerSer 480 Qy
1381 CGGGTGTGGGTGTCTACAGCCCGCAGCAGCCCTCGGGGGCCAGGAGACCCAGCCAGCAGC 1440 Db
481 SerCysSerArgSerHisArgArgLeuSerValHisIleLeuValHisIleHisHis 500 Qy
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501 HisHisHisHisTyrHisIleGlyAsnGlyThrLeuArgAlaProArgAlaSerProGlu 520 Qy
1501 CATCACCAACCATACCACTTGGGCAATGGGACCTCAGGGCCCCCGGGCCAGCCCGGAG 1560 Db
521 IleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProSerThrPro 540 Qy
1561 ATCCAGGACAGGATGCAATGGTCCCGCAGGCTCATGTGTGCAGCAACCCCTCGAGCGCT 1620 Db

541 AlaLeuSerGlyAlaProProGlyGlyAlaGluSerValHisSerPheTyrHisAlaAsp 560 Qy
1621 GCCCTTCCGGGGCCCCCTTGTGTGGCGCAGAGTCTGTGCACAGCTTCTTACCATGCGCAC 1680 Db
561 CysHisLeuGluProValArgCysGlnAlaProProProArgSerProSerGluAlaSer 580 Qy
1681 TGCCACTTAGAGCCAGTCCGCTGCCAGCGCCCCCTCCAGGTCCCATCTGAGGCAATCC 1740 Db
581 GlyArgThrValGlySerGlyLysValTyrProThrValHisThrSerProProGlu 600 Qy
1741 GGCAGACTGTGGGCGAGCGGAGAGGTGTATCCACCGGTGCACACAGCCCTCCACCGGAG 1800 Db
601 ThrLeuLysGluLysAlaLeuValGluValAlaAlaSerSerGlyProProThrLeuThr 620 Qy
1801 ACCTGTAAGGAGGACACTAGTAGAGGTGGTGGCAGCTCTGGGCCCCCAACCTCTACC 1860 Db
621 SerLeuAsnIleProProGlyProTyrSerSerMetHisLysLeuLeuGluThrGlnSer 640 Qy
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641 ThrGlyAlaCysGlnSerSerCysLysIleSerSerProCysLeuLysAlaAspSerGly 660 Qy
1921 ACAGTGTCTGCCAAGCTCTTGAAGATCTCCAGCCCTTGTCTGAAAGCAGACAGTGG 1980 Db
661 AlaCysGlyProAspSerCysProTyrCysAlaArgAlaGlyAlaGlyGluValGluLeu 680 Qy
1981 GGCTGTGTCTCAGACAGCTGCCCTTACTGTGCCCGGGCGGGGAGGTGGAGCTC 2040 Db
681 AlaAspArgGluMetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAla 700 Qy
2041 GCGACCGGTGAATGCTGACTCAGACAGGAGGAGCTTATGAGTTTACACAGAGATGCC 2100 Db
701 GlnHisSerAspLeuArgAspProHisSerArgArgGlnArgSerLeuGlyProAspAla 720 Qy
2101 CAGCAGACGACCTCCGGGACCCCAACAGCGCGCGCAACGAGGCTGGGCCAGATGCA 2160 Db
721 GluProSerSerValLeuAlaPheTrpArgLeuIleCysAspThrPheArgLysIleVal 740 Qy
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2281 GGCATCGAATACCAGCAGCAGCGCGGAGCTTACCACGCCCTAGAAATCAGCAATC 2340 Db
781 ValPheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuValTyrGlyProPhe 800 Qy
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2521 GTGTGAAGCTGTGTGCTTCTTCCCGCGCTGCAGCGGAGCTGGTGGTGCATGAAG 2580 Db
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881 IleLeuGlyMetHisLeuPheGlyCysLysPheAlaSerGluArgAspGlyAspThrLeu 900 Qy
2641 ATCTTGGCATGTCATCTCTTGGCTGCAAGTTTGCCTCTGAGCGGGATGGGGACACCTGTG 2700 Db

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 3944 TGGCAAGTCTGCTCAGGGCCCTTGGCCGGGCTCTGCGGCTGATGACCCCTTGGG 4003
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 1240 eArgAlaArgLeuProAlaCysTyrLeuGluArgAspSerTrpSerAlaTyrIlePhePr 1260
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QY 1260 oProGlnSerArgPheAraGluLeuCysHisArgIleThrHisLysMetPheAspHi 1280
DB 4124 TCCTCAGTCCAGGTTCCGCCCTCCTGTGTACCGGATCATCCACAGAGATGTTGACCA 4183
QY 1280 sValValLeuValIlePheLeuAasnCysIleThrIleAlaMetGluArgProLysIl 1300
DB 4184 CGTGGCTCTGTGCATCATCTTCTTAAGTGCATCATCCATCCGATGGAGCGCCCAAT 4243
QY 1300 eAspProHisSerAlaGluArgIlePheLeuThrLeuSerAsnThrIlePheThrAlaVa 1320
DB 4244 TGACCCCCACAGCGGTGAACGCATCTTCTGACCCCTCTCCAATTACATCTTTCACCGCAGT 4303
QY 1320 lPheLeuAlaGluMetThrValLysValValAlaLeuGlyTrpCysPheGlyGluGlnAl 1340
DB 4304 CTTTCTGGCTGAAATGACAGTGAAGGTGGTGGCACTGGGCTGGTGGTGGGAGCAGGC 4363
QY 1340 aTyrLeuArgSerSerTrpAsnValLeuAspGlyLeuLeuValLeuIleSerValIleAs 1360
DB 4364 GTACTCGGAGCAGTGGAGCGTGTGGACGGCTGTGTGTGTCTCATCTCCGTATCGA 4423
QY 1360 pIleLeuValSerMetValSerAspSerGlyThrLysIleLeuGlyMetLeuArgValLe 1380
DB 4424 CATTCGTGTCTCATGTCTCTGACAGCGGCACCAAGATCTCGGCATGCTGAGGGTGCT 4483
QY 1380 uArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeuLysLe 1400
DB 4484 CGCGCTGCTGGGACCCCTCGCCCGCTCAGGGTGATCAGCGCGGCAGCGGGCTGGAAGCT 4543
QY 1400 uValValGluThrLeuMetSerSerLeuLysProIleGlyAsnIleValValIleCysCy 1420
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QY 1420 sAlaPhePheIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPhePheVa 1440
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QY 1440 lCysGlnGlyGluAspThrArgAsnIleThrAsnLysSerAspCysAlaGluAlaSerTy 1460
DB 4664 GTGCCAGGCGGAGATACAGGAACATCCCAATAATCGGACTGTGCCGAGGCGCAGTTA 4723
QY 1460 rArgTrpValArgHisLysTyrAsnPheAspAsnLeuGlyGlnAlaLeuMetSerLeuPh 1480
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QY 1633 hrValIlePheValLeuGluSerValPheLysLeuValAlaPheGlyPheArgArgPheP 1653
DB 5264 CTGTTCATCTTGTCTTGGAGTCAGTTTTCAAACTTGTGGCCTTGTGGTTCTCGTGGTTCT 5323
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DB 5324 TCCAGGACAGTGAACAGCTGACCTGGCCATTGTGCTGTCTCCATCATGAGGCATCA 5383
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QY 1870 erProPheLeuTrpProGlyValGluGlyProAspSerProAspSerProLysProGlyA 1890
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QY 1909 ----- 1909
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QY 1909 ----- 1909

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Qy	1910	-----MetGlnProHisProThrGlu	1916
Db	6344	GACATGCACACACTCTTACTTAGTGCCTGGAGAGCAATATGACGCCGCCACCCACCGAG	6403
Qy	1917	LeuProGlyProAspLeuThrValArgIysSerGlyValSerArgThrHisSerLeu	1936
Db	6404	CTCCAGAGCCAGACTTACTGACTGTGGGAAAGTCTGGGGTCAGCCGAAACCACTCTCTG	6463
Qy	1937	ProAsnAspSerTyrMetCysArgHisGlySerThrAlaGluGlyProLeuGlyHisArg	1956
Db	6464	CCCAATGACAGCTACATGTGTGGCATGGAGCACTGCCGAGGGGCCCTCGGACACAGG	6523
Qy	1957	GlyTyrGlyLeuProIlysalGlnSerGlySerValLeuSerValHisSerGlnProAla	1976
Db	6524	GGCTGGGGGCTCCCAAGCTCAGTCAGGCTCGCTTGTGCGTTTCATCTCCAGCCAGCA	6593
Qy	1977	AspThrSerTyrIleLeuGlnLeuProIlyAspAlaProHisLeuLeuGlnProHisSer	1996
Db	6584	GATACCAAGCTACATCTGAGCTTCCCAAGATGCACCTCATCTCTCCAGCCCCACAGC	6643
Qy	1997	AlaProThrTyrGlyThrIleProIlyLeuProProGlyArgSerProLeuAlaGln	2016
Db	6644	GCCTCAACCTGGGGCCACCATCCCAACTGCCCCACAGGAGCTCCCTTTGGCTCAG	6703
Qy	2017	ArgProLeuArgArgGlnAlaAlaIleArgThrAspSerLeuAspValGlnGlyLeuGly	2036
Db	6704	AGGCCACTCAGGGCCGACGAGCAGCAATPAGACTGACTCTCTTGACGTTCCAGGTCGGC	6763
Qy	2037	Ser-ArgGluAspLeuLeuAlaGluValSerGlyProSerProProLeuAlaArgAlaTyr	2056
Db	6764	AGCCGGGAAGACCTGCTGGCAGAGGTGAGTGGGCCCTCCCGCCCTTGGCCCGGCCCTA	6823
Qy	2056	rSerPheTyrGlyGlnSerSerThrGlnAlaGlnHisSerArgSerHisSerIleI	2076
Db	6824	CTCTTTCTGGGGCCAGTCAAGTACCAGCAGCAGCAGCACTCCGACGCCACAGCAAGAT	6883
Qy	2076	eSerIlyHisMetThrProProAlaProCysProGlyProGluProAsnTyrGlySerG	2096
Db	6884	CTCCAAGCACATGACCCCGCCAGCCCTTCCCGAGGCCAGAACCCAACTGGGGGAAGGG	6943
Qy	2096	yProProGluThrArgSerSerLeuGluLeuAspThrGluLeuSerTyrIleSerGlyAs	2116
Db	6944	CCCTCCAGAGACCAGACAGCTAGAGTTGGACAGCAGAGCTGAGCTGATTTTCAGGAGA	7003
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Db	7004	CTCTCTGCCCCCTGGCGCCAGGAGGAGCCCCCATCCCAACCGGACCTGAAGAAGTGCTA	7063
Qy	2136	rSerValGluAlaGlnSerCysGlnArgArgProThrSerTyrLeuAspGluArgArg	2156
Db	7064	CAGCGTGGAGGCCAGAGCTCCAGCCCGGCCCTAGCTCTGCTGGATGAGCAGAGGAG	7123
Qy	2156	qHisSerIleAlaValSerCysLeuAspSerGly-SerGlnProHisLeuGlyThrAspP	2176
Db	7124	ACACTTATCCCGCTCAGCTGCTGGACGCGGCTCCCAACCCCACTGGGCGACAGACC	7183
Qy	2176	toSerAsnLeuGlyGlyGlnProLeuGlyGlyProGlySerArgProIlyLysLeuS	2196
Db	7184	CCTCTAACTTTGGGGGCCAGGCTCTTGGGGGCCCTGGAGCCGCGCCCAAGAAAACTCA	7243
Qy	2196	exProProSerIleThrIle-AspProProGluSerGlnGlyProArgThrProProSer	2215
Db	7244	GCCCCCTTAGTATACCAATTAGACCCCGCCAGAGCCAGGTCCTCGGACCCCGCCAGC	7303
Qy	2216	Pro-GlyIleCysLeuArgArgAlaProSerSerAspSerIlyAspProLeuAlaSe	2235
Db	7304	CCTGGGTNTCTGCTCCGAGAGGGGCTCCCTCCAGGAGCTCCCAAGGATCCCTTGGCCCT	7363
Qy	2235	xGlyProPro--AspSerMetAlaAlaSerProSerProIlyLysAspValLeuSerLeu	2254

Db	2701	TTGCCAGACCGGAGAAATTTCCGACTCCCTGCTCTGGGCCATCGTCACTGCTTTTTCAGATT	2760	3781	TTTCTCTCTCAGTCAAGGTTTCGTTCTCTCTGTTGTACCGGATCATCAACCCACAAAGATGTTT	3840
Qy	920	LeuThrGlnGluAspTrpAsnLysValLeuTyrAsnGlyMetAlaSerThrSerTrp	939	1279	AspHisValValLeuValIlePheLeuAsnCysIleThrIleAlaMetGluArgPro	1298
Db	2761	CTGACTCAGGAAGACTGGAAATAAGTCTCTACACGGGATGGCTCCACATCGTCTTGG	2820	3841	GACCATGTGGTCTCGTCATCATCTTCTCACTGATATCACCATCGTATGGAGCGCCCC	3900
Qy	940	AlaAlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuLeu	959	1299	LysIleAspProHisSerAlaGluArgIlePheLeuThrLeuSerAsnTyrIlePheThr	1318
Db	2821	GCTGCTCTTTTACTTCATCGCCCTCATGACTTTTGGCACTATGTCTTTTAACTGTCTG	2880	3901	AAAATTGACCCCAACAGCGTGGCGCATCTTCTGACCCCTCTCCAACATACATCTTCACG	3960
Qy	960	ValAlaIleLeuValGluGlyPheGlnAlaGluIleSerLysArgGluAspAlaSer	979	1319	AlaValPheLeuAlaGluMetThrValLysValAlaLeuGlyTyrCysPheGlyGlu	1338
Db	2881	GTGGCCATTTCTGTGAAGGATTCACGACAGAGAAATCGCAACCGGAAGATGCGAT	2940	3961	GCAGTCTTTCTAGCTGAATGACAGTGAAGTGTGTGGACGGTCTGTGTGCTCATCTCGCTC	4020
Qy	980	GlyGlnLeuSerCysIleGlnLeuProValAspSerGlnGlyAlaAsnLysSer	999	1339	GlnAlaTyrLeuArgSerSerTrpAsnValLeuAspGlyLeuLeuValLeuSerVal	1358
Db	2941	GGACAGTTAAGCTGTATTACGTCCTGTCACTCTCAGGGGGAGATGCCACCAAGTCT	3000	4021	CAGGCTTACCTTCGGCAGCAGCTGGAAATGTGTGGACGGTCTGTGTGCTCATCTCGCTC	4080
Qy	1000	GluSerGluProAspPhePheSerProSerLeuAspGlyAspGlyAspArgLysLysCys	1019	1359	IleAspIleLeuValSerMetValSerAspSerGlyThrLysIleLeuGlyMetLeuArg	1378
Db	3001	GAGTCAGAGCCTGATTTCTTTTCGCCAGTGTGGATGTGTATGGGGACAGAAAGCGC	3060	4081	ATCGACATCTCTGCTCCATGGTCTCCGACACGGCCACCAAGATCTTGGCATGCTGAGG	4140
Qy	1020	LeuAlaLeuValSerLeuGlyGluHisProGluLeuArgLysSerLeuProLeu	1039	1379	ValLeuArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeu	1398
Db	3061	TTGGCCCTGTGGTCTTGGGAGAACACCGCGAACTACGAAAGAGCCTTTTGCACCCCTC	3120	4141	GTGCTGGCGTCTCGGACCCCTGGTCCATCTCAGGGTCACTCAGCGGGCCAGGAGCTG	4200
Qy	1040	IleIleHisThrAlaAlaThrProMetSerLeuProLysSerThrThrGlyLeuGly	1059	1399	LysLeuValValGluThrLeuMetSerSerLeuLysProIleGlyAsnIleValIle	1418
Db	3121	ATCATCCATACGGCTGCGACACCATATGTCACTACCAAGAGCTCCAGCACAGGTGTGGG	3180	4201	AGCTGGTGGTAGAGACTCTGATGTCTCAACCCCATTTGGCAACATTTGGTCAAT	4260
Qy	1060	GluAlaLeuGlyProAlaSerArgThrSerSerSerGlySerAlaGluProGlyAla	1079	1419	CysCysAlaPhePheIleIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPhe	1438
Db	3181	GAAGCACTGGCTCTGGCTCTCGAGTACCATGTCAGTGGTGGCTGGAGCT	3240	4261	TGCTGTGCTCTTCTCATCTTTTGGAAATCTTCGGGGTGCAGCTCTTCAAGGGAAGTTC	4320
Qy	1080	Ala---HisGluMetLysSerProSerAlaArgSerSerProHisSerProTrpSer	1098	1439	PheValCysGlnGlyGluAspThrArgAsnIleThrAsnLysSerAspCysAlaGluAla	1458
Db	3241	GGCCACCATGAGATGAATCTCCGCCAAGTGCCTCCGACCTCCCGCACAGTCTCGGAGT	3300	4321	TTCTGTGTGTCAGGTCAGGACACAGGACATCACTAAACAAATCCGACTGCGCTGAGGCC	4380
Qy	1099	AlaAlaSerSerTrpThrSerArgArgSerSerArgAsnSerLeuGlyArgAlaProSer	1118	1459	SerTyrArgTrpValArgHisLysTyrAsnPheAspAsnLeuGlyGlnAlaLeuMetSer	1478
Db	3301	CGGGCAAGCAGCTGGACACGAGCGGCTCCAGCAGAAACAGCTGGCGGGCGGCCCGCAGC	3360	4381	AGCTACCGATGGTCCGGCACCAAGTACAACTTTGACACCTGGCGGCAGGCTCTGATGTC	4440
Qy	1119	LeuLysArgArgSerProSerGlyGluArgArgSerLeuLeuSerGlyGluGlnGlu	1138	1479	LeuPheValLeuAlaSerLysAspGlyTyrValAspIleMetTyrAspGlyLeuAspAla	1498
Db	3361	CTAAACGGAGGAGCCGAGCGGGAGCGAGGTCCCTGCTCTCTGGAGGGCCAGGAG	3420	4441	CTGTTTGTCTGGCTTCCAAAGGATGTTGGTGTGACATCATGTATGATGGCTGATGTC	4500
Qy	1139	SerGlnAspGluGluSerSerGluGluArgAlaSerProAlaGlySerAspHis	1158	1499	ValGlyValAspGlnGlnProIleMetAsnHisAsnProTrpMetLeuLeuTyrPheIle	1518
Db	3421	AGTCAGGATGAGCAGGAAAGTTTCAGAAAGAGGACCGGGCCAGCCAGCGAGTACCAT	3480	4501	GTGGTGTGGATCAGCAGGCCCATCATGAACCAACACCCCTGGATGCTGTACTTCTATC	4560
Qy	1159	ArgHisArgGlySerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeu	1178	1519	SerPheLeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValValGlu	1538
Db	3481	CGCCACAGGGGTTCCTTGGAACTGAGCGGCAAGATTCCTTTGACCTGCTGACACTGTG	3540	4561	TCCTTCTCTCATCTGCTGGCTCTTCTTCTGAAACATGTTTGTGGCGTGGTGGAG	4620
Qy	1179	GlnValProGlyLeuHisArgThrAlaSerGlyArgGlySerAlaSerGlnHisGlnAsp	1198	1539	AsnPheHisLysCysArgGlnHisGlnGluGluAlaArgArgGluGluLys	1558
Db	3541	CAGTGGCGGGCTGCACCGCACAGCCAGCGCGCGGAGCTCTGCTCTGAGCACCAAGAC	3600	4621	AACTTCCATAAGTCACACAGCACAGCAGGAGGAGGAGCGGCGGTGAGGAGAAG	4680
Qy	1199	CysAsnGlyLysSerAlaSerGlyArgLeuAlaArgAlaLeuArgProAspProPro	1218	1559	ArgLeuArgArgLeuGluLysLysArgArg-	1568
Db	3601	TGTAATGGCAAGTCCGCTTCAGGCGGTTTGGCCCGCACCTGAGGACTGATGACCCCAA	3660	4681	CGACTACGAGGCTGGAGAGAAAAGAGAGGAATCTAATGTTGGACGATGTAATGTTCTTC	4740
Qy	1219	LeuAspGlyAspAlaAspAspGluGlyAsnLeuSerLysGlyGluArgValArgAla	1238	1569	-----LysAlaGlnCysLysProTyrTyrSerAspTyrSer	1580
Db	3661	CTGATGGGGATGATGATCAATGATGAGGAAATCTGAGCAAGGGAACATACACAGCC	3720	4741	GGCAGCTCAGCCGCGCTCGCTCAGAGCCCGAGTGCAGGCCCTACTACTCTGACTACTCG	4800
Qy	1239	TrpIleArgAlaArgLeuProAlaCysTyrLeuGluArgAspSerTrpSerAlaTyrIle	1258	1581	ArgPheArgLeuLeuValHisIleSerHisSerHisTyrLeuAspLeuPheIleThr	1600
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Qy	1259	PheProGlnSerArgPheArgLeuLeuCysHisArgIleIleThrHisLysMetPhe	1278	4861	GGTGTCTCGGGCTGAACGTGTGCTCACTATGCGCCATGGAACATTACCAAGCCCGGAGATC	4920


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; EARLIER FILING DATE: 1999-01-27
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 7285
; TYPE: DNA
; ORGANISM: Rattus sp.
US-09-383-894-3

Alignment Scores:
Pred. No.: 0 Length: 7285
Score: 11111.00 Matches: 2135
Percent Similarity: 94.80% Conservative: 35
Best Local Similarity: 93.27% Mismatches: 95
Query Match: 93.34% Indels: 24
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QY 41 ProGlySerAlaAspSerGluAlaGluGlyLeuProTyrProAlaLeuAlaProValVal 60
DB 277 CCGGACGCGGAGTCTCCGAGCGGAGGGGTCTCCGAGTCCCGCGGTACCCCGGTGT 336
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Dbb TTTGGCTACATTAAGATCCCTACAAATCTTTGATGCTGTGTCATTTGGTTCATCAGTGTG 2616
820 TrpGluIleValGlyGlnGlnGlyGlyLeuSerValLeuArgThrPheArgLeuMet 839
Dbb TGGAGAGATTGGGCGCCACAGCAGGAGTGGCTGTGGTGTGGCGACCTTCGCGCTCATG 2676
840 ArgValLeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMet 859
Dbb CGGTGTCTGAAGCTGTGTGCGCTTCTGCGCGCCCTGACGCGCCAGCTGTGGTGTCTCATG 2736
860 LysThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePhe 879
Dbb AAGACCATGGACAACGTGGCCACCTTCTGTCATGCTCTCTCATGCTTCTCATCTTCTTC 2796
880 SerIleLeuGlyMetHisLeuPheGlyCysLysPheAlaSerGluArgAspGlyAspThr 899
Dbb AGCATCTCTGGGCATGCATCTCTTTGGTTGGCAAGTTTCGCATCTGAACCGGATGGGACAG 2856
900 LeuProAspArgLysAsnPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIle 919
Dbb TTGCCAGACCGGAAGAATTTTCGATCTCCCTGCTCTGGGCGCATCGTCATCTTTTCAGATT 2916
920 LeuThrGlnGluAspTrpAsnLysValLeuTyrAsnGlyMetAlaSerThrSerTrp 939
Dbb CTGACTCAGGAAGACTGGAATAAGTCTCTACACCGGATGGCTCCACATCTCTTGG 2976
940 AlaAlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuLeu 959
Dbb GCTGCTCTTTACTTTCATCGCCCTCATGACTTTTGGCAACTATGTGTCTTTTAACTCTGTG 3036
960 ValAlaIleLeuValGluGlyPheGlnAlaGluGluIleSerLysArgGluAspAlaSer 979
Dbb GTGGCCATCTTGTGGAGGATTCAGGACAGAGAAATCGGCAACCGGGAAGATGCGAGT 3096
980 GlyGlnLeuSerCysIleGlnLeuProValAspSerGlnGlyGlyAspAlaAsnLysSer 999
Dbb GGACAGTTAAGCTGTATTACGTGCTGCTCAACTCTCAGGGGGGAGATGCCACCAAGTCT 3156

1000 GluSerGluProAspPhePheSerProSerLeuAspGlyAspGlyAspArgLysCys 1019
Dbb GAGTCAGAGCCTGATTTCTTTTCGCCAGTGTGATGTTGTTGAGGAGCAGAAAGAGCGC 3216
1020 LeuAlaLeuValSerLeuGlyHisProGluLeuArgLysSerSerLeuLeuProLeu 1039
Dbb TTTGGCCCTGTGGCTTTTGGGAGAACACCGGAACTACGAAAGAGCCTTTTGGCACCCTC 3276
1040 IleIleHisThrAlaAlaThrProMetSerLeuProLysSerThrSerThrGlyLeuGly 1059
Dbb ATCATTCATACCGCTGGCAGACCAATGTCTACCCCAAGAGCTCCAGCAGAGTGTGGG 3336
1060 GluAlaLeuGlyProAlaSerArgThrSerSerSerGlySerAlaGluProGlyAla 1079
Dbb GAAGCATCTGGGCTCTGGCTCTCGACGTACCAAGTAGCAGTGGGTCTCGCTGAGCCTGGAGCT 3396
1080 Ala---HisGluMetLysSerProProSerAlaArgSerSerProHisSerProTrpSer 1098
Dbb GCCCACCATGAGATGAATCTCCGCCAAGTCCCGCAGCTCCCGCAGCAGTCCCTGGAGT 3456
1099 AlaAlaSerSerTrpThrSerArgSerSerArgAsnSerLeuGlyArgAlaProSer 1118
Dbb CGGCAAGCAGCTGGACAGCAGCGCTCCAGCAGGAACAGCTTGGGCGGCGCCCGCCAGC 3516
1119 LeuLysArgSerProSerGlyGluArgArgSerLeuLeuSerGlyGluGlyGlu 1138
Dbb CTAAAGCGGAGGAGCCCGAGCGGGAGCGGAGTCTCTGTCTCTGGAGAGGGCCAGAG 3576
1139 SerGlnAspGluGluGluSerSerGluGluGluArgAlaSerProAlaGlySerAspHis 1158
Dbb AGTCAGATGAGGAGGAAAGTTTCAGAGAGAGACCGGCGCCAGCCAGCAGGAGTGCAT 3636
1159 ArgHisArgGlySerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeu 1178
Dbb CGCCACAGGGGCTCTTTGGAACTGAGGCCAACAGTCTCTTTGACCTGCCTGACACTCTG 3696
1179 GlnValProGlyLeuHisArgThrAlaSerGlyArgGlySerAlaSerGluHisGlnAsp 1198
Dbb CAGGTGCGGGGCTGACCCGACAGCGCGCGGAGCTCTGCTCTCTGACACCAAGAC 3756
1199 CysAsnGlyLysSerAlaSerGlyArgLeuAlaArgAlaLeuArgProAspAspProPro 1218
Dbb TGTAAATGGCAAGTCTGGCTTCAGGGCGTTTGGCCCGCACCTGAGGACTGATGACCCCAA 3816
1219 LeuAspGlyAspAspAlaAspAspGluGlyAsnLeuSerLysGlyGluArgValArgAla 1238
Dbb CTGGATCGGATGATGATCAATGATGAGGAAATCTGAGCAAAAGGGAACGATACAGACC 3876
1239 TrpIleArgAlaArgLeuProAlaCysTyrLeuGluArgAspSerTrpSerAlaTyrIle 1258
Dbb TGGGTCTAGATCCCGGCTTCTGCTGTGGCGAGCGAGATTCTCTGCTGGCTATATC 3936
1259 PheProGlnSerArgPheArgLeuLeuCysHisArgIleIleThrHisLysMetPhe 1278
Dbb TTTCTCTCTAGTCAAGTTCTGCTCTGTGTCTCCCGGATCATCATCCACCAAGATGTTT 3996
1279 AspHisValValLeuValIleIlePheLeuAsnCysIleThrIleAlaMetGluArgPro 1298
Dbb GACCATGTGTCTCTCTCATCTCTCAACTGTATCACCATCGCTATGGAGCGGCC 4056
1299 LysIleAspProHisSerAlaGluArgIlePheLeuThrLeuSerAsnTyrIlePheThr 1318
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1319 AlaValPheLeuAlaGluMetThrValLysValValAlaLeuLeuGlyTyrPhePheGlyGlu 1338
Dbb GCAGTCTTTCTAGCTGAATGACAGTGAAGTGTGGCAGCTGGGCTGGTGTGGGGAG 4176
1339 GlnAlaTyrLeuArgSerSerTrpAsnValLeuAspGlyLeuLeuValLeuIleSerVal 1358
Dbb CAGGCTTACCTGGCGCAGCAGCTGGAATGTCTGAGCGGCTTGTGGTGTCTCATCTCGTC 4236
1359 IleAspIleLeuValSerMetValSerAspSerGlyThrLysIleLeuGlyMetLeuArg 1378

Db 4237 ATCGACATCTGGTCTCCATGGTCTCCAGACGGGACCAAGATCTTGGCATGCTGAGG 4296
Qy 1379 ValLeuArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeu 1398
Db 4297 GTGCTGGCTGTGTGGGACCCCTGGCTCCACTCAGGCTCATCAGCGGGCCAGGAGCTG 4356
Qy 1399 LysLeuValValGluThrLeuMetSerSerLeuLysProIleGlyAenIleValIle 1418
Db 4357 AAGCTGGTGTAGAGACTCTGATGTATCCCTCAACCCCAATGGCAATGTGGTCAT 4416
Qy 1419 CysCysAlaPhePheIleIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPhe 1438
Db 4417 TGCCTGCTCTCTTCATCATTTTGGAAATCTCGGGGTGAGCTCTTCAAGGGAAGTTC 4476
Qy 1439 PheValCysGlnGlyGluAspThrArgAsnIleThrAsnLysSerAspCysAlaGluAla 1458
Db 4477 TTCGTGTGTAGGCTGAGGACACCCAGGAACATCACTAACAAATCCGACTCGCTGAGGCC 4536
Qy 1459 SerTyrArgTrpValArgHisLysTyrAsnPheAspAsnLeuGlyGlnAlaLeuMetSer 1478
Db 4537 AGCTACCGATGGGTCCGGCACAGTACAACTTTGCAACCTGGGCCAGGCTCTGATGTC 4596
Qy 1479 LeuPheValLeuAlaSerLysAspGlyTrpValAspIleMetTyrAspGlyLeuAspAla 1498
Db 4597 CTGTTTGTGCTGGCTCCCAAGGATGGTGGCTTCACATCATGATATGATGGCTGGATGCT 4656
Qy 1499 ValGlyValAspGlnGlnProIleMetAsnHisAsnProTrpMetLeuLeuTyrPheIle 1518
Db 4657 GTGGGTGTGGATCAGCAGCCCATCATCAACACACACCCCTGGATGCTGCTATATCTTCATC 4716
Qy 1519 SerPheLeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValValValGlu 1538
Db 4717 TCCCTTCTCTCTCATCTGGCCCTCTTGTCTCTGAACATGTTTGTGGCGTGGTGGAG 4776
Qy 1539 AsnPheHisLysCysArgGlnHisGlnGluGluAlaArgArgGluGluLys 1558
Db 4777 AACTTCCATAAAGTCAGACAGCACCAGGAGGAGGAGGCGGCGCTGAGGAGAAG 4836
Qy 1559 ArgLeuArgArgLeuGluLysLysArgArg 1568
Db 4837 CGACTACGGAGGCTGGAGAAAAGAGAAGGAATCTAATGTTGGAGGATGTAATGCTTCC 4896
Qy 1569 -----LysAlaGlnCysLysProTyrTyrSerAspTyrSer 1580
Db 4897 GCGACTCAGCCAGCGCTGGCTCAGAACGCCAGTGCAGAGCCCTACTACTCTGACTACTCG 4956
Qy 1581 ArgPheArgLeuLeuValHisLysLeuCysThrSerHisTyrLeuAspLeuPheIleThr 1600
Db 4957 AGATTCGGCTCTCTTGTCCACCATCTGTACCAAGCCACTACCTGGACCTCTTCATCACT 5016
Qy 1601 GlyValIleGlyLeuAsnValValThrMetAlaMetGluHisTyrGlnGlnProGlnIle 1620
Db 5017 GGTGTATCGGCTGAACTGTGCTACTATGGCCATGGACATACCAGCAGCCCAAGATC 5076
Qy 1621 LeuAspGluAlaLeuLysLysCysAsnTyrIlePheThrValIlePheValLeuGluSer 1640
Db 5077 CTGGAGGAGGCTCTGAAGATCTGCAATACATCTTTACCGTCATCTTGTCTTTGAGTCA 5136
Qy 1641 ValPheLysLeuValAlaPheGlyPheArgArgPheGlnAspArgTrpAsnGlnLeu 1660
Db 5137 GTTTTCAAACTTGTGGCTTTGGCTTCGCGCGTTCCTCCAGGACAGGTGGAAACAGCTG 5196
Qy 1661 AspLeuAlaIleValLeuLeuSerIleMetGlyIleThrLeuGluGluIleGluValAsn 1680
Db 5197 GACCTGGCTATTGTGCTTCTGTCCATCATGGGCATCAGCTGAGGAGATGAGGTCAAT 5256
Qy 1681 AlaSerLeuProIleAsnProThrIleIleArgIleMetArgValLeuArgIleAlaArg 1700
Db 5257 GCTTCGCTGCCATCAACCCCAACCATCATCCGTATCATGAGGGTGTCCGCAATGCTCGA 5316
Qy 1701 ValLeuLysLeuLeuLysMetAlaValGlyMetArgAlaLeuAspThrValMetGln 1720

Db 5317 GTTCTGAAGCTGTTGAAGATGGCTGTGGGCATGCGGGCACCTGTGGACACCGGTGATGCAG 5376
Qy 1721 AlaLeuProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPhePheIlePheAla 1740
Db 5377 GCGCTGCCCGCAGGTGGGAACTTGGACTTCTTTCATGTTATGTTTTCATCTTGCAC 5436
Qy 1741 AlaLeuGlyValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGluGly 1760
Db 5437 GCTCTGGCGCTGGAGCTCTTTGGAGACCTGGAGTGTGATGAGACACACCTTGTGAGGCG 5496
Qy 1761 LeuGlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgVal 1780
Db 5497 TTGGGTTCGCGATGCCACCTTTAGGAACCTTGGATGGCCCTTTCGACCCCTTTCGAGTC 5556
Qy 1781 SerThrGlyAspAsnTrpAsnGlyIleMetLysAspThrLeuArgAspCysAspGlnGlu 1800
Db 5557 TCCACTGTGTGACAACTGGAACTGGTATTATGAAGGACACCTCCGGGACTGTGACAGGAG 5616
Qy 1801 SerThrCysTyrAsnThrValIleSerProIleTyrPheValSerPheValLeuThrAla 1820
Db 5617 TCCACTGTCTACACACTGTCTATCTCCCTATCTACTTGTGTCTCTTGTCTGCTGCGGCC 5676
Qy 1821 GlnPheValLeuValAsnValValIleAlaValLeuMetLysHisLeuGluGluSerAsn 1840
Db 5677 CAGTTTGTGCTGTCAACGTGTCTAGCTGTGATGAAGCACCTTGAAGAAAGCAAC 5736
Qy 1841 LysGluAlaLysGluGluAlaGluLeuGluAlaGluLeuGluLeuMetLysThrLeu 1860
Db 5737 AAAGAGCCCAAGGAGGAGGCGGAGCTCGAGGCGGAGCTGGAGCTGGAGATGAAGCGCTC 5796
Qy 1861 SerProGlnProHisSerProLeuGlySerProPheLeuTrpProGlyValGluGlyPro 1880
Db 5797 AGCCCGCAGCCCACTCCCGCTGGGCAGCCCTTCTCTGGCCCCGGGTGGAGGTGTCTC 5856
Qy 1881 AspSerProAspSerProLysProGlyAlaLeuHisProAlaAlaHisAlaArgSerAla 1900
Db 5857 AACACTCTCGACAGCCCTAAGCTCTGGGCTCCACACACACCTGCCACATTGGAGCAGCC 5916
Qy 1901 SerHisPheSerLeuGluHisProThrMetGlnProHisProThrGluLeuPro----- 1918
Db 5917 TCGGGCTTCTCCCTTGGACACCCACGATGGTACCCACCCCGGAGGAGGTGCCAGTCCCC 5976
Qy 1919 ---GlyProAspLeuLeuThrValArgLysSerGlyValSerArgThrHisSerLeuPro 1937
Db 5977 CTAGGACCAAGCTGTCTGCTGAGGAACTGTGGTGTGAGCGGAGCAGCATCTCTGCGCC 6036
Qy 1938 AsnAspSerTyrMetCysArgHisGlySerThrAlaGluGlyProLeuGlyHisArgGly 1957
Db 6037 AATGACAGCTACATGTGCCCAATGGAGCACTGTCTGAGAGATCCCTTAGGACACAGGGGC 6096
Qy 1958 TrpGlyLeuProLysAlaGlnSerGlySerValLeuSerValHisSerGlnProAlaAsp 1977
Db 6097 TGGGGGCTCCCAAGCCAGTCAGGCTCCATCTTGTTCGTTTCACTCCCAACACGAGAC 6156
Qy 1978 ThrSerTyrIleLeuGlnLeuProLysAspAlaProHisLeuLeuGlnProHisSerAla 1997
Db 6157 ACCAGCTGCATCTCAGCTTCCCAAGATGTCACATATCTGTCTCCAGCTCATGGGCGC 6216
Qy 1998 ProThrTrpGlyThrIleProLysLeuProProGlyArgSerProLeuAlaGlnArg 2017
Db 6217 CCCACTGGGGCGCATCTCCCTAAACTACCCCACTGGCCGCTCCCTCTGGCTCAGAGG 6276
Qy 2018 ProLeuArgGlnAlaAlaIleArgThrAspSerLeuAspValGlnGlyLeuGlySer 2037
Db 6277 CCTCTAGGGCGCCAGGAGCAATAGGACTGATCCCTCGATGTGAGGCGCTGGGTAGC 6336
Qy 2038 ArgGluAspLeuLeuAlaGluValSerGlyProSerProProLeuAlaArgAlaTyrSer 2057
Db 6337 CGGGAAGCCCTGTGTGAGAGGTGAGTGGGCCCTCTCTGCCCTCTGTACCCGCTCTCATCC 6396
Qy 2058 PheTrpGlyGlnSerSerThrGlnAlaGlnHisSerArgSerHisSerLysIleSer 2077
Db 6397 TTCTGGGGCGGCTGAGCATCCAGGTGACGAGGTTCCGGGCATCCAGACGAAAGTCTTCC 6456

Db	1194	TACTTCGTAATGGACGCTCACTCTTCTACAACTTCACTTCACTTCTTCTCACTC	1253	Db	2274	GCAGAGCCTAGTCTGTGCTGGCTTTCTGGAGGCTGATCTGTGACACATTCGCGAAGATC	2333
Qy	381	ValGlySerPhePheMetIleAanLeuCysLeuValValIleAlaThrGlnPheSerGlu	400	Qy	740	ValAspSerIleValPheGlyArgGlyIleMetIleAlaIleLeuValAanThrLeuSer	759
Db	1254	GTGGGCTCTCTTTCATGATCAACCTGTGCTGGTGGTATTGCCAGGAGTTCCTCCGAG	1313	Db	2334	GTAGATAGCAAAATCTTTGGCCGGGGAATCATGATCGCCATCTTGGTCAATACACTCAGC	2393
Qy	401	ThrIysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAanAla	420	Qy	760	MetGlyIleGluTyrHisGluGlnProGluGluLeuThrAanAlaLeuGluIleSerAsn	779
Db	1314	ACCAAAACAGCGGAGAGTACGTGATGCGGGAGCAGCGGTACGATTCCTGTCCAATGCT	1373	Db	2394	ATGGCATCGAGTACCACGAGCAGCCGAGGAGCTCACCAACGCCCTGGAAATCAGCAAC	2453
Qy	421	SerThrLeuAlaSerPheSerGluProGlySerCysTyrGlnGluLeuLeuIleValLeu	440	Qy	780	IleValPheThrSerLeuPheAlaLeuMetLeuLeuIleValLeuValTyrGlyPro	799
Db	1374	AGCACCTTGGCAAGCTTCTCTGAGCCAGGAGCTGCTATGAGGAGCTACTCAAGTACCTG	1433	Db	2454	ATCGCTTTCACAGCCTCTTCGCTTGGAGATGCTGCTGAACCTGTCTACGGTCCC	2513
Qy	441	ValTyrIleLeuArgLysAlaAlaArgArgLeuAlaGlnValSerArgAlaAlaGlyVal	460	Qy	800	PheGlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleValValIleSerVal	819
Db	1434	GTGTACATCTCCGAAAAGCAGCCCGAAGGCTGGCCCGAGCTCTAGGGCTATAGCGGTG	1493	Db	2514	TTTGGCTACATTAAGATCCCTACAACTCTTTGATGGTGTCAITGTGTTCATCAGTGTG	2573
Qy	461	ArgValGlyLeuLeuSerSerProAlaProLeuGlyGlyGlnGlnThrGlnProSerSer	480	Qy	820	TrpGluIleValGlyGlnGlnGlyGlyLeuSerValIleLeuArgThrPheArgLeuMet	839
Db	1494	CGGGCTGGCTGCTCAGCAGCCAGTGGCCCGTAGTGGGCGAGGAGCCCGAGCCAGTGGC	1553	Db	2574	TGGGAGATTGTGGGCGCAGCAGGAGTGGCTGTGGTGTGGGACCTTCGGCTGTGATG	2633
Qy	481	SerCysSerArgSerHisArgArgLeuSerValHisIleLeuValHisHisHisHis	500	Qy	840	ArgValLeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMet	859
Db	1554	AGCTGCACTCGCTCACACCGTCTGCTGTCTCCACACCTGGTCCACCACTCACCAC	1613	Db	2634	CGGGTGTGAACTGGTGGCTTCTCGCGGCCCTGCGAGCCAGCTCGTGGTGTCTCATG	2693
Qy	501	HisHisHisIleTyrHisLeuGlyAsnGlyThrLeuArgAlaProArgAlaSerProGlu	520	Qy	860	LysThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePheIlePhe	879
Db	1614	CACCATCACCACTACCACTGGGTAAATGGGACGCTCAGAGTTCCCGGGCGAGCCAGAG	1673	Db	2694	AAAGCATCGACACACGCTGGCCACCTTCTGCATGCTCTCATGCTGTCTTCTCATCTTC	2753
Qy	521	IleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProSerThrPro	540	Qy	880	SerIleLeuGlyMetHisLeuPheGlyCysLysPheAlaSerGluArgAspGlyAspThr	899
Db	1674	ATCCAGGACAGGAGTGCCTGCTGGTCTCGCGGCTCATGCTACCAACCTCTTACACCC	1733	Db	2754	AGCATCTCGGCGATGCACTCTTTGTTGCAAGTTTCGATCTGAACGGGATGGGACACG	2813
Qy	541	AlaLeuSerGlyAlaProProGlyGlyAlaGluSerValHisSerPheTyrHisAlaAsp	560	Qy	900	LeuProAspArgLysAsnPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIle	919
Db	1734	ACTCCCTCTGGGGCCCTCCGAGGGTGGGAGTCTGTACACAGCTTCTACCATGTGAC	1793	Db	2814	TTGCCAGACCGGAAGATTTTCGACTCCCTGCTCTGGGCCATCTGCTACTGTCTTTT	2873
Qy	561	CysHisLeuGluProValArgCysGlnAlaProProProArgSerProSerGluAlaSer	580	Qy	920	LeuThrGlnGluAspTrpAsnLysValIleTyrAsnGlyMetAlaSerThrSerTrp	939
Db	1794	TGCCACTTGGAGCCAGTCCGTTGGCAGGACCCCTCCAGATGCCATCCAGCCCTCCAC	1853	Db	2874	CTGACTCAGGAAGACTGGAATTAAGTCTCTACAAGCGCATGGCTCCACATCGTCTGG	2933
Qy	581	GlyArgThrValGlySerGlyLysValTyrProThrValHisThrSerProProGlu	600	Qy	940	AlaAlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuLeu	959
Db	1854	GGTAGACTGTGGTAGTGGAGGTGTACCCCACTGTGCTATCCAGCCCTCCACACAG	1913	Db	2934	GCTGCTCTTACTTCTATCGCCCTCATGACTTTTGGCACTATGCTCTTTAACTGCTG	2993
Qy	601	ThrLeuLysGluLysAlaLeuValGluValAlaAlaSerSerGlyProProThrLeuThr	620	Qy	960	ValAlaIleLeuValGluGlyPheGlnAlaGluGluIleSerLysArgGluAspAlaSer	979
Db	1914	ATACTGAAGGATAAAGCACTAGTGGAGTGGCGCCCGCCAGCCCTGGGCCCCCCTCAC	1973	Db	2994	GTGGCCATTCTTGTGAAGGATTTCCAGGCGAGAG-----	3026
Qy	621	SerLeuAsnIleProProGlyProTyrSerSerMetHisLysLeuLeuGluThrGlnSer	640	Qy	980	GlyGlnLeuSerCysIleGlnLeuProValAspSerGlnGlyGlyAspAlaAsnLysSer	999
Db	1974	AGCTTCAACATCCACTGGGCCCCCTTCACTCTCATGCAACAGCTCTGGAGACACAGAGT	2033	Db	3027	-----GGAGTGCACCAAGTCT	3044
Qy	641	ThrGlyAlaCysGlnSerSerCysLysIleSerSerProCysLeuLysAlaAspSerGly	660	Qy	1000	GluSerGluProAspPhePheSerProSerLeuAspGlyAspGlyAspArgLysLysCys	1019
Db	2034	ACGGGAGCTGCTCATAGCTCTGCAAAATCTCCAGCCCTTGTCTCCAAAGGACACAGTGA	2093	Db	3045	GAGTCAGAGCTGATTTCTTTTTCGCCCACTGATGGTGTGATGGGACAGAAAGAGCGC	3104
Qy	661	AlaCysGlyProAspSerCysProTyrCysAlaArgAlaGlyValGluValGluLeu	680	Qy	1020	LeuAlaLeuValSerLeuGlyGluHisProGluLeuArgLysSerLeuLeuProProLeu	1039
Db	2094	GCCTGGGGCGGACAGTGTGCTCTGTGCTGCTGGCCGACAGGAGGAGGAGCCAGTCC	2153	Db	3105	TTGGCCCTGGTGGCTTTGGGAGAACACGCGGAATACGAAAGAGCCCTTTGCCACCCCTC	3164
Qy	681	AlaAspArgGluMetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAla	700	Qy	1040	IleIleHisThrAlaAlaThrProMetSerLeuProLysSerThrSerThrGlyLeuGly	1059
Db	2154	GCTGACCATGCTCATGCTGACTCAGACAGGAGGCTGTGTATGAGTTTACACAGGACGCT	2213	Db	3165	ATCATTCATACGGCTGGACACCAATGTCAACCCCAAGAGCTCCAGCACAGGTGTGGGG	3224
Qy	701	GlnHisSerAspLeuArgAspProHisSer---ArgArgGlnArgSerLeuGlyProAsp	719	Qy	1060	GluAlaLeuGlyProAlaSerArgArgThrSerSerSerGlySerAlaGluProGlyAla	1079
Db	2214	CAGCACAGTGACTTCCGGGATCCCCACAGCCGCGCGGACAGCGGAGCTTGGGCCAGAT	2273	Db	3225	GAAGCACTGGGCTCTGGCTCTCGACGTACAGTAGCAGTGGGTCGCTGAGCCCTGGAGCT	3284
Qy	720	AlaGluProSerSerValLeuAlaPheTrpArgLeuIleCysAspThrPheArgLysIle	739	Qy	1080	Ala---HisGluMetLysSerProProSerAlaArgSerSerProHisSerProTrpSer	1098
				Db	3285	GCCCAACATGAGATGAAATGTCCGCCAAGTGGCCGACAGTCCCGCACAGTCCCTGGAGT	3344

1099 AlaAlaSerSerTrpThrSerArgArgSerSerArgAenSerLeuGlyArgAlaProSer 1118
1119 LeuLysArgArgSerProSerGlyGluArgArgSerLeuLeuSerGlyGluGlyGlnGlu 1138
1479 LeuPheValLeuAlaSerLysAspGlyTrpValaAspIleMetTyrAspGlyLeuAspAla 1498
1485 CTGTTTGTGTGGCTCCAGGATGGTTGGGTGTGACATCATGTATGATGGGCTGATGCT 4544
1499 ValGlyValaAspGlnGlnProIleMetAsnHisAsnProTrpMetLeuLeuTyrPheIle 1518
4545 GTGGGTGTGGATCAGCAGCCCATCATGAACACACACACCCCTGGATGCTCTACTTATC 4604
1519 SerPheLeuLeuIleValAlaPhePheValLeuLeuMetPheValGlyValValGlu 1538
4605 TCCCTTCCTCCATCAYCTGGGCTTCTTGTCTGAACATGTTTGTGGGCTGGTGGTGAG 4664
1539 AsnPheHisLysCysArgGlnHisGlnGluGluAlaArgArgGluGluLys 1558
4665 AACTTCCATTAAGTCAGACAGCACACAGGAGGAGGAGGCGGCGGTGAGGAGAAG 4724
1559 ArgLeuArgArgLeuGluLysLysArgArg-----LysAlaGln 1571
4725 CGACTACGGAGGCTGGAGAAAAGAGAGAGTAAGGAGAAAGACAGATGGCCGAGCCAG 4784
1572 CyleysProTyrTyrSerAspTyrSerArgPheArgLeuLeuValHisHisLeuCysThr 1591
4785 TGAAGGCCCTACTACTCTGACTCTCGAGATTCGGGCTCTTGTCCACCATCTGTGTACC 4844
1592 SerHisTyrLeuAspLeuPheIleThrGlyValIleGlyLeuAsnValIleThrMetAla 1611
4845 AGCCACTACCTGGACCTCTTCTCATCTGGTGTCTCATCGGCTGACGCTGCTCATATGGC 4904
1612 MetGluHisTyrGlnGlnProGlnIleLeuAspGluAlaLeuLysIleCysAsnTyrIle 1631
4905 ATGGAACATTACACAGCAGCCAGATCTCTGACGAGGCTCTGAAGATCTGCAATTTACATC 4964
1632 PheThrValIlePheValLeuGluSerValPheLysLeuValAlaPheGlyPheArgArg 1651
4965 TTTACCGCTCATCTTGTCTTTGAGTTCAGTCTTTCACAACTTTGGGCTTTGGCTTCCGCGT 5024
1652 PhePheGlnAspArgTrpAsnGlnLeuAspLeuAlaIleValLeuLeuSerIleMetGly 1671
5025 TTTCTTCCAGGACAGGTGGACACAGCTGGACCTGGCTATTGTGCTTCTCTCATATGGC 5084
1672 IleThrLeuGluGluIleGluValAsnAlaSerLeuProIleAsnProThrIleIleArg 1691
5085 ATCACTTGGAGGAGATTAGGTCAATCTGTCTGCTGCCCATCAACCCACCATCATCGCT 5144
1692 IleMetArgValLeuArgIleAlaArgValLeuLysLeuLysMetAlaValGlyMet 1711
5145 ATCATGAGGGTGTCCCGATTTGCTGAGTTCGAGCTTGAAGCTGTGAAGATGGCTGTGGGATG 5204
1712 ArgAlaLeuLeuAspThrValMetGlnAlaLeuProGlnValGlyAsnLeuGlyLeuLeu 1731
5205 CGGCGCATCTGTGCACACGCTGATGCGGCCCTGCCCCAGGTGGGAACTTGGACTTCTC 5264
1732 PheMetLeuLeuPhePheIlePheAlaLeuGlyValGluLeuPheGlyAspLeuGlu 1751
5265 TTCATGTTATTTGTTTTTTCATCTTTGACGCTCTGGGCGTGGAGCTCTTTGGAGACCTGGAG 5324
1752 CysAspGluThrHisProCysGluGlyArgHisAlaThrPheArgAsnPheGly 1771
5325 TGTATGAGACACACCTTTGTGAGGGCTTTGGTGGGATGCCACCTTTAGGAACCTTTGGT 5384
1772 MetAlaPheLeuThrLeuPheArgValSerThrGlyAspAsnTrpAsnGlyIleMetLys 1791
5385 ATGGCCCTTCTGACCCCTCTTCCGAGTCTCCACTGGTGAACAACCTGGAATGGTATTATGAG 5444
1792 AspThrLeuArgAspCysAspGlnGluSerThrCysTyrAsnThrValIleSerProIle 1811
5445 GACACCTCCGGGACTGTGACGAGGTCCACCTGCTACACACTGTCTATCTCCCTATC 5504
1812 TyrPheValSerPheValLeuThrAlaGlnPheValLeuValAsnValIleAlaVal 1831

Oy 1459 SerTyrArgTrpValArgHisLysTyrAsnPheAspLeuGlyGlnAlaLeuMetSer 1478
Db 4425 AGCTACCGATGGGTCCGGGCAACAAGTACAACTTTTGACAACTGGGGCCAGGCTCTGATGTCC 4484
Oy 1479 LeuPheValLeuAlaSerLysAspGlyTrpValaAspIleMetTyrAspGlyLeuAspAla 1498
Db 4485 CTGTTTGTGTGGCTCCAGGATGGTTGGGTGTGACATCATGTATGATGGGCTGATGCT 4544
Oy 1499 ValGlyValaAspGlnGlnProIleMetAsnHisAsnProTrpMetLeuLeuTyrPheIle 1518
Db 4545 GTGGGTGTGGATCAGCAGCCCATCATGAACACACACACCCCTGGATGCTCTACTTATC 4604
Oy 1519 SerPheLeuLeuIleValAlaPhePheValLeuLeuMetPheValGlyValValGlu 1538
Db 4605 TCCCTTCCTCCATCAYCTGGGCTTCTTGTCTGAACATGTTTGTGGGCTGGTGGTGAG 4664
Oy 1539 AsnPheHisLysCysArgGlnHisGlnGluGluAlaArgArgGluGluLys 1558
Db 4665 AACTTCCATTAAGTCAGACAGCACACAGGAGGAGGAGGCGGCGGTGAGGAGAAG 4724
Oy 1559 ArgLeuArgArgLeuGluLysLysArgArg-----LysAlaGln 1571
Db 4725 CGACTACGGAGGCTGGAGAAAAGAGAGAGTAAGGAGAAAGACAGATGGCCGAGCCAG 4784
Oy 1572 CyleysProTyrTyrSerAspTyrSerArgPheArgLeuLeuValHisHisLeuCysThr 1591
Db 4785 TGAAGGCCCTACTACTCTGACTCTCGAGATTCGGGCTCTTGTCCACCATCTGTGTACC 4844
Oy 1592 SerHisTyrLeuAspLeuPheIleThrGlyValIleGlyLeuAsnValIleThrMetAla 1611
Db 4845 AGCCACTACCTGGACCTCTTCTCATCTGGTGTCTCATCGGCTGACGCTGCTCATATGGC 4904
Oy 1612 MetGluHisTyrGlnGlnProGlnIleLeuAspGluAlaLeuLysIleCysAsnTyrIle 1631
Db 4905 ATGGAACATTACACAGCAGCCAGATCTCTGACGAGGCTCTGAAGATCTGCAATTTACATC 4964
Oy 1632 PheThrValIlePheValLeuGluSerValPheLysLeuValAlaPheGlyPheArgArg 1651
Db 4965 TTTACCGCTCATCTTGTCTTTGAGTTCAGTCTTTCACAACTTTGGGCTTTGGCTTCCGCGT 5024
Oy 1652 PhePheGlnAspArgTrpAsnGlnLeuAspLeuAlaIleValLeuLeuSerIleMetGly 1671
Db 5025 TTTCTTCCAGGACAGGTGGACACAGCTGGACCTGGCTATTGTGCTTCTCTCATATGGC 5084
Oy 1672 IleThrLeuGluGluIleGluValAsnAlaSerLeuProIleAsnProThrIleIleArg 1691
Db 5085 ATCACTTGGAGGAGATTAGGTCAATCTGTCTGCTGCCCATCAACCCACCATCATCGCT 5144
Oy 1692 IleMetArgValLeuArgIleAlaArgValLeuLysLeuLysMetAlaValGlyMet 1711
Db 5145 ATCATGAGGGTGTCCCGATTTGCTGAGTTCGAGCTTGAAGCTGTGAAGATGGCTGTGGGATG 5204
Oy 1712 ArgAlaLeuLeuAspThrValMetGlnAlaLeuProGlnValGlyAsnLeuGlyLeuLeu 1731
Db 5205 CGGCGCATCTGTGCACACGCTGATGCGGCCCTGCCCCAGGTGGGAACTTGGACTTCTC 5264
Oy 1732 PheMetLeuLeuPhePheIlePheAlaLeuGlyValGluLeuPheGlyAspLeuGlu 1751
Db 5265 TTCATGTTATTTGTTTTTTCATCTTTGACGCTCTGGGCGTGGAGCTCTTTGGAGACCTGGAG 5324
Oy 1752 CysAspGluThrHisProCysGluGlyArgHisAlaThrPheArgAsnPheGly 1771
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Oy 1792 AspThrLeuArgAspCysAspGlnGluSerThrCysTyrAsnThrValIleSerProIle 1811
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Oy 1812 TyrPheValSerPheValLeuThrAlaGlnPheValLeuValAsnValIleAlaVal 1831

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 Qy 1932 LeuMetLysHisLeuGluSerAsnLysGluAlaLysGluAlaGluLeuGluAla 1851
 Db 5565 CTGATGAAGCACCCTGGGAAGAACACACAAAGAGCCCAAGAGAGCGCTCGAGGCC 5624
 Qy 1852 GluLeuGluLeuGluMetLysThrLeuSerProGlnProHisSerProLeuGlySerPro 1871
 Db 5625 GAGCTGGAGCTGGAGATGAAGACGCTCAGCCCGCAGCCCACTCCCGCTGGGACGCC 5684
 Qy 1872 PheLeuTrpProGlyValGluGlyProAspSerProAspSerProLysProGlyAlaLeu 1891
 Db 5685 TTCTCTGGCCGGGGTGGAGGTGTCAACAGTACTGACAGCCCTTAAGCCCTGGGGTCCA 5744
 Qy 1892 HisProAlaLysAlaArgSerAlaSerHisPheSerLeuGluHisProThrMetGln 1911
 Db 5745 CACACCCTGCCACATTTGGAGCAGCTCGGGCTTCTCCCTTGAGCACCCACGATGGTA 5804
 Qy 1912 ProHisProThrGluLeuPro-----GlyProAspLeuLeuThrValArgLysSer 1928
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 Qy 1929 GlyValSerArgThrHisSerLeuProAsnAspSerTyrMetCysArgHisGlySerThr 1948
 Db 5865 GGTGTGACCCGAGCAGCATCTCTGCCCAATGACAGCTACATGTCGCGCAATGGGAGCACT 5924
 Qy 1949 AlaGluGlyProLeuGlyHisArgGlyTrpGlyLeuProLysAlaGlnSerGlySerVal 1968
 Db 5925 GCTGAGAGATCCCTAGGACACAGGGGCTGGGGGCTCCCAAAGCCCACTCAGGCTCCATC 5984
 Qy 1969 LeuSerValHisSerGlnProAlaAspThrSerTyrLeuLeuGlnLeuProLysAspAla 1988
 Db 5985 TTGTCCGTCACTCCCAACACAGCACACACAGCTGATCCATCAGCTTCCCAAGATGTG 6044
 Qy 1989 ProHisLeuLeuGlnProHisSerAlaProThrTrpGlyThrLeuProLysLeuProPro 2008
 Db 6045 CACTATCTCTCAGCCTCATGGGCTCCACCTGGGGCGGCATCCCTAAACTACCCCA 6104
 Qy 2009 ProGlyArgSerProLeuAlaGlnArgProLeuArgArgGlnAlaAlaArgThrAsp 2028
 Db 6105 CCTGGCCGCTCCCTCTGGCTCAGAGGCTCTCAGGGCCGAGCAGCAATAGAGCTGAC 6164
 Qy 2029 SerLeuAspValGlnGlyLeuGlySerArgGluAspLeuLeuAlaValSerGlyPro 2048
 Db 6165 TCCTTGATGTGAGGGCTGGGTAGCCGGGAGACCTTGTCTCAGAGTGTGAGTGGGCC 6224
 Qy 2049 SerProLeuAlaAlaArgAlaTyrSerPheTrpGlyGlnSerSerThrGlnAlaGlnGln 2068
 Db 6225 TCCTGCCCTCTGACCCGGTCTCATCTTCTGGGGCGGTCTCAGCATCCAGGTGACGAG 6284
 Qy 2069 HisSerArgSerHisSerLysLysSerLysHisMetThrProAlaProCysProGly 2088
 Db 6285 CGTTCCGGCATCCAGAGCAAGTCTCAAGACATCCGCTGCGAGCCCTTGGCCAGGC 6344
 Qy 2089 ProGluProAsnTrpGlyLysGlyProProGluThrArgSerSerLeuGluLeuAspThr 2108
 Db 6345 CTGGAACCCAGCTGGGCCAAGGACCTCCAGAGACCAAGACAGCTTAGAGCTGGACAG 6404
 Qy 2109 GluLeuSerTrpLysSerGlyAspLeuLeuProProGlyGlyGlnGluGluProProSer 2128
 Db 6405 GAGCTGAGCTGGATTTTCAGAGACCTCTT---CCAGAGCCGAGGAGNACCCCTGTTC 6461
 Qy 2129 ProArgAspLeuLysLysCysTyrSerValGluAlaGlnSerCysGlnArgArgProThr 2148
 Db 6462 CCACGGACCTGAGAGTGTCTACAGTGTAGAGACCCAGAGCTGACGGCGCAGCCCTGGG 6521
 Qy 2149 SerTrpLeuAspGluGlnArgArgHisSerIleAlaValSerCysLeuAspSerGlySer 2168
 Db 6522 TTCTGGCTAGATGAACGCGGAGACACTCCATGTCTGCTGAGCTGTGGACAGCGCTCC 6581
 Qy 2169 GlnProHisLeuGlyThrAspProSerAsnLeuGlyGlyGlnProLeuGlyGlyProGly 2188

6582 CAACCCCGCCTATGTCAAGCCCTCAGCGGGGCCAACCTCTTGGGGGTCTCTGGG 6641
 2189 SerArgProLysLysLysLeuSerProProSerSerIleThrLeuAspProProGluSerGln 2208
 6642 AGCCGGCCTAGAAAAAACTCAGCCCAACCCAGTATCTCTATAGACCCCGGAGAGCCAG 6701
 2209 GlyProArgThrProProSerProGlyLysCysLeuArgArgAlaProSerSerAsp 2228
 6702 GGTCTCGGCCCCCATGCACTCTGTGCTCAGGAGGAGGGCGCGGCGCCAGTGAC 6761
 2229 SerLysAspProLeuAlaSerGlyProProAspSerMetAlaAlaSerProSerProLys 2248
 6762 TCTAAGATCCCTCGTCTCCAGCCCTTGACAGCAGCGTCTCACCCTCCCAAG 6821
 2249 LysAspValLeuSerLeuSerGlyLeuSerSerAspProAlaAspLeuAspPro 2266
 6822 AAAGACGCTGAGTCTCTCTGTGTTGTCTGTGACCAACAGACATGGACCCC 6875

RESULT 7
 US-10-930-301-51
 ; Sequence 51, Application US/10930301
 ; Publication No. US20050026207A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Issa, Jean-Pierre
 ; TITLE OF INVENTION: CACNA1G POLYNUCLEOTIDE POLYPEPTIDE AND
 ; TITLE OF INVENTION: METHODS OF USE THEREFOR
 ; FILE REFERENCE: JHUI590
 ; CURRENT APPLICATION NUMBER: US/10/930,301
 ; PRIOR FILING DATE: 2004-08-30
 ; PRIOR APPLICATION NUMBER: US/09/398,522
 ; PRIOR FILING DATE: 1999-09-15
 ; NUMBER OF SEQ ID NOS: 120
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 51
 ; LENGTH: 3993
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: CACNA1G - a gene encoding a T-type calcium channel
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (373)...(3993)
 ; US-10-930-301-51

Alignment Scores:
 Pred. No.: 0 Length: 3993
 Score: 6315.50 Matches: 1207
 Percent Similarity: 98.13% Conservative: 0
 Best Local Similarity: 98.13% Mismatches: 0
 Query Match: 53.05% Indels: 23
 Gaps: 19 DB:

US-09-611-257A-37 (1-2266) x US-10-930-301-51 (1-3993)

Qy 1 MetAspGluGluAspGlyAlaGlyAlaGluSerGlyGlnProArgSerPheMet 20
 Db 373 ATGACGAGGAGGAGGATGAGCGGGCGCGGAGAGTCGGGACAGCCCGAGGCTTCTG 432
 Qy 21 ArgLeuAsnAspLeuSerGlyAlaGlyGlyArgProGlyProGlySerAlaGluLysAsp 40
 Db 433 CGGTCAACACCTGTCTGGGGCGCGGGGCGCGGGCGGGGTCAGCAGAAAAGGAC 492
 Qy 41 ProGlySerAlaAspSerGluAlaGluGlyLeuProTyrProAlaLeuAlaProVal 60
 Db 493 CCGGCGCGCGGACTCCGAGCGGAGGGGTGCGGTACCGCGGCGTGGCCCGGTGGTT 552
 Qy 61 PhePheTyrLeuSerGlnAspSerArgProArgSerTrpCysLeuArgThrValCysAsn 80
 Db 553 TTCCTTCTACTTGAGCCAGACAGCCCGCGGAGCTGGTGTCTCCGACCGTCTGTAAAC 612
 Qy 81 ProTrpPheGluArgLysSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMet 100
 Db 613 CCCTGGTTGAGCGCATCAGCATGTTGTCTCTTCAACTGCTGCTGACCTCGGCAATG 672

QY 101 PheArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPhe 120
DB 673 TTCGGCCATCGAGGACATCGCTGTGACTCCAGCGCTCCCGGATCCTCGAGCCCTTT 732
QY 121 AspAspPheIlePheAlaPheAlaValGluMetValValIysMetValAlaLeuGly 140
DB 733 GATGACTTCATCTTTCCTCTCTTGGCGTGAGATGGTGGTGAAGATGGTGGCCCTGGGC 792
QY 141 IlePheGlyIysLysCysTyrLeuGlyAspThrTrpAsnArgLeuAspPheIleVal 160
DB 793 ATCTTTGGGAAAAAGTGTACTCGGGACACACTTGGAAACCGCTTGACTTTTTCATCGTC 852
QY 161 IleAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArg 180
DB 953 ATCCGAGGATGCTGGAGTACTCGCTGGACCTGCGAGAACGTCAGCTTCTCAGCTGTCCAGG 912
QY 181 ThrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeu 200
DB 913 ACAGTCCGTGTGTCGACCCGCTCAGGGCCATTAAACGGGTGCCAGCATCGCATCTT 972
QY 201 ValThrLeuLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePhe 220
DB 973 GTCACTGTGCTGGATACGCTGCCATGCTGGCAACGTCCTGCTCTGCTTCTTC 1032
QY 221 ValPhePheIlePheGlyIleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArg 240
DB 1033 GTCTTCTTCATCTTCGGCATCGTCGGCGTCAGCTGTGGCAGGGCTGCTTCGGAACCGA 1092
QY 241 CysPheLeuProGluAsnPheSerLeuProLeuSerValAspLeuGluArgTyrTyrGln 260
DB 1093 TGCTTCTTACCTGAGAAATTCAGCTCTCCCTGAGCGTGGACCTGGAGCGCTATTACGAG 1152
QY 261 ThrGluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArg 280
DB 1153 ACAGAGAACGAGGATGAGAGCCCTTCATCTGCTCCCGACCCAGCGAGAACGGCATCGG 1212
QY 281 SerCysArgSerValProThrLeuArgGlyAspGlyGlyGlyGlyProProCysGlyLeu 300
DB 1213 TCCTGCAAGAACGTGCCACACGCTCGCGGGGACCGGGGCGTGGCCACCTTGGCGTGTG 1272
QY 301 AspTyrGluAlaTyrAsnSerSerAsnThrThrCysValAsnTrpAsnGlnTyrTyr 320
DB 1273 GACTATGAGGCTTACAAACAGCTCCAGCAACACCACTCTGTGTCAACTGGAACAGTACTAC 1332
QY 321 ThrAsnCysSerAlaGlyGluHisAsnProPheLysGlyAlaIleAsnPheAspAsnIle 340
DB 1333 ACCAACTGCTCAGCGGGGAGACACAAACCCCTTCAAGGGCGCCATCACTTTTGACAACTT 1392
QY 341 GlyTyrAlaTrpIleAlaIlePheGlnValIleThrLeuGluGlyTrpValAspIleMet 360
DB 1393 GGCTATGCTGGATCGCCATCTCCAGGTCAATCAGCTGGAGGGCTGGGTGCACATCATG 1452
QY 361 TyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleIle 380
DB 1453 TACTTTGTGATGGATGCTCATCTCTTACAAATTCATCTACTTCACTCTCTCATCATC 1512
QY 381 ValGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGlu 400
DB 1513 GTGGGCTCTTCTTCATGATCAACCTGTGCTGGTGGTGAATGGCCACGCGAGTCTCAGAG 1572
QY 401 ThrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAla 420
DB 1573 ACCAAGCAGCGGAAAGCAGCTGATGCGGAGCAGCGTGTGCGGTCTCTGTCACACGCC 1632
QY 421 SerThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLeuTyrLeu 440
DB 1633 AGCACCTTGGCTAGCTTCTCTGAGCCCGAGCTGCTATGAGGAGCTCTCAAGTACCTG 1692
QY 441 ValTyrIleLeuArgLysAlaAlaArgArgLeuAlaGlnValSerArgAlaAlaGlyVal 460
DB 1693 GTGTACATCTCTCGTAAAGCAGCCCGCAGGCTGGCTCAGGCTCTCTCGGGCAGCAGGTGTG 1752

QY 461 ArgValGlyLeuLeuSerSerProAlaProLeuGlyGlyGlnGluThrGlnProSerSer 480
DB 1753 CGGTTTGGCTGTCTCAGAGCCCGAGCCTCTCGGGGCCAGGAGACCCAGCCAGAGC 1812
QY 481 SerCysSerArgSerHisArgArgLeuSerValHisLeuValHisHisHisHis 500
DB 1813 AGCTGCTCTCGTCCCAACCGCGCTATCGGTCCACCACTGGTGCACCAACCAACCA 1872
QY 501 HisHisHisHisTyrHisLeuGlyAsnGlyThrLeuArgAlaProArgAlaSerProGlu 520
DB 1873 CATCACCACTACCTACCACTGGGCAATGGGACGCTCAGGGCCCCCGGGCCAGCCCGAG 1932
QY 521 IleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProSerThrPro 540
DB 1933 ATCCAGACAGGATGCAATATGGGTCCCGCGCTCATGTGCCACCACTCTCAGCGCT 1992
QY 541 AlaLeuSerGlyAlaProProGlyGlyValAlaGluSerValHisSerPheTyrHisAlaAsp 560
DB 1993 GCGCTCTCGGGGCCCCCTGTGTGGCGCAGAGTCTGTGCACAGCTTCTACCATGCCGAC 2052
QY 561 CysHisLeuGluProValArgCysGlnAlaProProProArgSerProSerGluAlaSer 580
DB 2053 TGCCACTTAGAGCCAGTCCGCTGCCAGCGCGCCCTCCAGGTCCCATCTCTGAGGCACTCC 2112
QY 581 GlyArgThrValGlySerGlyLysValTyrProThrValHisThrSerProProProGlu 600
DB 2113 GGCAGGACTGTGGGCAGCGGAGGTGTATCCCACTGTCACACAGCCCTCCACCGGAG 2172
QY 601 ThrLeuLysGluLysAlaLeuValGluValAlaAlaSerSerGlyProProThrLeuThr 620
DB 2173 ACCTGAGGAGGAGGACACTAGTAGAGTGGTGCAGCTCTGGGCCCCCAACCTCACC 2232
QY 621 SerLeuAsnIleProProGlyProTyrSerSerMetHisLysLeuLeuGluThrGlnSer 640
DB 2233 AGCTCTAACTCCACCGCGGCCCTACAGCTCCATGCACAACTGTGTGAGACACAGAGT 2292
QY 641 ThrGlyAlaCysGlnSerSerCysLysIleSerSerProCysLeuLysLeuAlaAspSerGly 660
DB 2293 ACAGGTGCTGCCAAAGCTCTTGCAGATCTCCAGCCCTTCTGTAAGAGCAGAGTGGG 2352
QY 661 AlaCysGlyProAspSerCysProTyrCysAlaArgAlaGlyAlaGlyValGluLeu 680
DB 2353 GCGTGTGTCAGACAGCTGCCCTACTGTGTCGGCGGGCGGCGGAGGTGGAGCTC 2412
QY 681 AlaAspArgGluMetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAla 700
DB 2413 GCCAGCGTGAATGCTGCTCAGACAGCGAGGAGTATATGAGTTTCAACAGGATGCC 2472
QY 701 GlnHisSerAspLeuArgAspProHisSerArgArgGlnArgSerLeuGlyProAspAla 720
DB 2473 CAGCACAGCGACCTCCGGGACCCCAAGCGCGGCAACGAGCGCTGGGCCCCAGATGCA 2532
QY 721 GluProSerValLeuAlaPheTrpArgLeuIleCysAspThrPheArgLysIleVal 740
DB 2533 GAGCCAGCTCTGTGCTGGCTTCTGGAGGCTAATCTGTGACACTTCCGAAAGATTGTG 2592
QY 741 AspSerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerMet 760
DB 2593 GACAGCAAGTACTTTGGCGGGGAATCATGATGCCATCTCTGGTCAACACACTCAGCATG 2652
QY 761 GlyIleGluTyrHisGluGlnProGluLeuThrAsnAlaLeuGluIleSerAsnIle 780
DB 2653 GGCATCAAGTACCAACGAGCAGCGCGGAGGCTTACCACCGCCCTAGAAATCAGCAACATC 2712
QY 781 ValPheThrSerLeuPheAlaLeuGluMetLeuLysLeuValTyrGlyProPhe 800
DB 2713 GTCTTACCAGCTCTTTGGCTGGAGATGCTGTGAGAGTGTGTGTGTGTGTGTGTGTGT 2772
QY 801 GlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleValIleValIleSerValTrp 820
DB 2773 GGCTACATCAAGATCCCTACCAATCTTCCATGGTGTGATTTGGTTCATCAGCGGTGTG 2832
QY 821 GluIleValGlyGlnGlnGlyGlyLeuSerValLeuArgThrPheArgLeuMetArg 840

Db 2833 GAGATCTGGCGCCAGCAGGGGGCGGCTGTGCGTGTGCGGACCTTCGCGCTGATGCGT 2892
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Db 2893 GTGCTGAAGCTGTGCGCTTCTTCCGCGCGCTGCAGCGGCGAGTGGTGTCTCATGAAG 2952
Qy 861 ThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheLeuPheSer 880
Db 2953 ACCATGACCAAGTGGCGACCTTCTGCATGCTGTATGCTTCTCATCTTCATCTTCAGC 3012
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Qy 941 AlaLeuTyPheIleAlaLeuMetThrPheGlyAsnTyValLeuPheAsnLeuVal 960
Db 3193 GCCCTTTATTTCAATGCTCCCTCATGACCTTGGCACTACGTGCTCTTCAATTTGCTGTC 3252
Qy 961 AlaIleLeuValGluGlyPheGlnAlaGluIleSerLysArgGluAspAlaSerGly 980
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Qy 981 GlnLeuSerCysIleGlnLeuProValAspSerGlnGlyGlyAspAlaAsnLysSerGlu 1000
Db 3283 -----GGAGATGCCAACAGTCCGAA 3303
Qy 1001 SerGluProAspPheSerProSerLeuAspGlyAspArgLysLysCysLeu 1020
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Qy 1081 HisGluMetLysSerProProSerAlaArgSerSerProHisSerProTrpSerAlaAla 1100
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Qy 1101 SerSerTrpThrSerArgArgSerSerArgAsnSerLeuGlyArgAlaProSerLeuLys 1120
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Qy 1121 ArgArgSerProSerGlyGluArgArgSerLeuLeuSerGlyGluGlyGlnGluSerGln 1140
Db 3664 CGGAGAAGCCCAAGTGGAGAGCGGCGTCTGTTGTCCGGAGAGGCGGAGAGCGCAG 3723
Qy 1141 AspGluGluSerSerGluGluArgAlaSerProAlaGlySerAspHisArgHis 1160
Db 3724 GATGAAGAGAGAGCTCAGAGAGAGCGGCGCCGAGCCCTTGGCGGAGTGCACCATGCCAC 3783
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Db 3784 AGGGGTCTCTGAGCGGAGGCGCAAGAGTTCCTTTTCACTTGCAGACACACTGCGAGTGT 3843
Qy 1181 ProGlyLeuHisArgThrAlaSerGlyArgGlySerAlaSerGluHisGlnAspCysAsn 1200

Db 3844 CCAGGGCTGCTACGCTGCGAGTGGCGAGGGTCTCTTCTGTAGCACCAGGACTGCAT 3903
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Db 3904 GCGAAGTGGCTTTCAGGCGCTTGGCGGCGCTTGGCGGCTGATGACCCCCCACTGAT 3963
Qy 1221 GlyAspAspAlaAspAspGluGlyAsnLeu 1230
Db 3964 GGGGATGACGCCGATGACGAGGCGCAACCTG 3993
RESULT 8
US-10-377-139-8
; Sequence 8, Application US/10377139
; Publication NO. US20040175761A1
; GENERAL INFORMATION:
; APPLICANT: MacKinnon, Roderick
; APPLICANT: Jiang, Youxing
; APPLICANT: Lee Mackinnon, Alice
; APPLICANT: Ruta, Vanessa
; TITLE OF INVENTION: Voltage Sensor Domains of Voltage-Dependent Ion Channel Proteins
; FILE OF INVENTION: Uses Thereof
; FILE REFERENCE: Seq. Nos. 1-21 for 1119-9
; CURRENT APPLICATION NUMBER: US/10/377,139
; CURRENT FILING DATE: 2003-03-01
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 8
; LENGTH: 6990
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-377-139-8
Alignment Scores:
Pred. No.: 0 Length: 6990
Score: 5496.50 Matches: 1244
Percent Similarity: 60.31% Conservative: 216
Best Local Similarity: 51.38% Mismatches: 525
Query Match: 46.17% Indels: 437
Gaps: 60
US-09-611-257A-37 (1-2266) x US-10-377-139-8 (1-6990)
Qy 31 ArgProGlyProGlySerAlaGluLysAspProGlySerAlaAspSerGluAlaGluGly 50
Db 73 CAGCCCGGACCCCGAGCCCCCATCTCCCGCCAGGCTGGAGGAGCTCTGGATGGA 132
Qy 51 -----LeuProTyProAlaLeuAlaProValValPhePheTyLeuSerGln 66
Db 133 GCTGATCTCTATGCTCCACACACCCAGACCTGGCGCTTATTCCTTCTTCTGCTGCGACAG 192
Qy 67 AspSerArgProArgSerTrpCysLeuArgThrValCysAsnProTrpPheGluArgIle 86
Db 193 ACCACCGCCCGGAACTGGTGCATCAAGATGGTGTGCACCCGCTGGTGTGATGTGTC 252
Qy 87 SerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMetPheArgProCysGluAsp 106
Db 253 AGCATGTGTGTCTGCTGTAACCTGGTGACACTTGGCATGTACACGCGCTGCGACGAC 312
Qy 107 IleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPheAspPheIleAla 126
Db 313 ATGAGCTGCTGTCCGACCGCTGCAGATCTCTGAGGTCTTGTATGACTTCTATCTTATC 372
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; Sequence 1, Application US/09935541
; Patent No. US20020150911A1
; GENERAL INFORMATION:
; APPLICANT: Dietrich, Paul S.
; APPLICANT: McGivern, Joseph G.
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
; TITLE OF INVENTION: AND USES
; FILE REFERENCE: R00438-REG sequence listing
; CURRENT APPLICATION NUMBER: US/09/935,541
; CURRENT FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: 09/404,650
; PRIOR FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 1
; LENGTH: 6816
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (192)..(6716)
US-09-935-541-1

Alignment Scores:
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Score: 5492.50 Matches: 1236
Percent Similarity: 60.30% Conservative: 213
Best Local Similarity: 51.44% Mismatches: 506
Query Match: 46.14% Indels: 449
DB: 9 Gaps: 55

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Qy 727 -----AlaPheTyrArgLeuLeuCysAspThrPheArgLysIleValAspSerLysTyr 744
Db 1950 TCGCGGGATGTGCGGGAGACCGGACCGCAAGCTGCGCGCATCGTGAGCAGCAAGTAC 2009
Qy 745 PheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerMetGlyIleGluTyr 764
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Qy 765 HisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnIleValPheThrSer 784
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Qy 785 LeuPheAlaLeuGluMetLeuLeuLysAlaLeuValTyrGlyProPheGlyTyrIleLys 804
Db 2130 ATGTTTCCCTTGGAGATGATCTGAAGCTGCTGCTGCTTGGCTCTTCGACTACTGCTG 2189
Qy 805 AsnProTyrAsnIlePheAspGlyValIleValValIleSerValTrpGluIleValGly 824
Db 2190 AACCCTTACACATCTTCGACAGCATCATTTGTTCATCATCAGCATCTGGAGATCGTGGG 2249
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Qy 885 HisLeuPheGlyCysLysPheAlaSerGluArgAsp-----GlyAspThrLeuProAspArg 903
Db 2430 CATATTTTGGCTTCAAGTTTCAGCTCGCGACGACACTGGAGACACGGTCCCGACAGG 2489
Qy 904 LysAsnPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIleLeuThrGlnGlu 923
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Db 2550 GACTGGAACTGCTTCTTCAATGGCATGGCTTCCACTTCTTCCCTGGGCTCTCTCTAC 2609
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Qy 964 ValGluGlyPheGlnAlaGluIleSerLysArgGluAspAlaSerGlyGlnLeuSer 983
Db 2670 GTGGAGGCTTCCAGCGGAG----- 2690
Qy 984 CysIleGlnLeuProValAspSerGlnGlyAspAlaLeuLysSerGluSerGluPro 1003
Db 2691 -----GGTGACGCCAATCGCTCTCTACTCGACGAG 2720
Qy 1004 AspPhePheSerProSer-----LeuAspGlyAsp 1013
Db 2721 GACGAGAGCTCATCCAACTAGAAAGAGTTGATTAAGCTCCAGGAGGCTCGACAGCAGC 2780
Qy 1014 GlyAspArgLysLysCysLeuAlaLeuValSerLeuGlyGluHisProGluLeuArgLys 1033
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Qy 1034 SerLeuLeuProProLeuIleIleHisThrAlaAlaThrProMetSerLeuProLysSer 1053
Db 2826 -----CTGGACCCC-----AGTCTCCCATGGGT 2849
Qy 1054 ThrSerThrGlyLeuGlyGluAlaLeuGlyProAlaSerArgArgThr----- 1069
Db 2850 GGGCACCTAGTCTGCTGGGGCTGCGGGACCTGCCCGGACCTCTCACTGACGCGGAGC 2909
Qy 1070 -----SerSerSerGlySerAlaGluProGlyAlaAla 1080
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Qy 1140 GlnAspGluGluSerSerGluGlu-----GluArgAlaSerProAlaGlySerAsp 1157
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Qy 1158 His-----ArgHisArgGly 1162

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Db 5228 GCTCACCGCAGTTCGTGCTCATCAACGTTGGTGGTGTGCTGTCTCATGAGGACCTGGA 5287
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Qy 1876 yValicluGlyProAspSerProAsp----- 1884
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Qy 1885 -----SerProLySProGlyAlaLeu----- 1891
Db 5462 CTGCTACTCGCTGCCAGGACTCTTGGAGGGGAGGTGACCATCATCGACACCTGTC 5521
Qy 1892 -----HisProAlaAlaHisAla----- 1897
Db 5522 GGGCTCCATCTTCCACCACTACTCTCGCTGCCGGCTGCAAGAAGTGTACACGACAA 5581
Qy 1898 -----HisProAlaAlaHisAla----- 1901
Db 5582 GCAAGAGGTGAGTGGCTGAGACGAGGCGCTTCTCCCTGAACTCAGACAGTCTCTGTC 5641
Qy 1901 r-----HisPheSerLeuGluHisProThrMetGlnPro----- 1912
Db 5642 CATCTGCTGGGTGACGACCTGAGTCTCGAGGACCCACACGCTGCCACCTGGCCGCA 5701
Qy 1913 -----HisProThrGluLeuProGlyProAspLeuLeuThrValArgLySergly----- 1929
Db 5702 GGACAGCAAGGGTGAAGTGGACCCACCTGAGCCCATGCTGTGGGAGACCTGGGCGAATG 5761
Qy 1930 -----ValSerArgThrHisSerLeuProAsn---AspSerTyrMetCysArgHi 1945
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Qy 1945 sGlySerThrAlaGluGlyProLeuGlyHisArgGlyTyrGlyLeuProLySAlaGlnse 1965
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Qy 1965 rGlySerValLeuSerValHisSerGlnProAlaAspThrSerTyrLeuLeuGlnLeuPr 1985
Db 5870 CAGTCAAGCACCCCAAGTCTCTCCCGATGCTCCAGCGCTCTCTGTCGCGCATGCC 5929
Qy 1985 oLyAspAlaProHis-----LeuLeuGlnProHisSerAlaProTh 1999
Db 5930 AGCGGAGTTCTTCCACCTCGAGTGTCTGCAGGCGCAGAAAGCCCAAGAGGCGACTGG 5989
Qy 1999 rTrpGlyThrLeuProLySLeuProProGly-----ArgSerProLe 2014
Db 5990 CACTGGAACCTTCCCAAGATTGGCTCGCAGGGCTCTCGGGCATCTCTGGCGTCAACAG 6049
Qy 2014 uAlaGlnArgProLeuArgArgGlnAlaAlaAlaArgThrAspSerLeuAspValGlnGl 2034
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Qy 2034 yLeuGlySerArgGluAspLeuLeuAlaGluValSerGlyProSerProProLeuAlaAr 2054
Db 6102 -----GCCAGCCCCCAGCAGCTCCGCGGGCAG 6127
Qy 2054 gAlaTy-SerPheTrpGlyGlnSerSerThrGlnAlaGlnGlnHisSerArgSerHisSe 2074
Db 6128 CCTGACAGCACGCTCGAGGACGCTGACCTCGAGGACAGCCCGCGGTGCC----- 6182
Qy 2074 rLySLeSerLySHisMetThrProAlaProCysProGlyProGluProAsnTrpGl 2094
Db 6183 -----CTGGGGCGCGCGCGCTCTCCAGGACCCCGGGCGCGCTGTC 6226
Qy 2094 yLySLeGlyProGluThrArgSerSerLeuGluLeuAspThrGluLeuSerTrpLleSe 2114
Db 6227 C-----CCCCCGCTCGCGCGCGCTGAGCTG----- 6254
Qy 2114 rGlyAspLeuLeuProProGlyGlyGlnGluLupProProSerProArgAspLeuLyS 2134
Db 6255 -----CGCGCGCGCGCGCTCTTCAG 6274
Qy 2134 sCysTy-SerValGluAlaGlnSerCysGlnArgArgProThrSerTrpLeuAspGluGl 2154
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Qy 2154 nArgArgHisSerIleAlaValSerCysLeuAspSerGlySerGlnProHisLeuGlyTh 2174
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Db 6416 CTGAGACCTCTAGCAGCCTCTCGCTCACCTCTTCTGCGCGCGCGC----- 6467
Qy 2208 nGlyProArgThrProSerProGlyIleCysLeuArgArgAlaProSerSerAs 2228
Db 6468 -----CCGCGCGCAGCCCGCGCTCACCGCCCGCAGGAAGTTCAGCAGCAGCAG 6517
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RESULT 10
US-10-425-800-1
; Sequence 1, Application US/10425800
; Publication No. US20030180886A1
; GENERAL INFORMATION:
; APPLICANT: Dietrich, Paul S.
; APPLICANT: McGivern, Joseph G.
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
; TITLE OF INVENTION: AND USES
; FILE REFERENCE: R0043B-REG sequence listing
; CURRENT APPLICATION NUMBER: US/10/425,800
; CURRENT FILING DATE: 2003-04-29
; PRIOR APPLICATION NUMBER: US/09/404,650
; PRIOR FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 6816
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (192)..(6716)
; US-10-425-800-1

Alignment Scores:
Pred. No.: 0 Length: 6816
Score: 5492.50 Matches: 1236
Percent Similarity: 60.30% Conservative: 213
Best Local Similarity: 51.44% Mismatches: 506
Query Match: 46.14% Indels: 449
DB: 16 Gaps: 55

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Qy 51 -----LeuProTyrProAlaLeuAlaProValPhePheTyrLeuSerGln 66
Db 324 GCTGATCCTCATGTCCACACACCCAGACCTGGCGCTATTGCTTCTTCTGCTCGCAG 383
Qy 67 AspSerArgProArgSerTrpCysLeuArgThrValCysAsnProTrpPheGluArgGly 86
Db 384 ACCACGACCCCGGAACTGGTGCATCAAGATGTTGCAACCCCGCTGTTGATGTGTC 443
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DB	444	AGCATGCTGGTGATCTCTGCTGAACCTGCGTGACACTTGGCATGTACACAGCGGTGCGACGAC	503
QY	107	IleAlaCysAspSerGlnArgCysArgGIlleuGlnAlaPheAspAspPheIlePheAla	126
DB	504	ATGACTGCGCTTCGCGACCGCTCAGAGATCTCGAGGCTTTTGATGACTTCATCTTTATC	563
QY	127	PhePheAlaValGluMetValValLysMetValAlaLeuGlyIlePheGlyLysLysCys	146
DB	564	TTCTTTGCCATGGAGATGCTGCTCAAGATGGTGGCCCTGGGGATTTTGGCAAGAAGTGC	623
QY	147	TyrLeuGlyAspThrTrpAsnArgLeuAspPhePheIleValIleAlaGlyMetLeuGlu	166
DB	624	TACCTCGGGACACATGGAAACCGCTGGATTTCTTCATCGCTCATGGCAGGATGGTCGAG	683
QY	167	TyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArgThrValArgValLeuArg	186
DB	684	TACTCCCTGGACCTTCAGAACATCAACCTGTACGCCATCCGCACCGTGGCGCTCTGAGG	743
QY	187	ProLeuArgAlaIleAsnArgValProSerMetArgIleLeuValThrLeuLeuLeuAsp	206
DB	744	CCCCTCAAGCCATCAACCGCGTGCCTGCGATTCGCGATCTCTGTGAACCTGCTCTCGAC	803
QY	207	ThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePheValPhePheIlePheGly	226
DB	804	ACACTGCCCATGCTGGGGAATGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	863
QY	227	IleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArgCysPheLeuProGluAsn	246
DB	864	ATCATAGTGTGACGCTCTGGCGGGCTGCTGGGTAAACCGCTCTCTCTGGAGGAGAAC	923
QY	247	PheSerLeuProLeuSerValAspLeuGluArgTyrTyrGlnThrGluAsnGluAspGlu	266
DB	924	TTTACCATAAAGGGGATGTGGCTTTCGCCCCATPACTACCAGCGGAGGAGGATGATGAG	983
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DB	984	ATGCCCTTCATCTGCTCTGCTCGGGCGACAAUGGGATATGGCGTGCATGAGATCCCC	1043
QY	287	ThrLeuArgGlyAspGlyGlyGlyProProCysGlyLeu	300
DB	1044	CGGCTCAAGGAGCAG-----GGCGGTGAGTGCCTGCTCCAAAGGACGACGCTCAT	1094
QY	301	AspTyrGluAlaTyrAsnSerSerSerAsnThrThr	318
DB	1095	GACTTTGGGGGGGGCGGCGCAGACCTCAATGCCAGCGGCTCTGTGTCACTGGAACCGT	1154
QY	319	TyrTyrThrAsnCysSerAlaGlyGluHisAsnProPheLysGlyAlaIleAsnPheAsp	338
DB	1155	TACTACATGTGTCGGCACGGCGACGCCAACCCCCACAAGGGTGCCATCACTTTGAC	1214
QY	339	AsnIleGlyTyrAlaTrpIleAlaIlePheGlnValIleThrLeuGluGlyTrpValAsp	358
DB	1215	AACATCGGTTATGCTTGATTTGTCATCTTCAGGTGATCATCTCGAAGGCTGGGTGGAG	1274
QY	359	IleMetTyrPheValMetAspAlaHiserPheTyrAsnPheIleTyrPheIleLeuLeu	378
DB	1275	ATCATGTACTACGTGATGATGCTCATCTCTTACAACTTCATCTACTTCACTTCGCTT	1334
QY	379	IleIleValGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPhe	398
DB	1335	ATCATAGTGGGCTCTTCTTCATGATCAACCTGTGCTGCTGCTGCTGCTGCTGCTGCTG	1394
QY	399	SerGluThrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSer	418
DB	1395	TCGGAGACCAAGCAACGGGAGCACCGGCTGATGTGGAGCAGCGGCGCTACTCTGCT	1454
QY	419	AsnAlaSerThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLys	438
DB	1455	---TCCAGCAGCGTGGCGAGCTACGCCGAGCTGCGGAGCTGCTACGAGAGATCTTCAG	1511

Qy	439	TyrLeuValTyrIleLeuArgLysAlaAlaArgArgLeuAlaGlnValSerArgAlaAa	458
Db	1512	TATGTCTGCACATCTCTGCAGGCGC-----CGCGCCTG	1553
Qy	459	GlyValArgValGlyLeuLeuSerSerProAlaProLeuGlyGlnGluThrGlnPro	478
Db	1554	GGCTCTACAGGCTCTGCAGAGCGCGCCAGGCCTTGGC-----	1595
Qy	479	SerSerSerCysSerArgSerHisArgArgLeuSerValHisLeuValHisHis	498
Db	1595	-----	1595
Qy	499	HisHisHisHisHisTyrHisLeuGlyAsnGlyThrLeuArgAlaProArgAlaSer	518
Db	1595	-----	1595
Qy	519	ProGluIleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProSer	538
Db	1596	-----CGGAG	1601
Qy	539	ThrProAlaLeuSerGlyAlaProProGlyGlyAlaGluSerValHisSerPheTyrHis	558
Db	1602	GCCTCCGCCC-----CCCGCAAACTTGGCCCC-----CAC	1631
Qy	559	AlaAspCysHisLeuGluProValArgCysGlnAlaProProArgSerProSerGlu	578
Db	1632	GCCAAAG-----GAGCCCCGGCACTACCAGCTGTCCCGCAACATAGCCCTCGGAT	1682
Qy	579	AlaSerGlyArgThrValGlySerGlyLysValTyrProThrValHisThrSerProPro	598
Db	1683	GCGACGCCCCACACCCCTG-----GTGACGCCCATC	1712
Qy	599	ProGluThrLeuLysGluLysAlaLeuValGluValAlaAlaSerSerGlyProProThr	618
Db	1713	CCGCCACGCTG-----	1724
Qy	619	LeuThrSerLeuAsnIleProProGlyProTyrSerSerMethHisLysLeuLeuGluThr	638
Db	1724	-----	1724
Qy	639	GlnSerThrGlyAlaCysGlnSerSerCysLysIleSerSerProCysLeuLysAlaAsp	658
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Qy	659	SerGlyAlaCysGlyProAspSerCysProTyrCysAlaArg-----	672
Db	1725	-----GCTTCCGATCCCGCAGCTGGCTTGTTCGACGATCAGGACGCGCGCGCC	1778
Qy	673	AlaGlyAlaGlyGluValGluLeuAlaAspArgGluMetProAspSerAspSerGluAla	692
Db	1779	TCGGGGCTTGGCGACACCGAC-----TCGGCGCAGGAGGGCTCGGGCTCCGGAGCTCCGCT	1835
Qy	693	ValTyrGluPheThrGlnAspAlaGlnHisSerAspLeuArgAspProHisSerArgArg	712
Db	1836	GCTGCCAG-----GACGAGCGGATGGGACGCGGCCCGGACGACGAGGACGGAGCC	1889
Qy	713	GlnArgSerLeuGlyProAspAlaGluProSerSerValLeu-----	726
Db	1890	TCCTCAGAACTGGGGAAGGAGGAGGAGGAGGAGGAGCGGATGGCGGCTTGGCTG	1949
Qy	727	-----AlaPheTyrArgLeuIleCysAspThrPheArgLysIleValAspSerLysTyr	744
Db	1950	TGGGGGATGTGTGGCGGAGACCGCAGCCAGCTGCGCGCATCTGTGGACACGACATAC	2009
Qy	745	PheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerMetGlyIleGluTyr	764
Db	2010	TTCAACCGGGCAATCATATGGCCATCTCTGTCAACACCGCTCAGCATGGGCATCGAC	2065
Qy	765	HisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnIleValPheThrSer	784
Db	2070	CACGACGACCGGAGGAGCTGACCAATCTCTGGAGATCTGCATGTGGTCTTACCCAGC	2129
Qy	785	LeuPheAlaLeuGluMetLeuLeuLysLeuLeuValTyrGlyProPheGlyTyrIleLys	804

Qy	1480	eValLeuAlaSerLysAspGlyTirpValAspIleMetTyrAspGlyLeuAspAlaValG1	1500
Db	4208	TGTCTTGGCATCAAGATGTTGGTGAACATCATGTACAATGGATCGATGCTGTTCG	4267
Qy	1500	yValAspGlnGlnProIleMetAsnHisAsnProTirpMetLeuLeuTyrPheIleSerPh	1520
Db	4268	TGTGGACAGCAGCGCTGTGATCCAAACACACACCCCTGGATGCTGCTACTTTCATCTCC	4327
Qy	1520	eLeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValValValGluAsnPh	1540
Db	4328	CCTGCTCATGTCAGCTTCTTTGTGCTCAACATGTTTGGGTGTCTGGTGGAGAACTT	4387
Qy	1540	eHisLysCysArgGlnHisGlnGluGluGluAlaArgArgArgGluGluArgLe	1560
Db	4388	CCACAAGTCGGCAGCACCCAGCAGGCTGAAGAGGCACCGCGCGTGGAGGAAGCGGCT	4447
Qy	1560	uArgArgLeuGluLysArgArgLysAlaGlnCysLysProTyrTyrSerAspTyrSe	1580
Db	4448	CGCGCGCTGGAGAAGAAGCGCGGAAGGCCAGCGCTGCCCTACTATGCCCATTTATG	4507
Qy	1580	rArgPheArgLeuLeuValHisIshLeuCysThrSerHisTyrLeuAspLeuPheIlePh	1600
Db	4508	TCACACCGGCTGCTCATCCACTCCATGTGCACACGCCACTACTCGACATCTTCATCAC	4567
Qy	1600	rGlyValIleGlyLeuAsnValValThrMetAlaMetGluHisTyrGlnProGlnI1	1620
Db	4568	CTTCATCATCTGCTCAACGCTGTCAACATGTCCCTGGAGCACTACAATCAGCCCCAGTC	4627
Qy	1620	eLeuAspGluAlaLeuLysIleCysAsnTyrIlePheThrValIlePheValIleGluLuse	1640
Db	4628	CCTGGAGACAGCCCTCAAGTACTGCACACTATATGTCACCACTGTCTTTGTGCTGGAGG	4687
Qy	1640	rValPheLysLeuValAlaPheGlyPheArgArgPhePheGlnAspArgTirpAsnGlnLe	1660
Db	4688	TGTGCTGAAGCTGGTGGCATTTGGTCTGAGCGCTTCTTCAAGACCGATGGAACCACT	4747
Qy	1660	uAspLeuAlaIleValLeuLeuSerIleMetGlyIleThrLeuGluGluIleGluValAs	1680
Db	4748	GGACCTGGCCATTTGTCTACTGTCACTCACTGGGCATCACCCCTGGAGGAGATCGAGATCA	4807
Qy	1680	nAlaSerLeuProIleAsnProThrIleIleArgIleMetArgValLeuArgIleAlaAr	1700
Db	4808	TGCGGCCCTGCCCATCAATCCCACCATCATCCGCATCATGAGGTTCTGCGCATGCCCG	4867
Qy	1700	gValLeuLysLeuLeuLysMetAlaValGlyMetArgAlaLeuLeuAspThrValMetG1	1720
Db	4868	AGTCTGAAGCTGTTGAAGATGGCCACAGAAATGCGGGCCCTGCTGACACGCTGGTGCA	4927
Qy	1720	nAlaLeuProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPhePheIlePheAl	1740
Db	4928	AGCTTTGCCCCAGGTGGGCACCACTGGGCCCTCCTCTTCATGCTGCTCTCTTCATCTATGC	4987
Qy	1740	aAlaLeuGlyValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGluG1	1760
Db	4988	TGCTCTCGGGTGGAGCTCTTTGGGAAGCTGGTCTGCACGACGAGAACCCGTGCCAGGG	5047
Qy	1760	yLeuGlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgVa	1780
Db	5048	CATGACCGGCATGCCACCTTCGAGAACTTCGGCATGGCCCTTCTCACACTCTTCACAGT	5107
Qy	1780	lSerThrGlyAspAsnTrpAsnGlyIleMetLysAspThrLeuArgAspCys---AspG1	1799
Db	5108	CTCACCGGTGACAACTGGAAACGGGATCATGAAGGACACGCTCGGGACTGCAACCCACGA	5167
Qy	1799	nGluSerThrCysTyrAsnThrVal-----IleSerProIleTyrPheValSerPheVa	1817
Db	5168	CGAGCGAGCTGCCGTGAGCAGCTGCAGTTGTGTGCGCGCTGTACTTCTGTGAGCTTCGT	5227
Qy	1817	lLeuThrAlaGlnPheValLeuValAsnValValIleAlaValLeuMetLysHisLeuG1	1837
Db	5228	GCTCACCGCAGGTTCTGTGCTCATCAACGTGGTGGTGGCTGTGCTCATGAAGACCTGGA	5287

1837	Qy	uGluSerAsnLysGluAlaIylsGluCluAlaGlutLeuGluAlaGluLeuGluLeuGluMe	1895
:	:	:::::	:
5288	Dd	CGAGCAACAAGAGGGCCGAGGACGCCGAGATGGATGCGAGCTCGAGCTGGAGAT	5347
1857	Qy	t----LysThrLeuSerProGlnProHisSerProLeuGlySerProPheLeuTrpGln	1876
5348	Dd	GGCCCATGGCTTGGCCCTTGGCCGAGGTGCTACTACGGCTCCCCGGGGGCC--	5404
1876	Qy	yValGluGlyProAspSerProAsp-----	1884
5405	Dd	C---CGAGGGCCGGAGGGGGCGGGCGGGCGCACCAGAGGGCGGCTTGTCGGCGGC	5461
1885	Qy	-----SerProLysProGlyAlaLeu-----	1891
5462	Dd	CTGCTACTCGCCCTGCCACGAGACTCTTTGAGGGGGAGATTGACCATCATCGACAACTGTC	5521
1892	Qy	-----HisProAlaAlaHisAla-----	1897
5522	Dd	GGGCTCCATCTTCCACCACTACTCTCTCGCTGCGGCTGCAAGAAGTGTCAACACGACAA	5581
1898	Qy	-----ArgSerAlase-----	1901
5582	Dd	GCAAGAGGTGACCTGGCTGAGACGAGGGCTTCTCCCTGAATCTAGACAGGTCTCTGTC	5641
1901	Qy	r-----HisPheSerLeuGluHisProThrMetGlnPro-----	1912
5642	Dd	CATCTCTGCTGGGTGACGACCTGAGTCTCGAGGACCCCACAGCCCTGCCCCCGCAA	5701
1913	Qy	-----HisProThrGluLeuProGlyProAspLeuLeuThrValargLysSerGly-----	1929
5702	Dd	GGACAGCAAGGGTGGAGTGGACCCACTGAGCCCATGCGGTGTGGAGACCTGGGGCAATG	5761
1930	Qy	-----ValSerArgThrHisSerLeuProAsn---AspSerTyrMetCysArgHi	1945
5762	Dd	CTTCTTCCCTTGTCTCTACGGCGCTCTCGCGGATCCAGAGAACTTCTGTGTGAGAT	5821
1945	Qy	sGlySerThrAlaGluGlyProLeuGlyHisArgGlyTrpGlyLeuProLysAlaGlnSe	1965
5822	Dd	GGAGGAGATCCCATTAACGCTGTC-----CGTCTCTGG-----CTGAAAACATGACAG	5869
1965	Qy	xGlySerValLeuSerValHisSerGlnProAlaAspThrSerTyrIleLeuGlnLeuPr	1985
5870	Dd	CAGTCAAGCACCCCAAGTCCCTTCTCCCGGATGCTCCAGCCCTCTCTCGCCATGCC	5929
1985	Qy	oLysAspAlaProHis-----LeuLeuGlnProHisSerAlaProTh	1999
5930	Dd	AGCCGAGTTCTTCCACCTCGAGTGTCTGCAGCCAGAAAGGCCAAGAGGCACTGG	5989
1999	Qy	rTrpGlyThrIleProLysLeuProProProGly-----ArgSerProLe	2014
5990	Dd	CACTGGAACCTCTCCCAAGATTGCGTGCAGGGCTCTCTGGGCATCTCTCGGTCAACCAAG	6049
2014	Qy	wAlaGlnArgProLeuArgArgGlnAlaIalleArgThrAspSerLeuAspvalGlnGl	2034
6050	Dd	GGTCAACTGHTACCTCTCCGGCAGGCCACCGGAGGCGACACGTCTGCTGAC-----	6101
2034	Qy	yLeuGlySerArgGluAspLeuLeuAlaGluValSerGlyProSerProLeuAlaAr	2054
6102	Dd	-----GCCAGCCCCCAGCAGCTCCCGGGCGAG	6127
2054	Qy	aGalaty-SerPheTrpGlyGlnSerSerThrGlnAlaGlnGlnHisSerArgSerHisse	2074
6128	Dd	CTTCAGACCACTCTCAGGACAGCTGACCTGAGCGACAGCCCCCGGCTGCC-----	6182
2074	Qy	rLysIleSerLysHisMetThrProProAlaProCysProGlyProGluProAsnTrpGl	2094
6183	Dd	-----CTGGGGCGCGCGCGCTGCTTCCAGAACCCCGCGGCCCGGCTGTC	6266
2094	Qy	yLysGlyProProGluThrArgSerSerLeuGluLeuAspThrGluLeuSerTrpIleSe	2114
6227	Dd	C-----CCCCCGCTCGCGCCGCTGAGCCTG-----	6254
2114	Qy	rGlyAspLeuLeuProProGlyGlyGlnGluGluProProSerProArgAspLeuLysLy	2134

399 SerGluThrIysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSer 418
1395 TCGAGACCAAGCAAGCGGAGCACCGGCTGATCTGGAGCAGCGGAGCGCTACCTGCTC 1454
419 AsnAlaSerThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLeuLys 438
1455 ---TCCAGACGGTGGCCACCTACCGGAGCCTGGGACTGCTACGAGGAGATCTTCCAG 1511
439 TyrLeuValTyrLeuArgLysAlaAlaArgArgLeuAlaGlnValSerArgAlaAla 458
1512 TATGCTGTCACATCTCTCGCAAGGCGCAAGCGC-----CGCGCCCTG 1553
459 GlyValArgValGlyLeuLeuSerSerProAlaProLeuGlyGlnGluThrGlnPro 478
1554 GGCTCTACGAGGCGCTGCGAGCGCGCGCGCGCGCGCTGGGC----- 1595
479 SerSerSerCysSerArgSerHisArgArgLeuSerValHisHisLeuValHisHis 498
1595 ----- 1595
499 HisHisHisHisHisHisTyrHisLeuGlyAsnGlyThrLeuArgAlaProArgAlaSer 518
1595 ----- 1595
519 ProGluIleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProSer 538
1596 -----CGGAG 1601
539 ThrProAlaLeuSerGlyAlaProProGlyGlyAlaGluSerValHisSerPheTyrHis 558
1602 CCGCGCGC-----CGCGCAACCTGGGCGC-----CAC 1631
559 AlaAspCysHisLeuGluProValArgCysGlnAlaProProArgSerProSerGlu 578
1632 GCCAAG-----GAGCGCGCGACCTACGAGCTGCGCGCAACATAGCCCGCTGGAT 1682
579 AlaSerGlyArgThrValGlySerGlyLysValTyrProThrValHisThrSerProPro 598
1683 CGGAGCGCCACACCTG-----GTGAGCGCCATC 1712
599 ProGluThrLeuLysGluLysAlaLeuValGluValAlaAlaSerSerGlyProProThr 618
1713 CCGCGCACGCTG----- 1724
619 LeuThrSerLeuAsnIleProProGlyProTyrSerSerMetHisLysLeuLeuGluThr 638
1724 ----- 1724
639 GlnSerThrGlyAlaCysGlnSerSerCysLysIleSerSerProCysLeuLysAlaAsp 658
1724 ----- 1724
659 SerGlyAlaCysGlyProAspSerCysProTyrCysAlaArg----- 672
1725 -----GCTTCGATCCCGCAGCTGCTTGTCCAGCATGAGGAGCGCGCGCGCGCC 1778
673 AlaGlyAlaGlyGluValGluLeuAlaAspArgGluMetProAspSerAspSerGluAla 692
1779 TCGGCGCTGGGAGCAGCAGCAGC-----TCGGCGCAGGAGGCTCGGCTCGGAGCTCCGCT 1835
693 ValTyrGluPheThrGlnAspAlaGlnHisSerAspLeuArgAspProHisSerArgArg 712
1836 GGTGGCGAG-----GACGAGCGATGGGAGCGCGCGCGCGCGAGCAGCGAGCGAGGCC 1889
713 GlnArgSerLeuGlyProAspAlaGluProSerSerValLeu----- 726
1890 TCCTCAGAACTGGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1949
727 -----AlaPheTyrArgLeuIleCysAspThrPheArgLysIleValAspSerLysTyr 744
1950 TCGCGGAGTGTGGCGGAGAGCGGAGCAGCAAGCTGCGCGCATCTGTGAGCAGCAAGTAC 2009
745 PheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerMetGlyIleGluTyr 764

2010 TTCAACCGGGGCATCATGATGCCATCTGTGTCAACACCGTCAGCATGGGCATCGAGCAC 2069
765 HisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnIleValPheThrSer 784
2070 CACGAGCAGCGGAGGAGCTGACCAACATCTCTGGAGATCTGCATGTGGTCTTCACGAGC 2129
785 LeuPheAlaLeuGluMetLeuLeuLysLeuValTyrGlyProPheGlyTyrIleLys 804
2130 ATGTTTGGCTGGAGATCATCTGAAGCTGGCTGATTTGGCTCTTCGACTACCTGGCT 2189
805 AsnProTyrAsnIlePheAspGlyValIleValIleSerValTyrGluIleValGly 824
2190 AACCCCTCAACATCTTCGACAGCATCATTTGTCATCATGATCATGCGAGATCTGGGG 2249
825 GlnGlnGlyGlyGlyLeuSerValLeuArgThrPheArgLeuMetArgValLeuLysLeu 844
2250 CAGGCGGAGCGTGGCTGCTGGTGTGCGGACCTTCGGCTCGCGCTGCGGCTGCTGAACTG 2309
845 ValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetLysThrMetAspAn 864
2310 GTGGCTTCATGCTGCCCTGGCGGCGGAGCTGCTGTGTGCTCATGAAGACCATGACAC 2369
865 ValAlaThrPheCysMetLeuMetLeuPheIlePhePheSerIleLeuGlyMet 884
2370 GTGGCGACCTTGTGATGCTGCTCATGCTCTTCATCTTCATCTTCAGCATCTCTGGATG 2429
885 HisLeuPheGlyCysLysPheAlaSerGluArgAsp---GlyAspThrLeuProLeuArg 903
2430 CATATTTTGGCTGCAAGTTTCAGCTCCGCGGAGCAGCTGGAGACAGCGTGGCGGAGC 2489
904 LysAsnPheAspSerLeuLeuTyrAlaIleValThrValPheGlnIleLeuThrGlnGlu 923
2490 AAGAACTTCGACTCCCTGCTGTGGGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2549
924 AspTyrAsnLysValLeuTyrAsnGlyMetAlaSerThrSerSerTyrAlaAlaLeuTyr 943
2550 GACTGGAAGCTGCTTCTACATGTCAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2609
944 PheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuLeuValAlaIleLeu 963
2610 TTGTGCGCTCATGACTTCGCAACTATGTGCTTCAACCTGCTGCTGCTGCTGCTGCTGCTGCT 2669
964 ValGluGlyPheGlnAlaGluGluIleSerLysArgGluAspAlaSerGlyGlnLeuSer 983
2670 GTGGAGGGCTTCAGCGCGAG----- 2690
984 CysIleGlnLeuProValAspSerGlnGlyGlyAspAlaAsnLysSerGluSerGluPro 1003
2691 -----GGTGAGCGCAATCGCTCTCTACTCGGAGCAG 2720
1004 AspPhePheSerProSer-----LeuAspGlyAsp 1013
2721 GACGAGAGCTCATCAACATAGAGAGTTTGTATAGCTCCAGGAAGCCCTGGAGCAGCAGC 2780
1014 GlyAspArgLysCysLeuAlaLeuValSerLeuGlyGluHisProGluLeuArgLys 1033
2781 GGAGATCCCAAGCTCTGCCCAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCA 2825
1034 SerLeuLeuProProLeuIleIleHisThrAlaAlaThrProMetSerLeuProLysSer 1053
2826 -----CTGGAGCCCC-----AGTCTCCCACTGGGT 2849
1054 ThrSerThrGlyLeuGlyGluAlaLeuGlyProAlaSerArgThr----- 1069
2850 GGGCACCCTAGTCTGCTGGGCTGCGGAGCCTGCCCCCGGAGTCTCTCAGTCGAGCCGAGC 2909
1070 -----SerSerSerGlySerAlaGluProGlyAlaAla 1080
2910 CCATGCTGTGGCCCTGGGCTCCCGAAGAGCAGTGTCTGCTCTAGGAGGATCAGC 2969
1081 HisGluMetLysSerProProSerAlaArgSerSerProHisSerProTyrSerAlaAla 1100
----- 1100

2970	TATGACCA	CGCGCTCCCTGT	CCAGCTCCGCGAGTCTCTACTACGGGGCCATGGGGCCCGCAGC	3027							
1101	SerSer	ThrThr	ArgArg	SerSer	ArgArg	SerLeu	GluAla	ProSer	Leu	Leu	1120
3030	CGGCGCT	GGGCCAGCCGT	CGCTCCAGCTGGNAC	-----	-----	-----	-----	-----	-----	-----	3071
1121	ArgArg	SerPro	SerGly	GluArg	ArgSer	LeuLeu	SerGly	Glu-----	GlyGln	GluSer	1139
3072	CACAAGC	CGCGCTCGCGGAGCAT	GATGCTCCCTGTCTCTCGGAGCGCGCGGGCGCC	3131							
1140	GlnAsp	GluGlu	SerSer	GluGlu-----	GluArg	AlaSer	ProAla	GlySer	Asp	1157	
3132	CGGCTCG	GAGGTTGCGCGGAC	AGAGGGCGCGCGGCGGACCCCTGCCACACCCCA	3191							
1158	His-----	-----	-----	-----	-----	-----	-----	-----	-----	1162	
3192	CACGCCCA	CCATTATCAT	CGGGCCCATCTGGCGCACCGCACCGCACCGCCGCGG	3251							
1163	SerLeu	GluArg	GluAla	LeuSer	SerPhe	AspLeu	ProAsp	ThrLeu	GlnVal	ProGly	1182
3252	ACGCTGT	CCCTCGACAACAGAGGACT	CGGTGGACCTCGGTGGACCTGGCGAGCTGGTGGCGGGTGGGC	3311							
1183	LeuHis	ArgThr	AlaSer	GlyArg-----	GlySer	AlaSer	GluHis	GlnAsp	CysAsn	1200	
3312	GCCCAAC	CCCCGGCGCGCTGGAGGGCGGACGCCGCCCGGGCATAGAGACTGCAAT	3371								
1201	GlyLeu	SerAla	SerGly	ArgLeu	AlaArg	AlaLeu	ArgPro	AspAsp	ProPro	LeuAs	1220
3372	GGCAGAT	-GCCAGATCGC--	CAAGACGCTTCCACCAAGATGGGCACCGCGGGGA	3427							
1220	pGlyAsp	AspAla	AspAsp	GluGly	AsnLeu	SerLys	GlyGlu	ArgVal	ArgAla	TrpI	1240
3428	TCGCGGG	GAGGATGAGGAGGAAATCGACT	TACACCTGTGTTCGCGCTCCGCAAGATGAT	3487							
1240	eArgAla	ArgLeu	ProAla	CysTyr	LeuGlu	ArgAsp	SerTrp	SerAla	TyrIle	PhePr	1260
3488	CGACGTCT	AAAGCCCGACCTGGT	CGAGGTCGCGAAGACTGGTCTCTTACCTTCTCTC	3547							
1260	oProGln	SerArg	PheArg	LeuLeu	CysHis	ArgIle	IleThr	HisMet	PheAsp	Hi	1280
3548	TCCGAGA	CAGGTTCCGGTCTCTGTGT	CAGACCATTTATTGCCACAACTCTTCGACTA	3607							
1280	sValVal	LeuVal	IleIle	PheLeu	AsnCys	IleThr	IleAla	MetGlu	ArgPro	Ily	1300
3608	CGTCTCT	GGCCTTCACTTCTTCTCAACTGCAT	CACCATCCGCTGGAGCGGCTCAGAT	3667							
1300	eAspPro	HisSer	AlaGlu	ArgIle	PheLeu	ThrLeu	SerAsn	TyrIle	PheThr	AlaVa	1320
3668	CGAGCGC	GGCAGCACCAAGACGATCTTCTCACCGTGCACACTACATCTTCACGGCCAT	3727								
1320	lPheLeu	AlaGlu	MetThr	ValIys	ValAla	LeuGly	TrpCys	PheGly	GluGln	Al	1340
3728	CTTCTGG	GGCAGATGATCATGAA	GGFAGTCTCGCTGGGCTGTACTTCGGCAGCAGGC	3787							
1340	aTyrLeu	ArgSer	SerTrp	AsnVal	LeuAsp	GlyLeu	LeuVal	LeuIle	SerVal	IleAs	1360
3788	GTACCTAC	GACGAGCTGGAA	CGTGGATGGCTTTCTTGTCTTCGTGTCCATCATCGA	3847							
1360	pIleLeu	ValSer	MetVal	SerAsp	SerGly	ThrLys	IleLeu	GlyMet	LeuArg	ValLe	1380

QY	1440	lCysGlnGlycluaSpThrArgAsnIleThrAsnLysSerAspCysAlaGluAalaSerTy	1460
DB	4088	CTGTCTGGGGGTGGACACCCGCAACATCATCAACACCGCTCGAGCTGCGATGCCGCCCACTA	4147
QY	1460	rAqgTrrpValArgHisLysTyrrhenPheAspAsnLeuGlyGlnAlaLeuMetSerLeuPh	1480
DB	4148	CCGCTGGGTCCATCACAATAATACAACTTCGACACCACTGGCGCAGGCTCTGAATGTCCTCTT	4207
QY	1480	eValLeuAlaSerLysAspGlyTrrpValAspIleMetTyrAspGlyLeuAspAlaValG1	1500
DB	4208	TGTCTGGCATCCAGGATGGTGGGTGAACATCATGTACAAATGGACTGGATGCTGTTCG	4267
QY	1500	yValAspGlnGlnProIleMetAsnHisAsnProTrrpMetLeuLeuTyrPheIleSerPh	1520
DB	4268	TGTGGACCAAGCGCTGTGACCAACACACACCCCTGGATGCTGCTACTTCACTCTCCTT	4327
QY	1520	eLeuLeuIleValAlaPhePheValIleuAsnMetPheValGlyValValValGluAsnPh	1540
DB	4328	CCCTGCTCATGCTCAGCTCTTCTGTGCTCAACATGTTGTGGGTGCTGCTGGTGAGAACTT	4387
QY	1540	eHisLysCysArgGlnHisGlnGluGluGluAlaArgArgArgGluGluLysArgLe	1560
DB	4388	CCACAGTGGCGGACGACCAAGAGGCTGAAGAGGCACAGCGCGCGTGAGGAGAGCGGCT	4447
QY	1560	uArgArgLeuGluLysLysArgLysAlaGlnCysLysProTyrTyrSerAspTyrSe	1580
DB	4448	CGCGCGCTGGAGAAAGCGCGGAGGCGCCAGCGGCTGCGCTACTATGCCACCTATTG	4507
QY	1580	rArgPheArgLeuLeuValHisLysLeuCysThrSerHisTyrLeuAspLeuPheIleTh	1600
DB	4508	TCACACCGCGTGTCTATCCACTCCATGTGCACGACCACTACTCGACATCTTCATCAC	4567
QY	1600	rGlyValIleGlyLeuAsnValValThrMetAlaMetGluHisTyrGlnGlnProGlnI1	1620
DB	4568	CTTCATCATCTGCTCAACGTGTGCACATGCTCCCTGGAGCACTACAATCAGGCCCACTG	4627
QY	1620	eLeuAspGluAlaLeuLysIleCysAsnTyrrillePheThrValIlePheValLeuGluSe	1640
DB	4628	CCTGGAGACAGCCCTCAAGTACTGCAACTATATGTTCAACCACTGCTTTTGTGTGGAGGC	4687
QY	1640	rValPheLysLeuValAlaPheGlyPheArgArgPhePheGlnAspArgTrrpAsnGlnLe	1660
DB	4688	TGTCTCAAGCTGTGTGGCATTTGTGTGTGAGCGCTTCTTCAAGAGACCGATGGAACAGCT	4747
QY	1660	uAspLeuAlaIleValLeuLeuSerIleMetGlyIleThrLeuGluGluIleGluValAs	1680
DB	4748	GGACCTGGCCATTTGTGCTACTGTGAGTCATGGGCATCACCTGGAGAGATCGAGATCAA	4807
QY	1680	nAlaSerLeuProIleAsnProThrIleIleArgIleMetArgValLeuArgIleAlaAr	1700
DB	4808	TGCGGCCCTGCCCATCATCCACCATCATCCGCATCATGAGGGTTCTGGCATTCGCCG	4867
QY	1700	gValLeuLysLeuLeuLysMetAlaValGlyMetArgAlaLeuLeuAspThrValMetG1	1720
DB	4868	AGTGCTGAAGCTGTGAAGATGGCCACAGAAATGCGGGCCCTGCTGCGACACGCTGGTCCA	4927
QY	1720	nAlaLeuProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPhePheIlePheAl	1740
DB	4928	AGCTTTGCCCCAGGTGGGCAACTGGGCGCTCTTCTTTCATGCTGCTCTTCTTCACTATGC	4987
QY	1740	aAlaLeuGlyValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGluG1	1760
DB	4988	TGCTCTCGGGGTGGAGCTCTTTGGGAAGCTGGTCTGCACGACGAGAACCCGTGCCAGGG	5047
QY	1760	yLeuGlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgVa	1780
DB	5048	CATGAGCGCGCATGCCACCTTCAGAACTTCGCGCATGGCCCTCCTCACACTCTTCCAGGT	5107
QY	1780	lSerThrGlyAspAsnTrrpAsnGlyIleMetLysAspThrLeuArgAspCys---AspG1	1799
DB	5108	CTCCACGGGTGACAACTGGAACGGGATCATGTAAGGACAGCTGTCGGGACTGCACCCACA	5167

Qy 1799 ngluSerThrCysTyrAsnThrVal-----IleSerProIleTyrPheValSerPheVa 1817
Db 5168 CGAGCGCAGCTGCTGAGCAGCTGCAGTTGTGTGCGCGCTACTCTGTGAGCTTCGT 5227
Qy 1817 lLeuThrAlaGlnPheValLeuValAsnValIleAlaValLeuMetLysHisLeuG 1837
Db 5228 GCTCACCAGCGAGTTCTGTCTCATCAACGTGGTGGTGGTGTCTCATGAAGCACCTGA 5287
Qy 1837 uGluSerAsnLysGluAlaLysGluAlaGluLeuAlaGluLeuLysHisLeuG 1857
Db 5288 CGACAGCAACAGAGCGCAGAGGAGCGCGAGATGAGTGCAGCTCGAGCTGAGAT 5347
Qy 1857 t---LysThrLeuSerProGlnProHisSerProLeuGlySerProPheLeuTrpProG 1876
Db 5348 GGCCTATGGCTGGCCCTGCGCGAGGCTGCTTACCGGCTCCCGGGCGCC---CCTGG 5404
Qy 1876 yValGluGlyProAsp----- 1881
Db 5405 C---CGAGGCGCGGAGGGGGCGGCGCGGCGCACCGAGGGCGCTGTGTGCGGCG 5461
Qy 1882 -----SerPro----- 1883
Db 5462 CTGCTACTCGCTGCCAGGAGAACCTGTGTGCTGCAGACGCTCTCTTTAATCATCAAGGA 5521
Qy 1884 -----AspSerProLysProGlyAlaLeuHis----- 1892
Db 5522 CTCCTTGGAGGGGAGCTGACCATCATCGAACACTGTCTGGGCTCCATCTTCCACCACTA 5581
Qy 1893 -----ProAlaAla----- 1895
Db 5582 CTCCTCGCTGCGGCTGCAAGAGTGTCAACAGCACAGAGGAGTGCAGCTGGCTGA 5641
Qy 1896 -----HisAlaArgSerAlaSer-----HisPh 1903
Db 5642 GACGAGAGCCTTCTCCCTGAACACTCAGACAGTCTCTGTCATCTCTGCTGGGTGAGACCT 5701
Qy 1903 eSerLeuGlnHisProThrMetGlnPro-----HisProThrGluLeuPr 1918
Db 5702 GAGTCTCAGAGACCCACAGCTGCCACCTGCGCGGCGAAGACAGCAAGGTGAGCTTGA 5761
Qy 1918 oGlyProAspLeuThrValArgLysSerGly-----ValSerArgTh 1933
Db 5762 CCCACTGAGCCATCGTGTGGAGACCTGGGCGAATGCTTCTTCCCTTGTCTCTAC 5821
Qy 1933 rHisSerLeuProAsn---AspSerTyrMetCysArgHisGlySerThrAlaGluGlyPr 1952
Db 5822 GGCCTCTGCGGATCCAGAGAACCTCTGTGTGAGATGAGGAGATCCCATCAACCC 5881
Qy 1952 oLeuGlyHisArgGlyTrpGlyLeuProLysAlaGlnSerGlySerValLeuSerValHi 1972
Db 5882 TGTC-----CGTCTCTG-----CTGAACATGACAGCAGTCAAGCACCCCAAGTCC 5929
Qy 1972 sSerGlnProAlaAspThrSerTyrIleLeuGlnLeuProLysAspAlaProHis----- 1990
Db 5930 CTTCTCCCGGATGCTCAGCGCTCTCTGCGCATGCCAGCGAGTCTTCCACCTGCG 5989
Qy 1991 -----LeuLeuGlnProHisSerAlaProThrTrpGlyThrIleProLysLe 2006
Db 5990 AGTGTCTGCCAGCAGAAAGGCCAGAAAGGGCACTGGCAGTGAACCTCCCAAGAT 6049
Qy 2006 uProProProGly-----ArgSerProLeuAlaGlnArgProLeuArgAr 2021
Db 6050 TCGCTGCGAGGCTCTCTGGGCATCTCTGCGGTCAACCAAGGGTCACTGTACCTCTCTCG 6109
Qy 2021 gGlnAlaAlaIleArgThrAspSerLeuAspValGlnGlyLeuGlySerArgGluAspLe 2041
Db 6110 GCAGGCCCGGAGCGCACCTGCTGGAC----- 6140
Qy 2041 uLeuAlaGluValSerProSerProProLeuAlaArgAlaTyrSerPheTrpGlyG 2061
Db 6141 -----GCCAGCCAGCAGCTCGCGGCGCAGCTGCAGACACCGCTCGAGGA 6187
Qy 2061 nSerSerThrGlnAlaGlnHisSerArgSerHisSerLysIleSerLysHisMetTh 2081

Db 6188 CAGCCTGACCTTGAGCGAGACAGCCCGCGCTGCC-----CTGGG 6226
Qy 2081 rProProAlaProCysProGlyProGluProAsnTrpGlyLysGlyProProGluThrAr 2101
Db 6227 GCGGCGCGGCTGTCTCCAGGACCCCGGCGCGCTGTCC-----CCGCGCGCTCG 6277
Qy 2101 gSerSerLeuGluLeuAspThrGluLeuSerTrpIleSerGlyAspLeuLeuProProG 2121
Db 6278 CCGCGCTCTGAGCTG----- 6293
Qy 2121 yGlyGlnGluGluProProSerProArgAspLeuLysCysTyrSerValGluAlaGl 2141
Db 6294 -----CGCGCGCGGCGCTCTTCAGCCTCGCGGCGCTCGCGGCG----- 6332
Qy 2141 nSerCysGlnArgArgProThrSerTrpLeuAspGluArgArgHisSerIleAlaVa 2161
Db 6333 -----CATCAGCGCAGCCACAGCAGCGGGG 6358
Qy 2161 lSerCysLeuAspSerGlySerGlnProHisLeuGlyThrAspProSerAsn----- 2178
Db 6359 CTCC---ACCAGCCCGGCTGCACCCACGACTCCATGACCCCTCGGACGAGAGGG 6415
Qy 2179 -LeuGlyGlnProLeuGlyGlyProGlySerArgProLysLysLysLeuSerProPr 2198
Db 6416 CCGCGTGGCGGCGCGCGCGCGCGCGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 6475
Qy 2198 oSerIleThr-----IleAspProProGluSerGlnGlyProArgThrProProSe 2215
Db 6476 CTCGCTACCTCTCTCTTCTGCGCGCGGCG-----CCGCGCGCAGC 6517
Qy 2215 rProGlyIleCysLeuArgArgAlaProSerSerAspSer-----LysAs 2231
Db 6518 CCGCGGCTTCAAGCGCGCGCGCGAGGTTACAGCAGCAGCAGCAGCAGCAGCAGCAG 6577
Qy 2231 pProLeuAlaSerGlyProProAspSerMetAlaAlaSerProSerProLysLysAspVa 2251
Db 6578 CCGCGCAGCG 6635
Qy 2251 lLeuSerLeuSerGlyLeuSerSerAspProAlaAspLeuAspPro 2266
Db 6636 -----CGCAGCAAGACCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 6665

RESULT 12
US-10-425-800-3
Sequence 3, Application US/10425800
Publication No. US20030180886A1
GENERAL INFORMATION:
APPLICANT: Dietrich, Paul S.
TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
TITLE OF INVENTION: AND USES
FILE REFERENCE: R0043B-REG sequence listing
CURRENT APPLICATION NUMBER: US/10/425,800
CURRENT FILING DATE: 2003-04-29
PRIOR APPLICATION NUMBER: US/09/404,650
PRIOR FILING DATE: 1999-09-23
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
LENGTH: 6855
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (192)..(6755)
US-10-425-800-3
Alignment Scores:
Pred. No.: 0
Score: 5484.00
Percent Similarity: 59.93%
Best Local Similarity: 51.20%
Length: 6855
Matches: 1237
Conservative: 211
Mismatch: 507

Query Match:	46.07%	Indels:	462
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Dd	264	CAGCCCGACCCCGAGGCCCCCATCTTCCCCCGCAGGCCTGGAGGACCCTCTGTGTGA	323
Qy	51	-----LeuProTyPrAlaLeuAlaProValPhePheTyLeuSerGln	66
Dd	324	GCTGATCTCATGTCTCCACACCCAGACCTTGSGGCTATTGCCTTCTTCTGCTCGCACG	383
Qy	67	AspSerArgProArgSerTrpCysLeuArgThrValCysAsnProTrpPheGluArgIle	86
Dd	384	ACCACGACCCCGGAACTGCTGTCATCAAGATGTGTGCACACCCGCTGTTTTGAATGTCT	443
Qy	87	SerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMetPheArgProCysGluAsp	106
Dd	444	AGCATGCTGTGTATCTCTGCTGACTGCGTGACACTTGGCATGTACCGCGCTGGCAGC	503
Qy	107	IleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPheAspAspPheIlePheAla	126
Dd	504	ATGAGCTGCTGTCCGACCGCTGCAAGATCTCGAGGTCTTTGATGACTTTCATCTTATC	563
Qy	127	PhePheAlaValGluMetValLysMetValAlaLeuGlyIlePheGlyLysCys	146
Dd	564	TTCCTTGGCATGGAGATGTGCTCAAAGATGTGTGCGCTTGGGGATTTTGGCAAGAAGTC	623
Qy	147	TyrLeuGlyAspThrTrpAsnArgLeuAspPhePheIleValIleAlaGlyMetLeuGlu	166
Dd	624	TACCTCGGGACACATGAACCGCTGGATTTCTTCATCGTATGGCAGGAGTGTGCGAG	683
Qy	167	TyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArgThrValArgValLeuArg	186
Dd	684	TACTCCCTGGACCTTCAGAACATCAACCTGTGACGCATCCGACCGCTCGCGCTCCTGAGG	743
Qy	187	ProLeuArgAlaIleAsnArgValProSerMetArgIleLeuValThrLeuLeuLeuAsp	206
Dd	744	CCCCCTAAAGCCATCAACCGCGTCCACAGTAGTGGAGTCTCTGGTGAACCTGCTCTCGAC	803
Qy	207	ThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePheValPhePheIlePheCly	226
Dd	804	ACACTGCCCATGCTGGGAATGCTCTGCTGCTCTGCTTCTTTGTCTTCTTCATCTTTGGC	863
Qy	227	IleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArgCysPheLeuProGluAsn	246
Dd	864	ATCATAGTGTGCAGCTCTGGCGGGCTGTGCGGTAAACCGCTGCTTCTCTGGAGGAGAAC	923
Qy	247	PheSerLeuProLeuSerValAspLeuGluArgTyrTyrGlnThrGluAsnGluAspGlu	266
Dd	924	TTCACCATACAAGGGATGTGGCTTGCCCCCATACTACCAAGCCGAGGAGGATGTAG	983
Qy	267	SerProPheIleCysSerGlnProArgGluAsnGlyMetArgSerCysArgSerValPro	286
Dd	984	ATGCCCTTCATCTGCTCCCTGTGGCGGCACATGGGATAATGGGCTGCCATGACATCCCC	1043
Qy	287	ThrLeuArgGlyAspGlyGlyGlyProProCysGlyLeu-----	300
Dd	1044	CCGCTCAAGGAGCAG-----GGCGGTGAGTGTCTCCCTGTCCAAGGACGACGCTCAT	1094
Qy	301	AspTyrGluAlaTyraenSerSerSerAsnThrThr-----CysValAsnTrpAsnGln	318
Dd	1095	GACTTTGGCGCGGGCGCAGGACCTCAATGCCAGCGGCTCTGTGTCACTGGAACCGT	1154
Qy	319	TyrTyrThrAsnCysSerAlaGlyGluHisAsnProPheLysGlyAlaIleAsnPheAsp	338
Dd	1155	TACTACAATGTGTCCGCACGGGACGCGCAACCCCAAGGGTGCATCACTTTGAC	1214
Qy	339	AsnIleGlyTyraIaTrpIleAlaIlePheGlnValIleThrLeuGluGlyTrpValAsp	358
Dd	1215	AACATCGGTATGTCTGATTGTCACTTCAGGTGATCACTCTGGAAGCTGGGTGGAG	1274

Qy 1400 uValValGluThrLeuMetSerSerLeuLeuProIleGlyAsnIleValValIleCysCy 1420
Db 3968 GGTGGTGAGACATCATCTCTCCCTCAAGCCCATCGGCAACATCGTGCTCATCTGCTG 4027
Qy 1420 sAlaPhePheIleIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPhePheVa 1440
Db 4028 TGCCTTCTTCATCATCTTGGCATCTTGGAGTGGAGCTCTTCAAGGCAAGTCTTACCA 4087
Qy 1440 lCysGlnGluAspThrArgAsnIleThrAsnLysSerAspCysAlaGluAlaSerTy 1460
Db 4088 CTGTCTGGGCTGGACACCCGCAACATCACCAACCGCTCGGACTGCATGGCGGCAACTA 4147
Qy 1460 rArgTTPValArgHisLysTyAsnPheAspAsnLeuGlyGlnAlaLeuMetSerLeuPh 1480
Db 4148 CCGCTGGGTTCATCACAAATACACTTCGACAACCTCGGCCAGGCTCTGATGTCTCTCTT 4207
Qy 1480 eValLeuAlaSerLysAspGlyTTPValAspIleMetTyAspGlyLeuAspAlaValG1 1500
Db 4208 TGTCTGGCATCCAAAGATGGTGGTGGAGCATCATGTACATGATGGATGGATGTGTTC 4267
Qy 1500 yValAspGlnGlnProIleMetAsnHisAsnProTTPMetLeuLeuTyPheIleSerPh 1520
Db 4268 TGTGGACAGCAGCTGTGACCAACCAACCAACCCCTGGATGTCTGTACTTCACTCTCTT 4327
Qy 1520 eLeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValValValGluAsnPh 1540
Db 4328 CCTCTCATCTGCTAGCTCTTGTGTCTCAACATGTTGTGGGTGTCTGTGGAGAACTT 4387
Qy 1540 eHisLysCysArgGlnHisGlnGluGluGluAlaArgArgGluGluLysArgLe 1560
Db 4388 CCACAGTGGCGGAGACACAGAGAGGTGAAGAGCGACGGCGGTGAGGAGAGCGCT 4447
Qy 1560 uArgArgLeuGluLysLysArgLysAlaGlnCysLysProTyTyrsSerAspTyrs 1580
Db 4448 GCGCGCTGTGGAGAGAGCGCGGAGGCGCCAGCGCTGCTCTACTATGCCACTATTG 4507
Qy 1580 rArgPheArgLeuLeuValHisHisLeuCyThrSerHisTyTyrsLeuAspLeuPheIleTh 1600
Db 4508 TCACACCGCGGTGCTCATCTCACTCATGTGTGACAGCCACTACCTGGACATCTTTCATCAC 4567
Qy 1600 rGlyValIleGlyLeuAsnValValThrMetAlaMetGluHisTyTyrsGlnProGlnI1 1620
Db 4568 CTTTCATCTGCTCAACGTGGTGCATCATGTCTGAGGAGCTACATACAGCCACAGTC 4627
Qy 1620 eLeuAspGluAlaLeuLysIleCysAsnTyTyrsIlePheThrValIlePheValLeuGluse 1640
Db 4628 CTTGGAGACGCTCTCAAGTACTGCAACTATATGTTCACCACTGTCTTGTGTGGAGGC 4687
Qy 1640 rValPheLysLeuValAlaPheGlyPheArgArgPhePheGlnAspArgTTPAsnGlnLe 1660
Db 4688 TGTCTGAAGCTGGTGGCATTTGTCTGAGGCGCTTCTTCAAGGACCGATGGAAACCACT 4747
Qy 1660 uAspLeuAlaIleValLeuLeuSerIleMetGlyIleThrLeuGluGluIleGluValAs 1680
Db 4748 GGACTGGCCATTTGTCTACTGTGAGTATGGGATCATCCCTGGAGAGATCGAGATCAA 4807
Qy 1680 nAlaSerLeuProIleAsnProThrIleIleArgIleMetArgValLeuArgIleAlaAr 1700
Db 4808 TGGCGCTTGGCCATCAATCCACCATCATCCGATCATGAGGTTCTGCGCATTTGCCG 4867
Qy 1700 gValLeuLysLeuLeuLysMetAlaValGlyMetArgAlaLeuLeuAspThrValMetGl 1720
Db 4868 AGTCTGAAGCTGTGAAGATGGGCACAGGAATGGGCGCTCTTTCATGTCTTCTTCATCATGC 4927
Qy 1720 nAlaLeuProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPheIlePheAl 1740
Db 4928 AGCTTTGGCCAGGTGGCAACCTGGGCTCTCTTTCATGTCTTCTTCTTCATCATGC 4987
Qy 1740 aAlaLeuGlyValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGluGl 1760
Db 4988 TGTCTCTGGGTGGAGCTCTTTGGAGAGCTGTCTGCAACGACGAGAACCGCTGCGAGGG 5047

Qy 1760 yLeuGlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgVa 1780
Db 5048 CATGAGCGGATGCCACCTTCGAGAACTTCGGCATGGCCCTTCCTCACACTCTTCCAGGT 5107
Qy 1780 lSerThrGlyAspAsnTTPAsnGlyIleMetLysAspThrLeuArgAspCys---AspG1 1799
Db 5108 CTCCACGGGTGACAACTGGAAACGGGATCATGAAGACACACGCTGCGGAGCTGCACCCACGA 5167
Qy 1799 nGluSerThrCysTyrsAsnThrVal-----IleSerProIleTyPheValSerPheVa 1817
Db 5168 CGAGCGAGCTGCTGAGCAGCTGCGAGTTTGTGTCGCGCTGTACTTCGTGAGCTTCTGT 5227
Qy 1817 lLeuThrAlaGlnPheValLeuValAsnValIleAlaValLeuMetLysHisLeuGl 1837
Db 5228 GCTCACCGCGAGTTCGTGTCTCATCAACGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5287
Qy 1837 uGluSerAsnLysGluAlaLysGluGluAlaGluLeuGluAlaGluLeuGluGluMe 1857
Db 5288 CGACAGCAACAGAGGCGGAGGAGGAGCGCGAGATGGATGCGAGCTCGAGCTGGAGAT 5347
Qy 1857 t---LysThrLeuSerProGlnProHisSerProLysSerProLysSerProPheLeuTTProGl 1876
Db 5348 GGCCTATGGCTGGGCGCTGCGCGAGGCTGCTTACCGGCTCCCGGCGCGCC---CCTGG 5404
Qy 1876 yValGluGlyProAsp----- 1881
Db 5405 C---CGAGGCGCGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 5461
Qy 1882 ---SerPro----- 1883
Db 5462 CTGCTACTCGCTGCCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 5521
Qy 1884 ---AspSerProLysProGlyAlaLeuHis----- 1892
Db 5522 CTCTCTGAGGCGGAGCTGACCATCATCGAACCTGTGCGGCTCCATCTTCCACCACCTA 5581
Qy 1893 ---ProAlaAla----- 1895
Db 5582 CTCTCTGCGCTGCGGCTGCAAGAGTGTCAACAGCAAGAGGAGGAGGAGGAGGAGGAGGAG 5641
Qy 1896 ---HisAlaArgSerAlaSer-----HisPh 1903
Db 5642 GACGAGGCGCTTCTCCCTGAACTCAGACAGGTCCTGCTCCATCTCTGCTGGGTGAGCAGCT 5701
Qy 1903 eSerLeuGluHisProThrMetGlnPro-----HisProThrGluLeuPr 1918
Db 5702 GAGTCTCGAGGACCCACAGCAGCTGCGCCACCTGCGCGCAAGACAGCAAGGAGTGGAGTGA 5761
Qy 1918 oGlyProAspLeuThrValArgLysSerGly-----ValSerArgTh 1933
Db 5762 CCCACCTGAGCCCATGCGTGTGGAGACCTGGGCGAATGCTTTCGCCCTTGTCTCTAC 5821
Qy 1933 rHisSerLeuProAsn---AspSerTyMetCysArgHisGlySerThrAlaGluGlyPr 1952
Db 5822 GCGCTCTCGCGGATCCAGAACTTCTGTGTGAGATGGAGGAGATCCCATTCACCC 5881
Qy 1952 oLeuGlyHisArgGlyTTPGlyLeuProLysAlaGlnSerGlySerValLeuSerValHi 1972
Db 5882 TGTC-----CGGTCTCTG-----CTGAACATGACAGCAGTCAAGCACCACCCCAAGTCC 5929
Qy 1972 sSerGlnProAlaAspThrSerTyTyrsLeuGlnLeuProLysAspAlaProHis----- 1990
Db 5930 CTTCTCCCGGATGCTCCAGCCCTCTCTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5989
Qy 1991 -----LeuLeuGlnProHisSerAlaProThrTTPGlyThrIleProLysLe 2006
Db 5990 AGTGTCTGCCAGCAGCAAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 6049
Qy 2006 uProProProGly-----ArgSerProLeuAlaGlnArgProLeuArg 2021
Db 6050 TGGCTCGAGGCTCTCTGGGATCTCTGCGGTGCTACCAAGGAGTCACTGATACCTCTCTCG 6109
Qy 2021 gGlnAlaAlaIleArgThrAspSerLeuAspValGlnGlyLeuGlySerArgGluAspLe 2041

Db	6110	GCAGGCGACCGGAGGCACAGCTCGCTGGAC-----	6140
Qy	2041	uLeuAlaGluValSerGlyProSerProProLeuAlaAlaArgAlaTy-SerPheTrpGlyG1	2061
Db	6141	-----GCCAGCCCAAGACAGCTCCGGGGAGCCTCCACACACAGCTCGAGGA	6187
Qy	2061	nSerSerThrGlnAlaGlnGlnHisSerArgSerHisSerLysIleSerLysHisMetW	2081
Db	6188	CAGCCTGACCTGAGCGACAGACCCCGCGCGTGC-----CTGGG	6226
Qy	2081	rProProAlaProCysProGlyProGluProAsnTrpGlyLysGlyProProGluThrAr	2101
Db	6227	GCGCGCGCGCGCTGCTCCAGAGCCCGCGCGCGCTGTCC-----CCCGCGCTCG	6277
Qy	2101	gSerSerLeuGluLeuAspThrGluLeuSerTrpIleSerGlyAspLeuLeuProG1	2121
Db	6278	CCGCGCGCTGAGCTG-----	6293
Qy	2121	yGlyGlnGluGluProProSerProArgAspLeuLysLysCysTy-SerValGluAlaG1	2141
Db	6294	-----CGCGCGCGGGCGCTTCAGCGCTCGGGGGCTCGGGCG-----	6332
Qy	2141	nSerCysGlnArgArgProThrSerTrpLeuAspGluGlnArgArgHisSerIleAlaVa	2161
Db	6333	-----CATCAGCGGACGCACAGCAGCGGGG	6358
Qy	2161	lSerCysLeuAspSerGlySerGlnProHisLeuGlyThrAspProSerAsn-----	2178
Db	6359	CTCC--ACCAGCCCGGGCTGCACCCACCAACAGACTCCATGCAGCCCTCGACAGGAGGG	6415
Qy	2179	-LeuGlyGlyGlnProLeuGlyGlyProGlySerArgProLysIleLysLeuSerProPr	2198
Db	6416	CCGCGGTGGCGGGCGGGCGGGCGGGAGGAGCACTCGGAGACCTCTACAGACCT	6475
Qy	2198	oSerIleThr-----IleAspProProGluSerGlnGlyProArgThrProProse	2215
Db	6476	CTCGCTCACCTCCCTCTTCTGCGCGCGCGCC-----CCGCGCGCCAGC	6517
Qy	2215	rProGlyIleCysLeuArgArgAlaProSerSerAspSer-----LysAS	2231
Db	6518	CCCCGGCTCACGCCCGCGCAGGAAGTTTCAGCAGACCAAGCAGCTGCGCCGCCCGCGCGC	6577
Qy	2231	pProLeuAlaSerGlyProProAspSerMetAlaAlaSerProSerProLysLysAspVa	2251
Db	6578	CCCCACGCCCGCGCTGGGCCACGGCTGGCCCGGAGCCCTCTGTTGGGCGCGGAC--	6635
Qy	2251	lLeuSerLeuSerGlyLeuSerSerAspProAlaAspLeuAspPro	2266
Db	6636	-----CGCACAAGAGCCCCCGCGGGCGGCACCG	6665

RESIST 13

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RES001 13
US-09-935-541-12
; Sequence 12, Application US/09935541
; Patent No. US20020150911A1
; GENERAL INFORMATION:
; APPLICANT: Dietrich, Paul S.
; APPLICANT: McGivern, Joseph G.
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
; TITLE OF INVENTION: AND USES
; FILE REFERENCE: R0043B-REG sequence listing
; CURRENT APPLICATION NUMBER: US/09/935,541
; CURRENT FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: 09/404,650
; PRIOR FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 6503
; TYPE: DNA
; ORGANISM: Rattus sp.
US-09-935-541-12

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Alignment Scores:
 Pred. No.: 0 Length: 6503
 Score: 5418.50 Matches: 1212
 Percent Similarity: 60.41% Conservative: 209
 Best Local Similarity: 51.57% Mismatches: 446
 Query Match: 45.52% Indels: 484
 DB: 9 Gaps: 53

US-09-611-257A-37 (1-2266) x US-09-935-541-12 (1-6503)

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Db	320	GGAATCACTGAGCAGCGGGCCCGAGCTCCCTCCATCCCTCCAGCGCTGGAGGAG	379
Qy	47	GluAlaGlyGly-----LeuProTyrProAlaLeuAlaProValValPhePhe	62
Db	380	CCATTGGAGGAACCAACCTGACGTCCACATCCAGACCTGGCTCCTGTTCTTCTTC	439
Qy	63	TyrLeuSerGlnAspSerArgProArgSerTyrCysLeuArgThrValCysAsnProTyrP	82
Db	440	TGCTCGCCGAGACACGAGCCACGAACTGGTGATCAAGATGGTTTGTAAACCGTGG	499
Qy	83	PheGluArgIleSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMetPheArg	102
Db	500	TTCAGTGTGTGAGCATGCTGGTATTCTGTCTGAATGTGTGACCTGGGCATGTACCA	559
Qy	103	ProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPheAsp	122
Db	560	CCATGTATGACATGAGTGCCTGTGGACCGTTGCAAGATCCTGCAGGTCCTCGATG	619
Qy	123	PheIlePheAlaPhePheAlaValGluMetValValLysMetValAlaLeuGlyIlePhe	142
Db	620	TTCATCTTCATCTCTTGGCAGGAGATGGTCTTAAAGATGGTGGCCCTGGGCATTTT	679
Qy	143	GlyIlyIlyCysTyrLeuGlyAspThrTyrAsnArgLeuAspPheIleValIleAla	162
Db	680	GGCAAGAAGTGTACCTCGGAGACACATGNAACCGCTGGATTCTTCATTGTCTATGG	739
Qy	163	GlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArgThrVal	182
Db	740	GGGATGTTGAGTACTCTCTGGACCTACAGAACATCAACCTGTTCAGCCATCCGCATG	799
Qy	183	ArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeuValThr	202
Db	800	CGTGTCTGAGGCGCTCTCAAGAGCATCAACCGGTATCCAGCATCGGATCTCTGGTGA	859
Qy	203	LeuLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPheValPhe	222
Db	860	CTGTGCTCGACAGCTGCCCATGCTGGGAAACGTGTCTCTGTCTTCTTCTCTCTTC	919
Qy	223	PheIlePheGlyIleValGlyValGlnLeuThrAlaGlyLeuLeuArgAnArgCysPhe	242
Db	920	TTCATCTTCGGCATCATGTGGCGTGCAGCTCTGGCAGGCGTGTACGGAACCGCTGCT	979
Qy	243	LeuProGluAsnPheSerLeuProLeuSerValAspLeuGluArgTyrTyrGlnThrGlu	262
Db	980	CTGGAAGAGAACTTCACCATACAGGGGATGTGGCCCTGCCCCCTTATTACCAACGAG	1039
Qy	263	AsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArgSerCys	282
Db	1040	GAGGATGACGAGATGCCCTTTATCTGCTCCCTGACTGGGAGCAATGGCATCATGGGCTG	1099
Qy	283	ArgSerValProThrLeuArgGlyAspGlyGlyProCysGlyLeu-----	300
Db	1100	CACGAGATCCCCCAGCTGAGGAGCAG-----GGCCGGGAATGCTGCTGTCCAA	1150
Qy	301	-----AspTyrGluAlaTyrAsnSerSerSerAsnThrThr-----CysVal	314
Db	1151	GATGATGTGTATGACTTCGGGGGGGGCGCCAGGACCTCAACGCCAGCGGTCTGTGCGTC	1210
Qy	315	AsnTrpAsnGlnTyrTyrThrAsnCysSerAlaGlyGluHisAsnProPheIlyGlyAla	334
Db	1211	AACTGGGACCGCTACTCAACGCTCTGGCAGCGGGCAACGCCAACCTCTCAACAGGGGCC	1270

[illegible]

QY	689	AspSerGluAlaValTyrGluPheThrGlnAspAla---GlnHisSerAsp-LeuArgAs	707
DB	1892	GGTGGCTCTGCAGAGCGCGAAGCAATGGGGATGGACTCCAGAGCAGTGAAGGATGGGCT	1951
QY	707	pProHisSer-----ArgArgGlnArgSerLeuGlyProAspAlaGluProSerSe	724
DB	1952	TCCTCGACACTGGGAAGGAGGAGGAACAGGACGCGG-----CAGCCGACTG	2002
QY	724	rValLeuAlaPheTrpArgLeuIleCysAspThrPheArgLysIleValAspSerLysTy	744
DB	2003	TGTGGG-GATGTGTGGCGCGAGACACGAAAAAGCTGCGGGGCATCGTGACAGCAAGTA	2061
QY	744	rPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerMetGlyIleGluTy	764
DB	2062	CTTCAACAGAGGTATCATGATGCTATCTCTGGTGAACACAGTACAGATCGGCATCCAG	2121
QY	764	rHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnIleValPheThrSe	784
DB	2122	CCAGAACACGCCGAGGAGCTGACCAACATCTCTGGAGATCTGCANGTGGTCTTACCAG	2181
QY	784	rLeuPheAlaLeuGluMetLeuLysLeuLeuValTyrGlyProPheGlyTyrIleTy	804
DB	2182	TATGTTTGGCTTGGAGATGATCTGAAACTGGCGGCTTTGGGCTCTCTGACTACCTGCG	2241
QY	804	sAsnProTyrAsnIlePheAspGlyValIleValValIleSerValTrpGluIleValGI	824
DB	2242	GAACCTTTACAACATCTTTGACAGCATCTGTCATCATCAGCATCTGGGAAATCGTGGG	2301
QY	824	YGlnGlnGlyGlyGlyLeuSerValLeuArgThrPheArgLeuMetArgValLeuLysLe	844
DB	2302	CGAGCGGACGGTGGGCTGTCTGTGTGGCGACCTTCCGGGTCTCGGGGTCTGAAGCT	2361
QY	844	uValArgPheProAlaLeuGlnArgGlnLeuValValLeuMetLysThrMetAspAs	864
DB	2362	GGTGGCTTTCATGCGCGGCTGGCGGCCAGCTCGTGGTCTCATGAAGACCATGACAA	2421
QY	864	nValAlaIaThrPheCysMetLeuLeuMetLeuPheIlePheIlePheSerIleLeuGlyMe	884
DB	2422	CGTGGCCACCTTCTGCATGTACTCATGTGTGTTCATCTTTCATCTTCCAGCATCTCGGAT	2481
QY	884	tHisLeuPheGlyCysLysPheAlaSerGluArgAsp---GlyAspThrLeuProAspAr	903
DB	2482	GCATATCTTTGGCTGCAATTCAGCCTCCGCACGGACACGGGAGACACCGTCTCTGACAG	2541
QY	903	qLysAsnPhAspSerLeuLeuTrpAlaIleValThrValPheGlnIleLeuThrGlnGI	923
DB	2542	GAAGAACTTCGATTCCTTACTGTGGGCCATCGTCACAGTGTCCAGATCCTCCTCAGGA	2601
QY	923	uAspTrpAsnLysValLeuTyTrAsnGlyMetAlaSerThrSerSerTrpAlaAlaLeuTy	943
DB	2602	GGACTGAAGCTTGTCTGTACAAATGGCATGGGCTCCACACCCCTGGGGCTCTCCCTCTA	2661
QY	943	rPheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuLeuValAlaIleLe	963
DB	2662	TTTGTGTGGCTCATGACCTTTGGCAACTACGTTCTTCAATCTCTGGTGGCTATCCT	2721
QY	963	uValGluGlyPheGlnAlaGluGluIleSerLysArgGluAspAlaSerGlyGlnLeuSe	983
DB	2722	GGTAGAGGGTTTCAGGCTGAG-----LeuAspGlyAs	2743
QY	983	rCysIleGlnLeuProValAspSerGlnGlyGlyAspAlaAsnLysSerGluSerGluPr	1003
DB	2744	-----GGTGATGCTAATCGTTCCTGCTCTCATGA	2772
QY	1003	oAspPheSerProSer-----LeuAspGlyAs	1013
DB	2773	GGACCAAGAGCTCATCCAATTTGGAGGAGTTTGACAAGCTCCACAGAGGGCTCGACACAG	2832
QY	1013	pGlyAspArgLysLysCysLeuAlaLeuValSerLeuGlyGluHisProGluLeuArgLy	1033
DB	2833	TAGNATCTCAAGCTCTGGCCAATACCCATGACCAACCAATGGACAC-----	2878
QY	1033	sSerLeuLeuProProLeuIleIleHisThrAlaAlaIaThrProMetSerLeuProLysSe	1053

Db	2879	-----CTGGACCCCT-----				2896
Qy	1053	rThrSerThrGlyLeuGlyGluAlaLeuGlyProAla-			AGCCTCCCT	1065
Db	2897	-----CTGGGTGGCATCTGGGTCTCTGTGTACCATGGTACTGCCCCCG			2943	
Qy	1066	-----SerArgThrSerSerSe			1072	
Db	2944	CCTCTCACTGACGACCGCGTACTGGTGGCCCTAGACTCTCGAAAGCAGTCTCAT			3003	
Qy	1072	rGlySerAlaGluProGlyAlaAlaHisGluMetLysSerProSerAlaArgSerSe			1092	
Db	3004	GTCCCTGGGCGAG-----ATGAGCTATGATCAGCGATCTTGTTCAGCTCCCGAGCTC			3057	
Qy	1092	rProHisSerProTrpSerAlaAlaSerSerTrpThrSerArgArgSerSerArgLenSe			1112	
Db	3058	CTACTACGGGCGCTGGGGCGCAGCTGGGCTAGCGCGCTCCAGCTCGGAAC--			3115	
Qy	1112	rLeuGlyArgAlaProSerLeuLysArgArgSerProSerGlyGluArgArgSerLeuLe			1132	
Db	3116	-----AGCCTGAACACAAAGCCGCTAGCGCGCTCCAGCTCGGACTTACT			3159	
Qy	1132	userGlyGluGlyGlnGluSerGlnAspGluGlu-----GluSerSerGluGluGlu			1149	
Db	3160	GTCTGGGAGGTGGAGTACTGCTCGTCAGGGCCTGTGAGGGCGCCCGGAGGCGGCC			3219	
Qy	1150	-----ArgAlaSerProAlaGlySerAspHis-----			1158	
Db	3220	AACTCGCACCGCACCCCTGCTATCCACACGCGCACCGCACCATGGACCCACCT			3279	
Qy	1159	-----ArgHisArgGlySerLeuGluAlaLysSerSerPheAs			1173	
Db	3280	GGCACACCGTCAACGACACCCCGCGGACTCTGTCCCTTCATACCGGACTCTGTGA			3339	
Qy	1173	pLeuProAspThrLeuGlnValProGlyLeuHisArgThrAlaSer-----GlyArgG			1191	
Db	3340	CCTGGGAGAGCTGGTCCCGTGGTGGTGGTCCACTCACGGCGCGCTTGGAGGGGGCGG			3399	
Qy	1191	ySerAlaSerGluHisGlnAspCysAsnGlyLysSerAlaSerGlyArgLeuAlaArgAl			1211	
Db	3400	TCAGGCCCCCTGGGCGACGAGGACTGCAATGGCAGATGCCAACATAGCCCAAGGATGCTT			3459	
Qy	1211	aLeuArgProAspAspProProLeuAspGlyAspAlaAspAspGlyGluGlyAsnLeuSe			1231	
Db	3460	CACCAAGATGATGATACCGCGCGGACCGCGGGAGGAC--GAGGAGGAGATCGACTATAC			3516	
Qy	1231	rLysGlyGluArgValArgAlaTrpIleArgAlaArgLeuProAlaCysTyrLeuGluAr			1251	
Db	3517	CCTGTGTTTCCGGTCCGCAAGATGATGTGTACAGCGCGGACTGGTGGAGTCCG			3576	
Qy	1251	gAspSerTrpSerAlaTrpIlePheProProGlnSerArgPheArgLeuLeuCysHisAr			1271	
Db	3577	CGAGGACTGGTGGTCTACTCTTCTCCCGGAGAACAGTTCCGGATCTGTGTGCAGAC			3636	
Qy	1271	gIleIleThrHisLysMetPheAspHisValValLeuValIleIlePheLeuAsnCysIl			1291	
Db	3637	CATCATGTCTCAACACTTTTGGTACTGCTGTGTCTTGGCTTTATCTCTCAACTGAT			3696	
Qy	1291	eThrIleAlaMetGluArgProLysIleAspProHisSerAlaGluArgIlePheLeuTh			1311	
Db	3697	CACCATTTGCTGGAGAGACCCAGATTGAAGCTGGTACACTGAGCGCACTTCTCTAC			3756	
Qy	1311	rLeuSerAsnTrpIlePheThrAlaValPheLeuAlaGluMetThrValLysValValAl			1331	
Db	3757	GGTGTCTACTACTACTCTTCACAGCCATCTTGGGGCGAGATGACACTCAAGGTGGTTTC			3816	
Qy	1331	aLeuGlyTrpCysPheGlyGluGlnAlaTyrLeuArgSerSerTrpAsnValLeuAspGl			1351	
Db	3817	TCGGGCGCTGACTTTGGTGGAGAGCGGCTACCTCGCTAGCAGCTGGAATGTACTGATGG			3876	
Qy	1351	yLeuLeuValLeuLeuSerValIleAspIleLeuValSerMetValSerAspSerGlyTh			1371	

Db	3877	TTTCCTGGTCTTTGTGTCCATCATCGATATCGTAGTGTCCGTGGCTCTCTGCTGGGGGAGC	3936
Qy	1371	rLysIleLeuGlyMetLeuArgValLeuArgLeuLeuArgThrLeuArgProLeuArgVa	1391
Db	3937	CAAGATTCTGGGGTCTCTCCGGGTCTCGGGTCTCTGCGTACCTTACCTTACCTCTTGGGGT	3996
Qy	1391	lIleSerArgAlaGlnGlyLeuLysLeuValValGluThrLeuMetSerSerLeuLysPr	1411
Db	3997	TATCAGCCGGGCCCTCGGCTGAAGCTGGTGTAGAGACGCTCATCTCTCCCTCAAGCC	4056
Qy	1411	oIleGlyAsnIleValIleCysCysAlaPhePheIleIlePheGlyIleLeuGlyVa	1431
Db	4057	CATTGGGAACATCGCTCATCTGTGTGGCTCTTTCATCATCTTCGGCATCTCTGGGGT	4116
Qy	1431	lGlnLeuPheLysGlyLysPhePheValCysGlnGlyGluAspThrArgAsnIleThrAs	1451
Db	4117	GCAGTTTTTCAAGCGAAGTTCTACCATTTGTTGGAGTGGACACCCGAAACATCACAA	4176
Qy	1451	nLysSerAspCysAlaGluAlaSerTyrArgTrpValArgHisLysTyrAsnPheAspAs	1471
Db	4177	CGATCTGACTGCTGGCGGCCAATACCTACCTGGGTGCATCACAAATACAACTTTTGACA	4236
Qy	1471	nLeuGlyGlnAlaLeuMetSerLeuPheValLeuAlaSerLysAspGlyTrpValAspIl	1491
Db	4237	CCTGGCCAGGCAATGTATGCTCTTGTCTTGGCTCCAAAGGACGCGTGGTGAACAT	4296
Qy	1491	eMetTyrAspGlyLeuAspAlaValGlyValAspGlnGlnProIleMetAsnHisAsnPr	1511
Db	4297	CATGTATATGATGTAGATGCTGTGTGGACGAGCAGCAGGACCAACCAACCC	4356
Qy	1511	oTrpMetLeuTyrPheIleSerPheLeuLeuIleValAlaPhePheValLeuAsnMe	1531
Db	4357	CTGGATGCTACTGTACTTCAATTCGTTCTGTCTCATCTGTCAGCTCTTTTGTCTCAACAT	4416
Qy	1531	tPheValGlyValValGluAsnPheHisLysCysArgGlnHisGlnGluGluGl	1551
Db	4417	GTTTGTGGCGGTGCTCGTGAGAACTTCCCAAGTCCGCGCAGCACCCAGGAGCTGAGGA	4476
Qy	1551	uAlaArgArgArgGluGluLysArgLeuArgLeuGluLysLysArgArgLysAlaGl	1571
Db	4477	GGCGCGAGCGCTGAGGAGAAACCGCTGGCGGCTTGGAAAGAAAGCGCCGTAGGCTCA	4536
Qy	1571	nCysLysProTyrTyrSerAspTyrSerArgPheArgLeuLeuValHisLysLeuCysTh	1591
Db	4537	GAGGCTGCCCTACTATGCTACCTACTGTCCCAAGGTGCTCATCCACTCCATGTGCAC	4596
Qy	1591	rSerHisTyrLeuAspLeuPheIleThrGlyValIleGlyLeuAsnValThrMetAl	1611
Db	4597	CAGCCACTACTGGACATCTTCAATTCATCTCATCTCGCTCAATGTTGTCCCAATGTC	4656
Qy	1611	aMetGluHisTyrGlnGlnProGlnIleLeuAspGluAlaLeuLysIleCysAsnTyrIl	1631
Db	4657	CTGGAGCACTACAACAGCCTATACCTCCCTAGAGACAGCCCTTAAGTACTGCAACTACAT	4716
Qy	1631	ePheThrValIlePheValLeuGluSerValPheLysLeuValAlaPheGlyPheArgAr	1651
Db	4717	GTTCAACCACTCTTTGTGTGTGGAGGTGTGTGAAGCTGTGTGGCTATTGGCCCTGAGGG	4776
Qy	1651	gPhePheGlnAspArgTrpAsnGlnLeuAspLeuAlaIleValLeuLeuSerIleMetGl	1671
Db	4777	TTTCTTCAAGGACCGATGGAAACAGCTGGACCTGGCCATTTGCTGTCTGCTCCGTCATGG	4836
Qy	1671	yIleThrLeuGluGluIleGluValAsnAlaSerLeuProIleAsnProThrIleIleAr	1691
Db	4837	CATCACACTGGAGAGATCGAGATCAATGCGCCCTTCCCATCAACCCCACTCATCCG	4896
Qy	1691	gIleMetArgValLeuArgIleAlaArgValLeuLysLeuLeuLysMetAlaValGlyMe	1711
Db	4897	TATCATCGGTCTTCTGGGTATCGCCGGGTGTGAAGCTATTGAAGATGCGCACAGAT	4956
Qy	1711	tArgAlaLeuLeuAspThrValMetGlnAlaLeuProGlnValGlyAsnLeuGlyLeuLe	1731
Db	4957	CGGGGCCCTGCTGACACACAGTGGTACAGGCTCTGCCCCAGGTGGGCAACCTGGGCTGCT	5016

QY 724 rValLeuAlaPheTrpArgLeuIleCysAspThrPheArgIysIleValAspSerLysTy 744
DB 2003 TGTGGG-GATGTGTGGCGCGAGACACGAAAAAAGCTCGCGGCATCTGTGGACAGCAAGTA 2061
QY 744 rPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerMetGlyIleGluTy 764
DB 2062 CTTCAACAGAGTATCATGATGGGTATCTCTGTGTGACACAGTCAGCATGGGCATCGAGCA 2121
QY 764 rHisGluGlnProGluLeuThrAsnAlaLeuGluIleSerAsnIleValPheThrSe 784
DB 2122 CCAGCAACAGCCCGAGGAGCTGACCAACATCTCTGGAGATCTGCAATGTGTCTTCACCAAG 2181
QY 784 rLeuPheAlaLeuGluMetLeuLeuLysLeuValTyArgIlePheGlyTyIleLe 804
DB 2182 TATGTGTTCCTGGAGATGATCTCTGAAACTGGCGCCTTTGGGCTCTTCGACTACCTGGCG 2241
QY 804 sAsnProTyAsnIlePheAspGlyValIleValIleValIleSerValTrpGluIleValG 824
DB 2242 GAACCCCTTACACATCTTTGACACATCATCTGTCATCATGATCTCTGGGAATCTGTGGG 2301
QY 824 yGlnGlnGlyLeuSerValLeuArgThrPheArgLeuMetArgValLeuLysLe 844
DB 2302 GCAGCGGAGCGGTGCTGTGTGTGGCGACCTTCGGGTGTGGGTGTGTAAGCT 2361
QY 844 uValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetLysThrMetAspAs 864
DB 2362 GGTGCGCTTATGTCGCGCGCTGCGCGCCAGCTCGTGTGTCTCATGAAGACCATGGACAA 2421
QY 864 nValAlaThrPheCysMetLeuLeuMetLeuPheIlePheIlePheSerIleLeuGlyMe 884
DB 2422 CGTGGCCACCTTCTGCATGCTACTCATGCTGTTCATCTTCATCTTCAGCATCTTTGGGAT 2481
QY 884 tHisLeuPheGlyCysLysPheAlaSerGluArgAsp---GlyAspThrLeuProAspAr 903
DB 2482 GCATATCTTTGGCTGCAATTCACCTCCGCGACGACACGGGACACCGCTCTCTGACAG 2541
QY 903 gLysAsnPheAspSerLeuTrpAlaIleValThrValPheGlnIleLeuThrGlnG 923
DB 2542 GAAGAACTTCGATTCCTTACTGTGGCCATCGTCACAGTGTTCAGATCTCTCACTCAGGA 2601
QY 923 uAspTrpAsnLysValLeuTyArgGlyMetAlaSerThrSerTrpAlaAlaLeuTy 943
DB 2602 GGACTGGAAGCTTGTCTGTACATGGCATGGCTCCACACCCCTGGGCTCTCCCTCTA 2661
QY 943 rPheIleAlaLeuMetThrPheGlyAsnTyValLeuPheAsnLeuValAlaIleLe 963
DB 2662 TTTTGTGGCCTCATGACCTTTGGCACTAGTTCTCTCAATCTCTCTGGTGGCTATCCT 2721
QY 963 uValGluGlyPheGlnAlaGluIleSerLysArgGluAspAlaSerGlyGlnLeuSe 983
DB 2722 GGTAGAGGGTTTCAGGCTGAG----- 2743
QY 983 rCysIleGlnLeuProValAspSerGlnGlyIysAlaAsnLysSerGluSerGluPr 1003
DB 2744 -----GGTGTGCTTAATGTTCTGCTCTGATGA 2772
QY 1003 oAspPhePheSerProSer-----LeuAspGlyAs 1013
DB 2773 GGACAGAGCTCATCCATTTGGAGAGTTTGACAGCTCCAGAGGCTGGACACAG 2832
QY 1013 pGlyAspArgLysCysLeuAlaLeuValSerLeuGlyGluHisProGluLeuArgLy 1033
DB 2833 TAGAGATCTCAAGCTCTGCCCAATACCATGACACCAATGACAC----- 2878
QY 1033 sSerLeuLeuProLeuIleIleHisThrAlaAlaThrProMetSerLeuProLysSe 1053
DB 2879 -----CTGGACCTT-----AGCCTCCCT----- 2896
QY 1053 rThrSerThrGlyLeuGlyGluAlaLeuGlyProAla----- 1065
DB 2897 -----CTGGGTGGCATCTGGGTCTCTGTTACCATGGTACTGGTCCGCCCG 2943

QY 1066 -----SerArgArgThrSerSerSe 1072
DB 2944 CCTCTCACTGACCGACAGCCCGTACTGTGTGGCCCTAGACTCTCGGAAAGAGCATGTGCAT 3003
QY 1072 rGlySerAlaGluProGlyAlaAlaHisGluMetLysSerProProSerAlaArgSerSe 1092
DB 3004 GTCCCTGGGAGG-----ATGAGCTATGATCAGCGATCTTGTTCAGCTCCCGAGCTC 3057
QY 1092 rProHisSerProTrpSerAlaAlaSerSerTrpThrSerArgArgSerSerArgAenSe 1112
DB 3058 CTACTACGGGCCCTGGGGCGCGAGTGGAGCTGGGTAGCGCGCTCCAGCTCCAGCTGGAAC-- 3115
QY 1112 rLeuGlyArgAlaProSerLeuLysArgArgSerProSerGlyGlyArgArgSerLeuLe 1132
DB 3116 -----AGCCTGAAACACAACAGCGCCCTCAGCTGAGCATGATGATCTCTTACT 3159
QY 1132 uSerGlyGluGlyGlnGluSerGlnAspGluGlu---GluSerSerGluGluGlu----- 1149
DB 3160 GTCTGGGAGGTTGGAGTGTAGCTGCTGAGGGCTGTGTAGAGCGCCCGGAGGAGGCGCC 3219
QY 1150 -----ArgAlaSerProAlaGlySerAspHis----- 1158
DB 3220 AACTCGCACCGCACCCCTGCATGCTCCACACGCGCACCCAGCGCCATGCAGCCACCT 3279
QY 1159 -----ArgHisArgGlySerLeuGluArgGluAlaLysSerSerPheAs 1173
DB 3280 GGCACACCTGACCGACACCGCGGACTCTGTCTCTGTATACAGGAGACTCTGTGA 3339
QY 1173 pLeuProAspThrLeuGlnValProGlyLeuHisArgThrAlaSer-----GlyArgG 1191
DB 3340 CTTGGGAGAGCTGTCCTGCGCTGGTGGTGGCCACTACAGCGCGCTTGGAGGGGGCGGG 3399
QY 1191 ySerAlaSerGluHisGlnAspCysAsnGlyLysSerAlaSerGlyArgLeuAlaArgAl 1211
DB 3400 TCAGGCCCTCGGCGACGAGACTGCAATGGCAGAAATGCCCAACATAGCAAGGATGCTT 3459
QY 1211 aLeuArgProAspAspProLeuAspGlyAspAspAlaAspAspGluGlyAsnLeuSe 1231
DB 3460 CACCAAGATGANTGACCGCGCGACCGCGGGGAGGAC---GAGGAGGAGATCGCATATAC 3516
QY 1231 rLysGlyGluArgValArgAlaTrpIleArgAlaArgLeuProAlaCysTyLeuGluAr 1251
DB 3517 CTTGTGTTTCCGGTTCGCAAGATGATTGATGTGTACAGCCGGACTGGTTCGGAAGTCCG 3576
QY 1251 gAspSerTrpSerAlaTyIlePheProProGlnSerArgPheArgLeuLeuCysHisAr 1271
DB 3577 CGAGGACTGTGTCTACTCTCTTCCCGGAGAACAGTTCGGATCTCTGTCTGACAG 3636
QY 1271 gIleIleThrHisLysMetPheAspHisValValLeuValIleIlePheLeuAsnCyAl 1291
DB 3637 CATCATTTGCTCACAAGCTTTTTCAGTACGTGGTCTTGGCCCTTTATCTCTCAACTGTAT 3696
QY 1291 eThrIleAlaMetGluArgProLysIleAspProHisSerAlaGluArgIlePheLeuTh 1311
DB 3697 CACCATTTGCTCTGGAGAGACCCAGATTGAAGCTGTGTAGCACTGAGCGCATCTTCTCAC 3756
QY 1311 rLeuSerAsnTyIlePheThrAlaValPheLeuAlaGluMetThrValLysValValAl 1331
DB 3757 GGTGTCTTAATCATCTTTCAGCGCATCTTCGTGGCGGAGATGACACTGAAGGTGGTTTC 3816
QY 1331 aLeuGlyTrpCysPheGlyGlnGlnAlaTyLeuArgSerSerTrpAsnValLeuAspG 1351
DB 3817 TCTGGGCTGTACTTTGTGAGCAGCGGTACTCTCGGTAGCAGCTGGGAATGTACTGGATGG 3876
QY 1351 yLeuLeuValLeuLeuSerValIleAspIleLeuValSerMetValSerAspSerGlyTh 1371
DB 3877 TTTCTCTGCTTTTGTGTCATCATCGATATCGTAGTGTCTGTGGCCCTCTCTCTGGGGAGC 3936
QY 1371 rLysIleLeuGlyMetLeuArgValLeuArgLeuLeuArgThrLeuArgProLeuArgVa 1391
DB 3937 CAAGATTCTGGGGTCTCTCGGGTCTCTCGGCTCTCTCGTACCTTACCTCTCTTGGGGGT 3996
QY 1391 lIleSerArgAlaGlnGlyLeuLysLeuValValGluThrLeuMetSerSerLeuLysPr 1411

Db	3997	TATCAGCGCGCCCTGGGCTGAAGCTGGTGGTAGAGAGCTCATCTCTCCCTCAAGCC	4056	Db	5077	CTGCAATCAGCAACCCGCTGTGAGGGCATGAGCGGCAGCCACCTTTGAAAACTTCGG	5136
Qy	1411	oileGlyAsnIleValValIleCysCysAlaPhePheIleIlePheGlyIleLeuGlyVa	1431	Qy	1771	yMetAlaPheLeuThrIleuPheArgValSerThrGlyAspAsnTrpAsnGlyIleMetLy	1791
Db	4057	CATTGGGAACATGCTCTCATCTGCTGCTGCTCTTCTTCATCATCTTCGGCATCTCGGGGT	4116	Db	5137	CATGGCCTTCTCCAGGCTCTCCAGGCTCCACAGGCGATTAACCTGGAAATGGAATTAAGA	5196
Qy	1431	lGlnLeuPheLysGlyLysPheValCysGlnGlyGluAspThrArgAsnIleThrAs	1451	Qy	1791	sAspThrLeuArgAspCys---AspGlnGluSerThrCysTyrAsnThrVal-----Il	1808
Db	4117	GCAGCTTTCAAAGGCAAGTTTACCATTTGTTGGAGTGGACACCGCAACATCACCAA	4176	Db	5197	GGACACCTTGGAGACTGTACCCATGATGAGCGCAGCTGCTTAAGCAGCCTCGAGTTGT	5256
Qy	1451	nLysSerAspCysAlaGluAlaSerTyrArgTTrpValArgHisLysTyrAsnPheAspAs	1471	Qy	1808	sSerProIleTyrPheValSerPheValLeuThrAlaGlnPheValLeuValAsnValVa	1828
Db	4177	CCGATCTGACTGCGTGGCGCCAACTACCGCTGGTGCATCACAATAACAACTTTGACAA	4236	Db	5257	GTACCGCTCTACTTGTGAGCTTCGTCTCACAGCTCAGTTCGTGCTCATCAACGTGT	5316
Qy	1471	nLeuGlyGlnAlaLeuMetSerLeuPheValLeuAlaSerLysAspGlyTrpValAspIl	1491	Qy	1828	lIleAlaValLeuMetLysHisLeuGluGluSerAsnLysGluAlaLysGluGluAlaGl	1848
Db	4237	CCTGGCCAGCATTTGATCTCTTCTTGTCTTGGCTCCAGGAGCGCTGGGTGAACAT	4296	Db	5317	GGTGGCCGTGCTGATGAACATCTGTGATGACAGCAGGAGGAGGAGGAGGAGGAGGAG	5376
Qy	1491	eMetTyrAspGlyLeuAspAlaValGlyValAspGlnGlnProIleMetAsnHisAsnPr	1511	Qy	1848	uLeuGluAlaGluLeuGluMet---LysThrLeuSerProGlnProHisSerPr	1867
Db	4297	CATGTATAATGCATTAGATGCTTGTGTGTGGACAGCAGCCAGTGACGAACCAACCC	4356	Db	5377	GATGGATGCTGAGATCGAGCTGGAGATGGCCATGGCTCGGCCCTGCCT-----	5428
Qy	1511	oTrpMetLeuTyrPheIleSerPheLeuIleValAlaPhePheValLeuAsnMe	1531	Qy	1867	oLeuGlySerProPheLeuTrpProGlyValGluGlyProAspSerProAspSerProly	1887
Db	4357	CTGGATGCTACTGACTTCATTCTGCTCTGCTCATCTGTCAGCTTCTTGTGCTCAACAT	4416	Db	5429	-----GGCCCTCG 5436	
Qy	1531	tPheValGlyValValGluAsnPheHisLysCysArgGlnHisGlnGluGluGl	1551	Qy	1887	sProGlyAlaLeuHisProAlaAlaHisArgSerAlaSerHisPheSerLeuGluHi	1907
Db	4417	GTTTGTGGCGTGTGCTGGAGAACTTCCAAAGTGGCGGAGCAGCAGGAGGCTGAGGA	4476	Db	5437	CCTTGT-----	5443
Qy	1551	uAlaArgArgGluGluLysArgLeuArgLeuGluLysArgLysArgLysAlaGl	1571	Qy	1907	sProThrMetGlnProHisProThrGluLeuProGlyProAspLeuLeuThrVal-	1925
Db	4477	GGCGGGAGGCGTGAGGAGAACGCTCGCGGCTTGAAAAGAGCGCCGCTAAGGCTCA	4536	Db	5444	-CCCTGCCCTGCCCTGCCCTGCTGCTGCCCGAGGCTGCCACCTAGTTCCACC	5502
Qy	1571	nCysLysProTyrTyrSerAspTyrSerArgPheArgLeuLeuValHisHisLysTh	1591	Qy	1926	-----ArgLysSerGlyValSerArgThrHisSerLeuProAsnAspSerTyr	1941
Db	4537	GAGGCTGCCCTACTATGCTACTACTCTCCACAGGCTGCTCATCCACTCCATGTGCAC	4596	Db	5503	TGGGGCTCGGGCGGAGGATCGGGGGGCGAGGCTGTGGAGGC---GACACCGAGAGTCA	5559
Qy	1591	rSerHisTyrLeuAspLeuPheIleThrGlyValIleGlyLeuAsnValValThrMetAl	1611	Qy	1941	rMetCysArgHisGlySerThrAlaGluGlyProLeuGlyHisArgGlyTrpGlyLeuPr	1961
Db	4597	CAGCCACTACCTGGACATCTTATACCTTCATCTGCTCAATCTGCTCAATGTGTCACCATGTC	4656	Db	5560	CCTGTGCCG-----	5569
Qy	1611	aMetGluHisTyrGlnGlnProGlnIleLeuAspGluAlaLeuLysIleCysAsnTyrIl	1631	Qy	1961	oLysAlaGlnSerGlySerValLeuSerValHisSerGlnProAlaAspThrSerTyrIl	1981
Db	4657	CTTGAGCAGCTACAAACAGCTTACCTCCTAGAGCAGCCCTTAAGTACTCCACTACAT	4716	Db	5569	-----	5569
Qy	1631	ePheThrValIlePheValLeuGluSerValPheLysLeuValAlaPheGlyPheArgAr	1651	Qy	1981	eLeuGlnLeuProLysAspAlaProHisLeuGlnProHisSerAlaProThrTrpGl	2001
Db	4717	GTTCACTGCTCTTGTGCTGGAGGCTGTGTAAGCTGTGGCATTTGGCTGAGGCG	4776	Db	5570	-----CACTGCTATTCTCCAGCCAGGAGACCCCTGTGG--	5602
Qy	1651	gPhePheGlnAspArgTTrpAsnGlnLeuAspLeuAlaIleValLeuSerIleMetGl	1671	Qy	2001	yThrIleProLysLeuProProGlyArgSerProLeuAlaGlnArgProLeuArgAr	2021
Db	4777	TTTCTTCAAGGACCGATGAACACGCTGACCTGGCCATTTGCTGCTGCTCCGATCGG	4836	Db	5603	-----CTGGACAG 5610	
Qy	1671	ylleThrLeuGluGluIleGluValAsnAlaSerLeuProIleAsnProThrIleIleAr	1691	Qy	2021	gGlnAlaAlaIleArgThrAspSerLeuAspValGlnGlyLeuGlySerArgGluAspLe	2041
Db	4837	CATCACCTGGAGGAGATCGAGATCAATGCCGCCCTTCCATCAACCCACCATCATCG	4896	Db	5611	CGTCTCTTTTAATCATCAGGACTCTCTTGAG-----GGGAGCTGACCAT	5655
Qy	1691	gIleMetArgValLeuArgIlleAlaArgValLeuLysLeuMetAlaValGlyWe	1711	Qy	2041	uLeuAlaGluValSer-GlyProSer-ProProLeuAlaAlaArgAlaTyrSerPheTrpGly	2060
Db	4897	TATCATGCTGTTCTGCTGATCGCCGGTGTGAAGCTATTGAAGATGGCCACAGGAAT	4956	Db	5656	CATTGACACCTGTCTGGTCCGTCTCCACCACTACGCTACGCTCAGCGCTGTGGCAA	5715
Qy	1711	tArgAlaLeuLeuAspThrValMetGlnAlaLeuProGlnValGlyAsnLeuGlyLeuLe	1731	Qy	2061	GlnSerSerThrGlnAlaGlnGlnHisSerArgSer-----HisSerLysIleSer	2077
Db	4957	GGCGGCCCTGCTGGACACAGTGTACAGGCTCTGCCAGGTGGGACCTGGGCTGCT	5016	Db	5716	GTGTCAACCATCACAAGCAAGACAGAGAGGCTCTTCATCATCTCTGCTGGGAGTACCTGAGT	5775
Qy	1731	uPheMetLeuLeuPhePheIlePheAlaAlaLeuGlyValGluLeuPheGlyAspLeuGl	1751	Qy	2078	LysHisMetThrProProAlaProCysProGlyProGluProAsnTrpGlyLysGlyPro	2097
Db	5017	CTTCATGCTGCTCTTCTTCTATCTATGCTGCTCTGGGAGTGGAGCTCTTCGGAAGCTGT	5076	Db	5776	-----CTTGAGGACCCACGCGCTGCCA-----CAGGGCCCC	5808
Qy	1751	uCysAspGluThrHisProCysGluGlyArgHisAlaThrPheArgAsnPheGl	1771	Qy	2098	ProGluThrArgSerSerLeuGluLeuAspThrGluLeuSerTrpIleSerGlyAspLeu	2117
				Qy	5809	AAGGAGAGCAAG-----GGTGAACATA 5829	

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QY 2118 LeuProProGlyGlyGlnGluGluProProSerProArgAspLeuLysCysTyr--- 2136
Db 5830 GAGCCTCG-----GAGCCCATGAGGCTGGAGACCTGGATGAATGCTTTGG 5877
QY 2137 -----SerVal----- 2138
Db 5878 CCCTTTGCCAAGCAGCAGCTGTCCACAGGCCAGAGACCTGTGTGCGAGATGGGGC 5937
QY 2139 ---GluAlaGlnSerCys-GlnArgArgProThrSerTrpLeuAspGluGlnArgHi 2157
Db 5938 CATTCATTCAACCTGTCCAG-----TCCTGGCTCAAAACACGAGAGCAGCCA 5985
QY 2157 sSerIleAlaValSerCysLeuAspSerGlySerGlnPro----- 2170
Db 5986 AGCACCCAGCAGCCCTTTCTCCCGGATGGCTCCAGCCCTCTCTGTAGATGCTGTGA 6045
QY 2171 -----HisLeuGlyThrAspProSerAsnLeuGlyGlnProLeuGlyGlyProG1 2188
Db 6046 GTTCTTCACCTGTGTGTCTGCCAGCCAGAGGGGAGAACCGGCATGATGTCAGG 6105
QY 2188 ySerArgProLysLysLeuSerProProSerIleThrIleAspProProGluSerG1 2208
Db 6106 AACCTGCCCCAAGATTGCCTTCAG-----GGGTCTCTG 6138
QY 2208 nGlyProArgThrProProSerProGlyIleCysLeuArgArgAlaProSerSerAs 2228
Db 6139 GGCATCGCTGAGTCAACCGAGTGTCACTGCACCCCTCTTGGCCGAGGCTACTGTAGTGA 6198
QY 2228 pSerLysAspProLeuAlaSerGlyProProAspSerMetAlaAlaSerProSerProLy 2248
Db 6199 CACGTCC-----TTGGATGCCAGTCTCTGAGCTCAGCGGCGAGCTTACAGACCACT 6252
QY 2248 sLysAspValLeuSerLeuSer 2255
Db 6253 GGAAGACAGTCTGACTCTGACT 6274
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RESULT 15

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US-09-030-482B-18
; Sequence 18, Application US/09030482B
; Patent No. US2002009772A1
; GENERAL INFORMATION:
; APPLICANT: Snutch, Terry
; TITLE OF INVENTION: NOVEL HUMAN CALCIUM CHANNELS AND RELATED
; TITLE OF INVENTION: PROBES, CELL LINES AND METHODS
; FILE REFERENCE: 38109-20007.00
; CURRENT APPLICATION NUMBER: US/09/030,482B
; PRIOR FILING DATE: 1998-02-25
; PRIOR FILING DATE: 1997-02-28
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 5562
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(5562)
; OTHER INFORMATION: Human alpha-1 partial sequence from BAC bx206c7
US-09-030-482B-18
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Alignment Scores:

Pred. No.:	3,25e-316	Length:	5562
Score:	3959.50	Matches:	908
Percent Similarity:	54.89%	Conservative:	158
Best Local Similarity:	46.76%	Mismatches:	361
Query Match:	33.26%	Indels:	515
DB:	9	Gaps:	42

US-09-611-257A-37 (1-2266) x US-09-030-482B-18 (1-5562)

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Db 229 GGAACAGAGATGACACAGGACCTTCCAGGAAGAGCTGAGCCCTGGTTCATCTCAGCAC 288
QY 40 AspProGlySerAlaAspSerGluAlaGluGlyLeuProTyrProAlaLeuAlaProVal 59
Db 289 CCGTGGCAGCAGGCGCATATACAGAGGTCACCCAGCCCGCCCGGCGATCCAC 348
QY 60 ValPhePheTyrLeuSerGlnAspSerArgProArgSerTrpCysLeuArgThrValCys 79
Db 349 TGCTGCTTTGTCTCTGAC-----TTGGTGTGC 375
QY 80 AsnProTrpPheGluArgIleSerMetLeuValIleLeuLeuAanCysValThrLeuGly 99
Db 376 ACG---TGGTTGAATGTGTGAGCATGTGTGATCTGTGAACTGGTGACACTTGGC 432
QY 100 MetPheArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAla 119
Db 433 ATGTACACGCGTGGCAGACATGGACTGCTGTCGACCCGCTGCAAGATCTTCAGGTC 492
QY 120 PheAspAspPheIlePheAlaPhePheAlaValGluMetValValLysMetValAlaLeu 139
Db 493 TTTGATGACTTCATCTTTATCTTCTTCCATGAGATGGTCTCAAGATGCTGGCCCTG 552
QY 140 GlyIlePheGlyLysCysTyrLeuGlyAspThrTrpAsnArgLeuAspPheIle 159
Db 553 GGGATTTTGGCAAGAAGTGTCTCTGGGACACATGGAAACCCGCTGGATTTCTTCATC 612
QY 160 ValIleAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAanValSerPheSerAlaVal 179
Db 613 GTCATGGCAGGC-----AACATCAACCTGTAGCCATC 645
QY 180 ArgThrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIle 199
Db 646 CGCACCGTGGCGCTCTGAGGCCCTCAAAGCCATCAACCGCTGCCAGTATGGGATC 705
QY 200 LeuValThrLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhe 219
Db 706 CTGGTGAACCTGCTCTGGACACATGCCCATGTGGGAAATGCTCTCTCTCTCTCTC 765
QY 220 PheValPheIlePheGlyIleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsn 239
Db 766 TTTGTCTTCTTCATCTTTGGCATCTAGGTGTGAGCTCTGGCGGGGCTCTCTGGCTAAC 825
QY 240 ArgCysPheLeuProGluAanPheSerLeuProLeuSerValAspLeuGluArgTyr 259
Db 826 CGCTGCTTCTGGAGGAGAACTTCACCATACAAGGGATGTGGCTTGGCCCGCCATAC 885
QY 260 GlnThrGluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMet 279
Db 886 CAGCCGGAGGAGGATGATGATGCCCTTCATCTCTCTCTCTCTCTCTCTCTCTCTCT 945
QY 280 ArgSerCysArgSerValProThrLeuArgGlyAspGlyGlyGlyProProCysGly 299
Db 946 ATGGGCTGCCATGATATCCCCCTCAAGAGGAG-----GGCCGTGAGTGTCTGC 996
QY 300 Leu-----AspTyrGluAlaTyrAsnSerSerSerAsnThrThr--- 312
Db 997 CTGTCCAGGACGAGCTCTACGACTTTGGGCGGGCGCCAGGACCTCAATGCCAGCGC 1056
QY 313 ---CysValAsnTrpAsnGlnTyrTrpAsnCysSerAlaGlyGluHiAsnProPhe 331
Db 1057 CTCTGTGTCAACTGGAACCGTTACTACAATGTGTGCGCAGCGGCGAGCAACCCCCAC 1116
QY 332 LysGlyAlaIleAsnPheAspAsnIleGlyTrpAlaTrpIleAlaIlePheGluValIle 351
Db 1117 AAGGGTCCATCAACTTTGACAAATCGGTTATGCTTGGATGTGATCTTCCAGGTATC 1176
QY 352 ThrLeuGluGlyTrpValAspIleMetTyrPheValMetAspAlaHisSerPheTyrAsn 371
Db 1177 ACTCTGGAGGCTGGGTGGAGATCATGTACTACGTGATGGATGTCTCTCTCTCTAC 1236
QY 372 PheIleTyrPheIleLeuLeuIleIle----- 380
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Qy 915 ThrValPheGlnIleLeuThrGlnGluAspTrpAsnIysValLeuTyrAsnGlyMetAla 934
Db 3106 ACTGTGTTCCAGATCTCTCACCAGAGGACTGGAAACGTCGTCTCTCAATATGGCATGGCC 3165
Qy 935 SerThrSerSerTrpAlaAlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrVal 954
Db 3166 TCCACTTCTCCCTGGGCTCTCTCTACTTTGTGCGCCCTCATGACTTTCGGCAACTATGTG 3225
Qy 955 LeuPheAsnLeuLeuValAlaIleLeuValGluGlyPheGlnAlaGlu---GluIleSer 973
Db 3226 CTCTTCAACCTGCTGTGGCCATCTGTGTGGAGGCTTCCAGGGCGAGGTGACTGTGTGTC 3285
Qy 974 LysArgGluAspAla----- 978
Db 3286 TTGGCAGAGGAAGCACCCTCAGGGCTCGAAAGACTGGCGGAGGAGGTGGCGCTG 3345
Qy 979 -----SerGlyGlnLeuSerCysIleGlnLeuPro 988
Db 3346 GATGGGGGAGGGCTGCAATTCTAAGCACTTCTAGCAGCAACTATCC---CTAAAGGAGGG 3402
Qy 989 ValAspSerGlnGlyGlyAspAlaAsnIysSerGluSerGluProAspPheSerPro 1008
Db 3403 GTTGTGATGAGTGGGTGACGCCAATCGCTCTACTCGGACGAGGACCAAGCTCATCC 3462
Qy 1009 Ser-----LeuAspGlyAspGlyAspArgLysIys 1018
Db 3463 AACATAGAAGATTGTGATAGCTCCAGGAAGCCCTGGACACGCGAGATCCCAAGCTC 3522
Qy 1019 CysLeuAlaLeuValSerLeuGlyGluHisProGluLeuArgLysSerLeuProPro 1038
Db 3523 TGCCCAATCCCATGACCCCAATGGGCAC-----CTGGACCCC 3561
Qy 1039 LeuIleIleHisThrAlaAlaThrProMetSerLeuProIysSerThrSerThrGlyLeu 1058
Db 3562 -----AGTCTCCCACTGGGTGGGCACCTAGGTCT 3591
Qy 1059 GlyGluAlaLeuGlyProAla----- 1065
Db 3592 GCTGGGGCTGGGACCTGCCCCCGACTCTCACTGCAGCGCGACCCCATGCTGGTGCC 3651
Qy 1066 -----SerArgAspThrSer----- 1070
Db 3652 CTGGGCTCCCGAAGACGAGCGTCTATGCTCTAGGAGGATGAGCTATGACCGGCTCC 3711
Qy 1071 -----SerSerGlySerAlaGluProGlyAlaAlaHisGluMetLys 1084
Db 3712 CTGGTGGGTGCTTTAGAGCCACAGCGGGGTGCAGGCTGCTTTGGGCACCTGCTGCC 3771
Qy 1085 SerPro-----ProSerAla 1089
Db 3772 CAGCCGTGGGTGCTGCTGGGGCGCTGACCCGAACCGGAACTCTTCCAGTCCAGCTCC 3831
Qy 1090 ArgSerSerProHisSerProTrpSerAlaAlaSerSerTrpThrSerArgSerSer 1109
Db 3832 CGGAGCTCTTACTACGGGCTATGGGGCGGCGGCGGCTTGGCCAGCGGCTGCTCCAGC 3891
Qy 1110 ArgAsnSerLeuGlyArgAlaProSerLeuLysArgArgSerProSerGlyGluArg 1129
Db 3892 TGGAAC-----AGCTCAAGCACACGCGCGCTGGCGGACCATGAG 3933
Qy 1130 SerLeuLeuSerGlyGlu---GlyGlnGluSerGlnAspGluGluGluSerSerGlu 1148
Db 3934 TCCCTGTCTCTGCGGAGCGGCGGCGGCGGCGGCTGCGAGGTTGCGCGGAGGAG 3993
Qy 1149 -----GluArgAlaSerProAlaGlySerAspHis----- 1158
Db 3994 GGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 4053
Qy 1159 -----ArgHisArgGlySerLeuGluArgGluAlaLysSerSer 1171
Db 4054 CATCTGGGCGCACCGCCACCGCCGCGGAGCTGTCTCTCGACACACGAGGACTCG 4113

Qy 1172 PheAspLeuProAspThrLeuGlnValProGlyLeuHisArgThrAlaSerGlyArg--- 1190
Db 4114 GTGACCTGGCCGAGCTGGTGGCGCGGTGGCGCCGCCACCCCGGGCGCTCGAGGCGC 4173
Qy 1191 ---GlySerAlaSerGluHisGlnAspCysAsnGlyLysSerAlaSerGlyArgLeuAla 1209
Db 4174 GCAGGCCCGGCCCGGCGCATGAGACTGCAATGCGAGGATGCCAGCATGCCCAAGAC 4233
Qy 1210 ArgAlaLeuArgProAspAspProProLeuAspGlyAspAlaAspAsp----- 1226
Db 4234 GTCTTCCACCAAGATGGCGGACCGCGGGGATCGCGGGGAGGATGAGGAATAATCGACTAC 4293
Qy 1227 -----GluGlyAsnLeuSerLysGlyGluArgValArgAlaTrpIle 1240
Db 4294 GTGAGTGGGGGGGGGGGAGGAGGAGCTGACCTGTGCTTCCCGGCGCGCAAGATGATC 4353
Qy 1241 ArgAlaArgLeuProAlaCysTyrLeuGluArgAspSerTrpSerAlaTyrIlePhePro 1260
Db 4354 GACGTCTATAAGCCGACTGCTGGAGGTCCGCGAAGACTGGTCTGTCTACTCTCTCTCT 4413
Qy 1261 ProGlnSerArgPheArg-----LeuLeuCys----- 1269
Db 4414 CCGAGAACAGGCTCAGGGATCTGGGCTGGGTAAAGCTCGAGTCCAGGGAAGGTGGGT 4473
Qy 1270 -----HisArgIleIleThrHisLys 1276
Db 4474 GACCTCTGTGTGGGTGTATGTGTGAGGAGGCGCGCCAGACCATTAITGCCACAAA 4533
Qy 1277 MetPheAspHisValValLeuValIleIlePheLeuAsnCysIleThrIleAlaMetGlu 1296
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Db 4654 TTCACGGCCACTTCTGCGGGCGAGATGACATTGAAGGTAGTCTCGCTGGGCGCTGTACTTC 4713
Qy 1337 GlyGluGlnAlaTyrLeuArgSerSerTrpAsnValLeuAspGlyLeuLeuValLeuIle 1356
Db 4714 GCGGAGCAGCGCTACCTACGACGAGCTGGAACTGTGTGGATGCTTCTGTCTCGTG 4773
Qy 1357 SerValIleAspIleLeuValSerMetValSerAspSerGlyThrLysIleLeuGlyMet 1376
Db 4774 TCCATCATCGACATCGTGTGTCTCGCCCTCAGCGGGGAGGCAAGATCTTGGGGGTC 4833
Qy 1377 LeuArgValLeuArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGln 1396
Db 4834 CTCCGAGTCTTGGCGCTCTGCGCACCTTACGCCCTTGGGTGTCTATCAGCGGGCGCGC 4893
Qy 1397 GlyLeuLysLeuValValGluThrLeuMetSerSerLeuLysProIleGlyAsnIleVal 1416
Db 4894 GGCCTGAAGCTGTGTGTGGAGACACTCATCTCTCTCCCTCAAGCCCATCGGCAACATCGTG 4953
Qy 1417 ValIleCysCysAlaPhePheIleIlePheGlyIleLeuGlyValGlnLeuPheLysGly 1436
Db 4954 CTCACTGCTGTGCTCTTCTTCTCATCTTTGGCATCTGCGAGTGCAAGTCTTCAAGGGC 5013
Qy 1437 LysPhePheValCysGlnGlyGluAspThrArgAsnIleThrAsnLysSerAspCysAla 1456
Db 5014 AAGTTCTACCACTGTCTGGGCGTGGACACCGCAACATCACCAACCGCTCGAGTGTATG 5073
Qy 1457 GluAlaSerTyrArgTrpValArgHisLysTyrAsnPheAspAsnLeuGlyGlnAlaLeu 1476
Db 5074 GCCGCCAACHTACCGCTGGTCCATCACAATATCAACTTCGACAACTTGGGCGCAGGCTCTG 5133
Qy 1477 MetSerLeuPheValLeuAlaSerLysAspGlyTrpValAspIleMetTyrAspGlyLeu 1496
Db 5134 ATGTCCTCTTTGTCCTGGCATCCCAAGGATGGTGGGTGAACATCATGTCAATGAGCTG 5193
Qy 1497 AspAlaValGlyValAspGlnGlnProIleMetAsnHisAsnProTrpMetLeuLeuTyr 1516

[illegible]

Search completed: April 16, 2005, 19:01:36
Job time : 3081 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 16, 2005, 02:17:06 ; Search time 14253 Seconds
(without alignments)
6051.613 Million cell updates/sec

Title: US-09-611-257A-37
Perfect score: 11904
Sequence: 1 MDEEFGAGAEESGQPRSPM.....PKXDVLSGLSSDPADLDP 2266

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-Q=/CGN2 1/USPTO.spool/US09611257/runat 13042005 170153 164/app.query.fasta_1.2439
-DB=EST -QMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09611257 @CGN 1 1 9104 @runat 13042005 170153 164 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:
1: gb_est1.*
2: gb_est2.*
3: gb_btc.*
4: gb_est3.*
5: gb_est4.*
6: gb_est5.*
7: gb_est6.*
8: gb_gse1.*
9: gb_gse2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	ID	Description
1	1703.5	14.3	6636 3 BC043482	BC043482 Mus muscu
2	1683.5	14.1	6035 3 BC051413	BC051413 Mus muscu
3	1382.5	11.6	1076 4 BM479323	BM479323 AGENCOURT
4	1314.5	11.0	879 7 CF548698	CF548698 AGENCOURT
5	1290.5	10.8	5666 9 AY416501	AY416501 Mus muscu
6	1281.5	10.8	1064 4 BM451648	BM451648 AGENCOURT
7	1257	10.6	793 6 CA319705	CA319705 UI-M-FW0
8	1223.5	10.3	5943 9 AY416499	AY416499 Homo sapi
9	1216	10.2	711 5 BM950154	BM950154 UI-M-EH0P

10	1215.5	10.2	771	5	BU058818
11	1215.5	10.2	990	4	BI905383
12	1212.5	10.2	784	7	CF742232
13	1187.5	10.0	810	5	BU709095
14	1185	10.0	736	4	BI160856
15	1183	9.9	939	2	BI736618
16	1178	9.9	973	2	BF783704
17	1174	9.9	4675	3	AK083220
18	1140.5	9.6	777	6	CA945335
19	1136	9.5	6822	9	AY406058
20	1132	9.5	715	7	CF745071
21	1130	9.5	676	4	BI917129
22	1130	9.5	843	5	BQ180375
23	1129.5	9.5	6813	9	AY406056
24	1116.5	9.4	777	5	BU708898
25	1107.5	9.3	710	5	BU704267
26	1104	9.3	952	7	CF584866
27	1103.5	9.3	845	6	CA327685
28	1101	9.2	707	7	CN216936
29	1092.5	9.2	918	6	CD557381
30	1084	9.1	647	6	BM518482
31	1081	9.1	693	5	BM949227
32	1074	9.0	708	5	BQ179746
33	1068.5	9.0	710	7	CR576255
34	1065.5	8.9	727	5	BQ443110
35	1058.5	8.9	731	7	CN534628
36	1055.5	8.9	803	6	CB245297
37	1051	8.8	773	4	BI249987
38	1025	8.6	640	6	CB056097
39	1024	8.6	588	2	BE781203
40	1018.5	8.6	684	5	BU262763
41	1012	8.5	726	5	BQ042267
42	1012	8.5	772	6	CB524438
43	1006	8.5	707	5	BU612176
44	995	8.4	1134	2	BF179657
45	993	8.3	957	4	BG298038

ALIGNMENTS

RESULT 1

LOCUS BC043482 6636 bp mRNA linear HTC 19-NOV-2003
DEFINITION Mus musculus calcium channel, voltage-dependent, alpha 1F subunit,
mRNA (CDNA clone IMAGE:5369391), containing frame-shift errors.

ACCESSION BC043482

VERSION BC043482.1 GI:28175783

KEYWORDS HTC.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 6636)

AUTHORS Klausner, R.D., Collins, F.S., Wagner, L.H., Grouse, L.H., Derge, J.G.,
Altschul, S.F., Zeeberg, B., Buettow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Heien, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullany, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Halton, E., Kettman, M., Madan, A., Rodriguez, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smallos, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

JOURNAL
MEDLINE
PUBMED
REFERENCE
2 (bases 1 to 6636)
AUTHORS
TITLE
JOURNAL

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16999-16903 (2002)
2238257
12477932
Strausberg, R.
Direct Submission
Submitted (09-JAN-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgaps-x@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
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Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
Leticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo
Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
Ness, Pawan Pandoh, Anna-Lilaea Prabhu, Parvaneh Saeedi, Jacqueline
Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott,
Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAK Plate: 86 Row: 0 Column: 1
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 9624972
This clone has the following problem: frame shifted.

FEATURES
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1..6636
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/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:536931"
/tissue_type="Eye, retina, mouse strain C57Bl/6"
/clone_lib="NIH_MGC_94"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6"

ORIGIN

Alignment Scores:
Pred. No.: 9.4e-107 Length: 6636
Score: 1703.50 Matches: 665
Percent Similarity: 38.49% Conservative: 331
Best Local Similarity: 25.70% Mismatches: 805
Query Match: 14.31% Indels: 792
DB: 3 Gaps: 98

US-09-611-257A-37 (1-2266) x BC043482 (1-6636)

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QY 21 ArgLeuAenAaspLeuSerGlyAlaGlyArgProGlyPro- 38
DB 57 -GGGACTGGCCCTGGCCCTGGAATGGGGGCTCTGTCT 92
QY 39 LysAaspPro- 54
DB 93 GGGCTCCAACTGTGGGACTGATACACAGCGGGGCTGAGCCCTGGGACCCCAAGA 152
QY 55 -AlaLeuAlaProValPhePheTyrLeu 64
DB 153 AGGACCCAGCACAAACACACAGACTGTGGCGGTGGCC- 191
QY 65 SerGlnAaspSerArgProArgSerTrpCysLeuArgThrValCysAenPro- 81

DB 192 AGTGCTCAGAGATCACCTCGAGCGCTCTTCTGCTCTCACCTTACTAATCCCAATCGTGG 251
QY 82 -TTP- -PheGluArgIleSerMetLeuValIleLeu 92
DB 252 TCCTGCATCAGCATTTGTAGAGTGAAGCTTTTGATATTCATCTCTCTCAATCTTT 311
QY 93 LeuAenCysValThrLeuGlyMetPheArgProCys- -GluAasp- 106
DB 312 GCACACTCGTGGCATTTGGGGTATATATCCCTTCCCTCGAGGAGACTCCCAACACTGT 371
QY 106 - 106
DB 372 AACCACACTTGTGAGGTCTACCCCATCCCAACAGACTGCAGTTCCTTTAGAGCTA 431
QY 107 -IleAlaCysAaspSerGlnArg- 113
DB 432 CAGATAAAACACCCAGAGCCAGACCCACCCCTCCGGGGCTTACCTTCTACTCTTGT 491
QY 114 - 114
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QY 115 ArgIle-LeuGlnAlaPheAasp- -AspH 123
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Qy 576 oSerGluAlaSerGlyArgThrValGly--SerGlyLysValTyrPro-----ThrVal 593
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Qy	1034	rLeuLeuProProLeuIleIleHisThrAlaAlaThrProMetSerLeuProLysSerTh	Qy	1393	rArgAlaGlnGlyLeuLysLeuValValGluThrLeuMetSerSerLeuLysProIleG1	1413
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Db	2630	ACATCACCATATCTTACCAGTCTCATCTAGTGTTCATCTCTAGTGTGTCTGCTGCTGCT	Db	3680	TAACTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	3739
Qy	1293	eAlaMetGluArgProLysIleAspProHisSerAlaGluArgIlePheLeuThrLeuSe	Qy	1641	lPheLysLeuValAlaPheGlyPheArgArgPhePheGlnAspArgTyrAsnGlnLeuAs	1661
Db	2690	GGCTGCTGAGGACCC-----ATCCGAGCTCACTCTCTCGAAACCATATCTCGGATATT	Db	3740	GCTCAAAATCATCGCTCTTAAACCCAGCATTTACTTTGAGATGCTGCTGCTGCTGCTGCT	3799
Qy	1313	rAsnTyrIlePheThrAlaValPheLeuAlaGluMetThrValLysValAlaLeuG1	Qy	1661	pLeuAlaIleValLeuSerIleMetGlyIleThrLeuGluGluIleGluValAsnAl	1681
Db	2747	TGATTATGCTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACT	Db	3800	TGCTCTATTGTAGTGGCAGTGTAGTGGCAGTGTAGTGGCAGTGTAGTGGCAGTGTAGT	3853
Qy	1333	yTrpCysPheGlyGluGlnAlaTyrLeuArgSerSerTrpAsnValLeuAspGlyLeuLe	Qy	1681	aSerLeuPro-----IleAsnProThrIleIleArgIleMetArgValLeuArgIleAlaArg	1700
Db		-----GAGGC	Db	3854	GACAGCTCCCGCATATCTATCATGCTCTTTCGCTCTTTCGCTCTTTCGCTCTTTCGCTCT	3907

ACCESSION BM479323
 VERSION BM479323.1 GI:18528365
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1076)
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
 Plate: LHAM12140 row: a column: 15
 High quality sequence stop: 692.
 Location/Qualifiers
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 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5502230"
 /tissue_type="retinoblastoma"
 /lab_hosts="DH10B (phage-resistant)"
 /clone_lib="NIH MGC 67"
 /notes="Organ: eye; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.75 kb. Library constructed by Life Technologies."
 ORIGIN
 Alignment Scores:
 Pred. No.: 1.13e-85 Length: 1076
 Score: 1382.50 Matches: 286
 Percent Similarity: 90.37% Conservative: 5
 Best Local Similarity: 88.82% Mismatches: 15
 Query Match: 11.61% Indels: 16
 DB: 4 Gaps: 3
 US-09-611-257A-37 (1-2266) x BM479323 (1-1076)
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 DB 3 AGGAACATCCCAATAAATCGACTGTGCCGAGCCAGTTACCGTGGGTCCGGCACAAG 62
 QY 1467 TyrAsnPheAspAsnLeuGlyGlnAlaLeuMetSerLeuPheValLeuAlaSerLysAsp 1486
 DB 63 TACAACCTTCACAACTTGGCCAGGCCCTGATGCTCTGTTGGCTCCAGGAT 122
 QY 1487 GlyTyrValAspIleMetTyrAspGlyLeuAspAlaValGlyValAspGlnProIle 1506
 DB 123 GGTGGTGGACATCATGTACGATGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 182
 QY 1507 MetAsnHisAsnProTyrMetLeuLeuTyrPheIleSerPheLeuLeuIleValAlaPhe 1526
 DB 183 ATGAACACAAACCCCTGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 242
 QY 1527 PheValLeuAsnMetPheValGlyValValValGluAsnPheHisLysCysArgGlnHis 1546
 DB 243 TTGTCTCTGAACATGTTTGTGGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 302
 QY 1547 GlnGluGlnGluAlaArgArgArgGluGluLysArgLeuArgLeuGluLysLys 1566
 DB 303 CAGGAG 362
 QY 1567 ArgArgLysAlaGlnCysLysProTyrTyrSerAspTyrSerArgPheArgLeuVal 1586

Db 363 AGAAGGAAGCCAGTGCAAACTTACTCCGACTACTCCGCTTCCGCTTCCGCTTCCGCTC 422
 QY 1587 HisHisLeuCysThrSerHisTyrLeuAspLeuPheIleThrGlyValIleGlyLeuAsn 1606
 Db 423 CACACTTTGTGCACAGCCACCTACCTGGACCTTTTATCACAGGTGTCTATCGGGTGAAC 482
 QY 1607 ValValThrMetAlaMetGluHisTyrGlnGlnProGlnIleLeuAspGluAlaLeuLys 1626
 Db 483 GTGGTCACCATGGCCATGGAGCAGTACCAGCAGCCAGATTCTGGATGGCTCTGAAG 542
 QY 1627 IleCysAsnTyrIlePheThrValIlePheValLeuGluSerValPheLysLeuValAla 1646
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 QY 1647 PheGlyPheArgArgPheGlnAspArgTyrAsnGlnLeuAspLeuAlaIleValLeu 1666
 Db 603 TTTGGTTTCGTCGGTCTTCCAGGACAGGTGGAAACAGCTGGACCTGGCATTTGCTG 662
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 Db 723 CCACCATCATCCGCATCATAGGGTGTCTGCCATTTGCCCGAGTGTGAAGCTCTGAA 782
 QY 1706 YsMetAlaValGlyMet-ArgAlaLeuLeuAspThrValMetGlnAla--LeuProGlnV 1725
 Db 783 AAATCGGTGTGGCATGCCGCCGCTGTGGACACCGTGTGATGACGCCCTGTCCCGGT 842
 QY 1725 alGlyAsnLeuGlyLeuLeuPheMet-----LeuLeuPhePheIlePheAlaLeuG 1743
 Db 843 GGGGAACCTGGGAGCTTTTCTCCAGCGCGTGTGTTTTCATCCCTCGCGCTCCTG 902
 QY 1743 IyVal-----GluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGlu 1759
 Db 903 GCGCGTGCAGCCTCTTTTGGAGAA-----CCTTGAAG 937
 RESULT 4
 CF548698 879 bp mRNA linear EST 22-SEP-2003
 LOCUS AGENCOURT_15594508 NICHD_XGC_Brn1 Xenopus laevis cDNA clone
 DEFINITION IMAGE:7018586 5', mRNA sequence.
 ACCESSION CF548698
 VERSION CF548698.1 GI:348885530
 KEYWORDS EST.
 SOURCE Xenopus laevis (African clawed frog)
 ORGANISM Xenopus laevis
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae; Xenopodinae; Xenopus; Xenopus.
 REFERENCE 1 (bases 1 to 879)
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Daniela S. Gerhard, Ph.D.
 Office of Cancer Genomics
 National Cancer Institute / NIH
 Bldg. 31 Rm10A07 Bethesda, MD 20892
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement:
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
 Plate: LHAM14738 row: j column: 24
 High quality sequence stop: 646.
 Location/Qualifiers
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 /organism="Xenopus laevis"
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FEATURES
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/db_xref="taxon:8355"
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 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NICHD XCC Brn1"
 /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.5 kb. Constructed by Life Technologies. Note: This is a Xenopus Gene Collection (XGC) library."

ORIGIN

Alignment Scores:
 Pred. No.: 4,47e-81 Length: 879
 Score: 1314.50 Matches: 255
 Percent Similarity: 94.79% Conservative: 18
 Best Local Similarity: 88.54% Mismatches: 13
 Query Match: 11.04% Indels: 2
 DB: 7 Gaps: 1

US-09-611-257A-37 (1-2266) x CP548698 (1-879)

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 Db 1 GAGCGATGGGTGGACATCATGTATGATGGATGGATGCTGCGAATTCACACGACGCA 60

QY 1506 IleMetAsnHisAsnProTrpMetLeuLeuTyrPheIleSerPheLeuLeuValAla 1525
 Db 61 GTGATGANTTACACCCCTTGGATGCTGTATATTTTCATCTCATTTTTCGATGTGGCA 120

QY 1526 PhePheValLeuAsnMetPheValGlyValValValGluAsnPheHisLysCysArgGln 1545
 Db 121 TTTTTCGTCTCAACATGTTTGTGGGTGTGGTGTGGAGAACTCCATAGTCCGCGCAG 180

QY 1546 HisGlnGluGluGluAlaArgArgArgGluGluLysArgLeuArgLeuGluLys 1565
 Db 181 CATCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 240

QY 1566 LysArgArgLysAlaGlnCysLysProTyrTyrSerAspTyrSerArgPheArgLeuLeu 1585
 Db 241 AAGAGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 300

QY 1586 ValHisHisLeuCysThrSerHisTyrLeuAspLeuPheIleThrGlyValIleGlyLeu 1605
 Db 301 ATCCATCAGATCTGTACAAGTCATATTATGGATTTGTTATTTACTGGGTCAATTGGATTG 360

QY 1606 AsnValValThrMetAlaMetGluHisTyrGlnGlnProGlnIleLeuAspGluAlaLeu 1625
 Db 361 AATGTTATCTACTATGGCAATGGAGCACTATCAGCAACCCAGGATTTGGTTGAAGCTCTA 420

QY 1626 LysIleCysAsnTyrIlePheThrValIlePheValLeuGluSerValPheLysLeuVal 1645
 Db 421 AATCTGTATTTACATCTTTTACCTCATTTTGTACTGGAACTCTGGTGCAAAATGATTA 480

QY 1646 AlaPheGlyPheArgPhePheGlnAspArgTrpAsnGlnLeuAspLeuAlaIleVal 1665
 Db 481 GCITTTGGCTTCGGCGATTCTTTAAAGACAGGTGGAAACAGTTGGATCTGGCCATCGTT 540

QY 1666 LeuLeuSerIleMetGlyIleThrLeuGluGluIleGluValAsnAlaSerLeuProIle 1685
 Db 541 CTTCCTCCATCATCGGAATCACACTGGAAAGATTTGAAGTCAATGCATCACTGCCCAT 600

QY 1686 AsnProThrIleIleArgIleMetArgValLeuArgIleAlaArgValLeuLysLeuLeu 1705
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QY 1706 LysMetAlaValGlyMetArgAlaLeuLeuAspThrValMetGlnAlaLeuProGlnVal 1725
 Db 661 AAGATGCGAGTCGATCGAGCGCTCTCTGATACGGTTCTGCAAGCGCTTCTCAAGTG 720

QY 1726 GlyAsnLeuGlyLeuLeuPheMetLeuLeuPhePheIlePheAlaLeuGlyValGlu 1745
 Db 721 GGAATCTCGGCTGCTCTTTATGCTGCTCTCTTTTAAATTTGCGGCTCTCGGAGTTGAA 780

1746 LeuPheGlyAspLeuGluCysAspGluThrHisProCysGlu-GlyLeuGlyArgHisAla 176
 Db 781 CTTTTCGTTGGTACATTAAAGACGACGTCGATCCCATCCCTGTGAAGGCTCTTCGACACTGC 840

QY 1765 aThrPheArgAsn---PheGly 1771
 Db 841 CACTTTTCAAGGAATTTTCGGG 862

RESULT 5
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 DEFINITION Mus musculus SCN8A gene, VIRTUAL TRANSCRIPT, partial sequence,
 genomic survey sequence.
 ACCESSION AY416501
 VERSION AY416501.1 GI:39772461
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 5666)
 AUTHORS Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
 Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
 Adams,M.D. and Cargill,M.
 TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
 gene trios
 JOURNAL Science 302 (5652), 1960-1963 (2003)
 PUBMED 14671302
 REFERENCE 2 (bases 1 to 5666)
 AUTHORS Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
 Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
 Adams,M.D. and Cargill,M.
 TITLE Direct Submission
 JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
 Rockville, MD 20850, USA
 COMMENT This sequence was made by sequencing genomic exons and ordering
 them based on alignment.
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 /organism="Mus musculus"
 /mol_type="genomic DNA"
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 ORIGIN
 Alignment Scores:
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 Score: 1290.50 Matches: 525
 Percent Similarity: 36.71% Conservative: 305
 Best Local Similarity: 23.22% Mismatches: 713
 Query Match: 10.84% Indels: 723
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 QY 45 -AspSerGluAlaGluGlyLeuProTyr-----CCGTACTATTTCGACGAGAAACTTTTGTAGTATTTAA 53
 Db 252 TGAC-----CCGTACTATTTCGACGAGAAACTTTTGTAGTATTTAA 293
 QY 54 -----ProAlaLeuAlaProValPhePh 62
 Db 294 CAGAGGAAACTCTCTTCAGATTATAGCGCCTCTCGCTCTG-----TA 338
 QY 62 eTyrLeuSerGlnAspSerArgProArgSerTrpCysLeuArgThrValCysAsnProTr 82


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Qy 736 heArgLys---IleValAspSerLysTyrPheGlyArgGlyIleMetIleAlaIleuV 755
Db |||||
2036 GACGAAGGAGCAGAACTCAACAGT-----ATAATGAGCGTTGTCA 2074
Qy |||||
755 alAenThrLeu----- 758
Db |||||
2075 CAAACACACTAGTGAAGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 2134
Qy ----- 758
Db -----
2135 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 2194
Qy ----- 758
Db -----
2195 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 2254
Qy ----- 759
Db -----
2255 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 2314
Qy 775 euGluIleSerAsnIleValPheThrSerLeuPheAlaLeuGluMetLeuLysLeuL 795
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2315 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 2374
Qy 795 euValTyrGlyPropheGlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleV 815
Db |||||
2375 TAGCCATGGATCCCTACTATTACTTCCAAGAGGCTGGAACATTTTGGCGATTATCG 2434
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2435 TCTCCCTCAGTTTAATGAGCTGGGCTTGCGAGCTGGAGGGCTCTCAGTGTGCGAT 2494
Qy 835 hrPheArgLeuMetArgValLeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnL 855
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Qy 855 euValValLeuMetLysThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuP 875
Db |||||
2555 TCAAGATCATTTGGGAACCTCCGTGGCGCCCTGGGCAACCTGACCTGCTGGTCCATCA 2614
Qy 875 heIlePheIlePheSerIleLeuGlyMetHisLeuPheGly----- 888
Db |||||
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Db |||||
2675 TCTGTAAGATCAGCCAGGAG-----TGCAAGCTCCCG---CGCTGGCAGCATGAACG 2722
Qy 908 erLeuLeuTrpAlaIleValThrValPheGlnIleLeuThrGlnGluAspTrpAsnLysV 928
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Db |||||
2785 -----GCTGAACTTATTCTGCGCTTG 2806
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Db |||||
2807 CTTCTGAGCTCTTTCAGCGCAGACAA----- 2832
Qy 988 roValAspSerGlnGlyCysAlaAsnLys-----SerGluSerGluProAspPheP 1006
Db |||||
2833 -----TCTGGCGGCCAGCGACGACGCGGAAATGAAACACCTGCATATCG 2881
Qy 1006 heSerProSerLeuAspGlyAspGlyAspArgLysLysCysLeuAlaLeuValSerLeuG 1026
Db |||||
2882 GTGATCCGGATCAAGAGGGCGTGGC----- 2907
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Qy 1026 lyGluHisProGluLeuArgLysSerLeuLeuProProLeuIleIleHisThrAlaAlaT 1046
Db ----- 2907
Qy 1046 hrProMetSerLeuProLysSerThrSerThrGlyLeuGlyGluAlaLeuGlyProAlas 1066
Db |||||
2908 -----CTGGGCCAAAGTGAAGGTGCATG-CCTTCAT 2937
Qy 1066 erArgArgThrSerSerSerGly-----SerAlaGluP 1077
Db |||||
2938 GCAGGCACACTTCAAGCAACGCGGAGCTGATGAAGTGAAACCTTTAGACGAGCTGT----- 2993
Qy 1077 roGlyAlaAlaHisGluMetLysSerProProSerAlaArgSerSerProHisSerPro- 1096
Db |||||
2994 -----ATGAGAAGAAAGGCCAATGCA-----TCGCCAACCAACCCGG 3030
Qy 1097 --TrpSerAlaAlaSerSerTrpThrSerArgArgSerSerArgAsnSerLeuGlyArgA 1116
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Qy 1116 laProSerLeuLysArgArgSerProSerGlyGluArgArgSerLeuLeuSerGlyGluG 1136
Db |||||
3091 CGGCAAAACCTG----- 3101
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Db |||||
3102 -----GACGATACAGCTCCTCAGAA----- 3122
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Db |||||
3123 -----GGAGTACCATCGACATCAAGC 3144
Qy 1175 roAspThrLeuGlnValProGlyLeuHisArgThrAlaSerGlyArgGlySerAlaSerG 1195
Db |||||
3145 CTGAGGTGGAAGAAGTCCCA----- 3164
Qy 1195 luHisGlnAspCysAsnGlyLysSerAlaSerGlyArgLeuAlaArgAlaLeuArgProA 1215
Db |||||
3165 -----GTGGAGCAGC 3174
Qy 1215 spAspProProLeuAspGlyAspAlaAspAspGluGly----- 1228
Db |||||
3175 CTGAGGAATACTTGGATCCAGACCCCTGCTTCACGAGGGTGTGTCCAGAGGTTCAAGT 3234
Qy 1229 -----AsnLeuSerLysGlyGluArgValArgAlaTrpIleArgAlaArgLeuP 1245
Db |||||
3235 GCTGCCAGGTCAACATCGAGGAAGGACTAGGCAAGTCTGCTGTGATC----- 3281
Qy 1245 roAlaCysTyrLeuGluArgAspSerTrpSerAlaTyrIlePheProGlnSerArgP 1265
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Qy 1265 heArgLeuLeuCysHisArgIleIleThrHisLysMetPheAspHisValValLeuValI 1285
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Qy 1285 leIlePheLeuAsnCysIleThrIleAlaMetGluArgProLysIleAspProHisSerA 1305
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3511 CCTGGTCTGTTGGACTTCTCTCATCTGCTGCTNNNNNNNNNNNNNNNNNNNNNNNN 3570
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RESULT 6
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LOCUS             AGENCOURT 6394764 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:5493169
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ACCESSION         BM451648
VERSION           BM451648.1 GI:18500688
KEYWORDS          EST.
SOURCE            Homo sapiens (human)
ORGANISM          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE         1 (bases 1 to 1064)
AUTHORS          NIH-MGC http://mgc.nci.nih.gov/.
TITLE            National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL          Unpublished (1999)
COMMENT          Contact: Robert Strausberg, Ph.D.
                  Email: cgapbs-remail.nih.gov
                  Tissue Procurement: ATCC
                  cDNA Library Preparation: Life Technologies, Inc.
                  cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                  DNA Sequencing by: Agencourt Bioscience Corporation
                  Clone distribution: MGC clone distribution information can be
                  found through the I.M.A.G.E. Consortium/LLNL at:
                  http://image.llnl.gov
                  Plate: LLAM12116 row: h column: 02
                  High quality sequence stop: 657.

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                     /note="Organ: eye; Vector: pCMV-SPORT6; Site 1: NotI;
                     Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
                     Average insert size 1.75 kb. Library constructed by Life
                     Technologies."

ORIGIN
Alignment Scores:
Pred. No.:         1..22e-78      Length:      1064
Score:             1281.50        Matches:     272
Percent Similarity: 78.36%        Conservative: 9
Best Local Similarity: 73.91%     Mismatches:  16
Query Match:       10.77%        Indels:      71
DB:                4              Gaps:        6

US-09-611-257A-37 (1-2266) x BM451648 (1-1064)
Qy 1464 ArgHisLysTyrAsnPheAspAsnLeuGlyClnAlaLeuMetSerLeupheValLeuAla 1483
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Db 61 TCCAAGGATGGTTGGGTGGACATCATGTACATGGCTGGATGCTGTGGGCGGTGGACCAG 120
Qy 1504 GlnProIleMetAsnHisAsnProTyrMetLeuLeuTyrPheIleSerPheLeuLeuIle 1523
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Db 121 CAGCCCATCATGAACCAACACCCCTGGATGCTGCTGTACTTCACTCTGTTCTTCTGCTCAT 180
Qy 1524 ValAlaPhePheValLeuAsnMetPheValGlyValValGluAsnPheHisLysCys 1543
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Db 181 GTGGCCTCTTTTGTCCTGAACATGTTTGTGGGTGGTGGTGGAGAACTTCCACAAAGTGT 240
Qy 1544 ArgClnHisGlnGluGluGluAlaAArgAArgGluGluLysArgLeuArgArgLeu 1563
|||
Db 241 CGGCAGCACAGGAGGAGGAGGAGCGCGCGCGGAGGAGGAGCGCTACGAAAGCATG 300

```

Email: csaps-r@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)

Seq primer: pYX-5.
Location/Qualifiers
1. 793
/organism="Mus musculus"
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/lab_host="DH10B (TI phase resistant)"
/clone_lib="NIH BMAP FW0"
/note="Organ: Brain; Vector: pYX- Asc; Site 1: EcoR I;
Site 2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is AGCAGACAG. This library was created for the University
of Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
program coordinator."

ORIGIN

Alignment Scores:
Pred. No.: 3.85e-77 Length: 793
Score: 1257.00 Matches: 241
Percent Similarity: 92.40% Conservative: 2
Best Local Similarity: 91.63% Mismatches: 2
Query Match: 10.56% Indels: 18
DB: 6 Gaps: 1

US-09-611-257A-37 (1-2266) x CA319705 (1-793)

QY 1433 LeuPheLysGlyLysPhePheValCysGlnGlyGluAspThrArgAsnIleThrAsnLys 1452
DB 3 CTCCTCAAGGGAAGTCTTCGTGTGTGAGGTGAGGACACAGCAATCACTAAACAAG 62
QY 1453 SerAspCysAlaGluAlaSerTyrArgTrpValArgHisLysTyrAsnPheAsnLeu 1472
DB 63 TCCGACTGTCTGAGGCCAGTTACCGGTGGGTGGGCGCAAGTACAACTTTGACAACTG 122
QY 1473 GlyGlnAlaLeuMetSerLeuPheValLeuAlaSerLysAspGlyTrpValAspIleMet 1492
DB 123 GCCCAGGCTCTGATGTCCTCTTCCTCCATCGTGGCTCCAGGATGGTGGTGTGACATCATG 182
QY 1493 TyrAspGlyLeuAspAlaValGlyValAspGlnGlnProIleMetAsnHisAsnProTrp 1512
DB 183 TATGATGAGTGGTGTGAGTGGACCAAGCCATCATGAACCAACCAACCTTGG 242
QY 1513 MetLeuLeuTyrPheIleSerPheLeuLeuIleValAlaPhePheValLeuAsnMetPhe 1532
DB 243 ATGCTGCTCTACTTCACTTCCTTCCTCCATCGTGGCTTCCTGCTCTGACATGTTT 302
QY 1533 ValGlyValValValGluAsnPheHisLysCysArgGlnHisGlnGluGluGluAla 1552
DB 303 GTGGGGCTGGTGGTGGAGAACTTCCATAAGTGCAGGCAGCACAGGAGGAGGAGGCG 362

QY 1553 ArgArgArgGluGluLysArgLeuArgArgGluLysLysArgArg----- 1568
DB 363 CGCGCGCGGAGGAGAGCGGACTAAAGAGGCTGGAGAGAAAGAGAGAGAAATCTAATGTG 422
QY 1569 -----LysAlaGlnCysLysPro 1574
DB 423 GACGATGTAATGTCTCCGGCAGCTCAGCCAGCCGCTCGGTGAGAGGCCAGTGCACACCC 482
QY 1575 TyrTyrSerAspTyrSerArgPheArgLeuLeuValHisLysCysThrSerHisTyr 1594
DB 483 TACTACTCTGACTACTCGGCTTCGGCTCTCTCCACCACTGTGTACCAGCCACTAC 542
QY 1595 LeuAspLeuPheIleThrGlyValIleGlyLeuValValThrMetAlaMetGluHis 1614
DB 543 CTGGACCTCTTCATCCTGCTGTCATCGGGCTGAATGTGTGTCAGCATGGCCATGAACAT 602
QY 1615 TyrGlnGlnProGlnIleLeuAspGluAlaLeuLysIleCysAsnTyrIlePheThrVal 1634
DB 603 TACCAGCAGCCCGAGATCTCGACGAGGCTCTGAGAGATCTGCACTACATCTTTACCGTC 662
QY 1635 IlePheValLeuGluSerValPheLysLeuValAlaPheGlyPheArgPhePheGln 1654
DB 663 ATCTTTGCTTGGAGTCAGTATTCANACTTGTGGCTTCGGCTTCGGCGGTCTTCACG 722
QY 1655 AspArgTrpAsnGlnLeuAspLeuAlaIleValLeuLeuSerIleMetGlyIleThrLeu 1674
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QY 1675 GluGluIle 1677
DB 783 GAAGAGATT 791

RESULT 8

AV416499 5943 bp DNA linear GSS 17-DEC-2003
LOCUS Homo sapiens SCNA gene, VIRTUAL TRANSCRIPT, partial sequence,
DEFINITION genomic survey sequence.
ACCESSION AY416499
VERSION AY416499.1 GI:39772459
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE

1 (bases 1 to 5943)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Perriera, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J.,
Adams, M.D. and Cargill, M.
Infering nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 5943)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Perriera, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J.,
Adams, M.D. and Cargill, M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES Location/Qualifiers
source 1. 5943
/organism="Homo sapiens"
/mol_type="genomic DNA"
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/locus_tag="HCM5911"

TITLE

JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 5943)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Perriera, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J.,
Adams, M.D. and Cargill, M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA

TITLE

JOURNAL Science 302 (5652), 1960-1963 (2003)
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REFERENCE 2 (bases 1 to 5943)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Perriera, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J.,
Adams, M.D. and Cargill, M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.

FEATURES

Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="genomic DNA"
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gene
ORIGIN

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663 lyPro ---AspSerCysProTyrCysAlaArgAlaGlyA 675
1902 GCGCAGCGTGAAGCGCAACAGCAGCGGTGGACTCAACGGCGTGTCTCCCTCATCGCGG 1961
675 laGlyGluValGluLeuAlaAspArgGluMetProAspSerAspSerGluAlaValTyrG 695
1962 CCGCGGTCC-CACATCGCGCGGTCTCTCGCAGAGGCTCAACACTGAGGTGAAATTA 2020
695 luPheThrGlnAspAlaGlnHisSerAspLeuArgAspProHisSerArgArgGlnArgS 715
2021 AG --- 2022
715 erLeuGlyProAspAlaGluProSerSerValLeuAlaPheTrpA-gLeuileCysAspT 735
2023 ---AAGAAAGCGCTGGATCTCTTTAGTTTCCATGGACCAATTAGCCTCCT 2071
735 hrPheArgLys---IleValAspSerLysTyrPheGlyArgGlyIleMetIleAlaIleL 754
2072 ACGGCGGAAGGAGCAGAAATCAACAGT ---ATAATGAGTGTG 2110
754 euValAsnThrLeu --- 758
2111 TTACAAATACACTAGTAGAAGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 2170
758 --- 758
2171 NNN 2230
758 --- 758
2231 NNN 2290
759 ---SerMetGlyIleGluTyrHisGluGlnProGluGluLeuThrAsnA 774
2291 NNN 2350
774 laLeuGluileSerAsnIleValPheThrSerLeuPheAlaLeuGluMetLeuLeuLysL 794
2351 NNN 2410
794 euLeuValTyrGlyProPheGlyTyrIleLysAsnProTyrAsnIlePheAspGlyValI 814
2411 TCATAGCCATCGATCCCTTACTATTATTTCCAAAGAGTTGGAACATTTTGACGGATT 2470
814 leValValIleSerValTrpGluileValGlyGlnGlnGlyGlyLeuSerValLeuA 834
2471 TTGTCCTCCCTCAGTTTAATGAACTGAGTCTAGCAGACGCTGAGGGGCTTTCAGTGTGC 2530
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2591 NNN 2650
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2651 TTATGTCTCTCATCTTTCGCGTGGGTGCAACTCTTTGGAAAAAGCTACAAAGAGT 2710
889 ---CysLysPheAlaSerGluArgAspGlyAspThrLeuProAspArgLysAsnPheA 907
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2759 ATGACTTTTTCATCTCTCTCTCATCTTTCGAGTGTTCGCGGGAG ---TGGATTG 2815
927 ysValLeuTyrAsnGlyMet ---AlaSerThrSerSerTrpAlaAlaLeuTyrPheIleA 946

2816 AGACCATGTGGACTGTCATGGAAGTGGCAGGCCAGGCATGTGCTCTATTGCTTTATGA 2875
946 laLeuMetThrPheGlyAsnTyrVal --- 954
2876 TGTCTGTGTGATGTGCAACTTGGTNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 2935
955 --LeuPheAsnLeuLeuValAlaIleLeuValGluGlyPheGlnAlaGluGluIleSerL 974
2936 NNN 2995
974 ysArgGluAspAlaSerGlyGlnLeuSerCysIleGlnLeuProValAspSerGlnGlyG 994
2996 NNN 3055
994 lyAspAlaAsnLysSerGluSerGluProAspPheSerProSerLeuAspGlyAspG 1014
3056 NNNNGCCCACTTTAAGCAGCGTGAAGCTGTAGAGTGAAGCCT ---CTGGATGAGTTGT 3112
1014 lyAspArgLys---LysCysLeuAla-LeuValSerLeuGlyGluHisProGluLeuArg 1032
3113 ATGAAAGAGGCAACTGTATCGCAATCA --- 3145
1033 LysSerLeuLeuProProLeuIleIleHisThrAlaAlaThrProMetSerLeuProLys 1052
3146 ---CGGTG 3151
1053 SerThrSerThrGlyLeuGlyGluAlaLeuGlyProAlaSerArgArgThrSerSer 1072
3152 CAGACATCCACCGAATG ---GTGACTTCCAGAAGATGCA --- 3190
1073 GlySerAlaGluProGlyAlaAlaHisGluMetLysSerProProSerAlaArgSer 1092
3191 ---ATGGCAACACCGCGCA --- 3208
1093 ProHisSerProTrpSerAlaAlaSerSerTrp ---ThrSerArgArgSerSerArg 1110
3209 ---TTGGCAGCAGCGTGGAGAGTACATCAT ---CATCAGGACCAC 3249
1111 AsnSerLeuGlyArgAlaProSerLeuLysArgSerProSerGlyGluArgArgSer 1130
3250 ATGCTCTTCATCAACAACCCCACTTGCTGTACGGGTACCC --- 3291
1131 LeuLeuSerGlyGlyGln ---GluSerGlnAspGluGluSerSerGluGluGlu 1149
3292 ATTGCTGTGGCGAGTCTGACTTTGAGAACCTCAACACAGAGGATGTTAGCAGCGAG --- 3348
1150 ArgAlaSerProAlaGlySerAspHisArgHisArgGlySerLeuGluArgGluAlaLys 1169
3349 ---TCGGATCTTGAAGCAGCAAGATAAATACTAGATGACACAGCTCCTCTGAAGCA --- 3402
1170 SerSerPheAspLeu ---ProAspThrLeuGlnValProGlyLeuHisArgThrAlaSer 1188
3403 AGCACCATGTATCAACACAGAGTAGAAGAGTCCCT --- 3441
1189 GlyArgLysSerAlaSerGluHisGlnAspCysAsnGlyLysSerAlaSerGlyArgLeu 1208
3441 --- 3441
1209 AlaArgAlaLeuArgProAspAspProProLeuAspGlyAspAlaAspGluGly 1228
3442 ---GTGGAACAGCTGAGGAATACTTGATCCAGATGCTGCTTACAGAAGGT 3492
1229 ---AsnLeuSerLysGlyGluArgValArgAla 1238
3493 TGTGTCCAGCGTTCAAGTCTGCCAGGTCAACATCGAGGAGGCTAGCAGTCTTGG 3552
1239 TrpIleArgAlaLeuLeuProAlaCysTyrLeuGluArgAspSerTrpSerAlaTrpIle 1258
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D	b		3559	- - - - -CTGCGGAAAAACCTGCTTCTCTCATCGTGGAGACCAACTGTGTTT	3600
Q	y		1279	AspHisValVallLeuValIlePheLeuAenCysIleThrIleAlaMetGluArgPro	1298
D	b		3601	GAGACCTTCATCATCTTCATGAATTCCTGTCAGCAGTGCGCCCTTCGAGGACATC	3660
Q	y		1299	LysIleAspProHisSerAlaGluArgIlePheLeuThrLeuSerAentYrIlePheThr	1318
D	b		3661	TACATTGAGCAGAGAAAGACCACCGCACCATCTCGGAATATGCTGCACAAGTCTTCACC	3720
Q	y		1319	AlaValPheLeuAlaGluMetThrValLysValIalalaLeuGlyTrpCysPheGlyGlu	1338
D	b		3721	TATATCTTCCTCGGAGATGTTCTCAAGTGGACAGCCCTATGGCTTCGTC-	3771
Q	y		1339	GlnAlaTyrlLeuArgSerSerTrpAsnValLeuAspGlyLeuLeuValLeuIleSerVal	1358
D	b		3772	--AAGTTCCTCACCAATGCTGGTGTGGCTGGACCTCTCATTTGGCTNNNNNNNN	3828
Q	y		1359	IleAspIleLeuValSerMetValSerAspSerGlyThrylsIleLeuGlyMetLeuArg	1378
D	b		3829	NN	3888
Q	y		1379	ValLeuArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeu	1398
D	b		3889	NNNNNNNNNNNNNNNNNN--NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN	3939
Q	y		1399	LysLeuValValGluThrLeuMetSerSerLeuLysProIleGlyAsnIleValIle	1418
D	b		3940	NNNGTGGTGGTGAATGCCCTGGTGGGGCCCATCCCCTCCATCATGATGTGCTGCTG	3999
Q	y		1419	CysCysAlaPhePheIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPhe	1438
D	b		4000	TGCTCATCTTCGGCTGATTTTCAGCATCATGGCAGTTAACTGTTTGGCGAAAGTAC	4059
Q	y		1439	PheValCysGlnGlyGlu-----AspThrArgAnlleThrAsnLys	1452
D	b		4060	CACTACTGCTTTTAATGAGACTTCGAAATCCGATTTGAAATGAAGATGCAACAATAA	4119
Q	y		1453	SerAspCysAlaGlu-----AlaSerTyrlArgTrpValArgHisLys	1466
D	b		4120	ACTGAATGTGAAAGCTTATGGAGGGGAAACAATACAGATCATGATGGAAGACGTGAAG	4179
Q	y		1467	TyrAsnPheAspAenLeuGlyGlnAlaLeuMetSerLeuPheValLeuAlaSerLysAsp	1486
D	b		4180	ATCAACTTTCACAATGTGGCGCAGGATACCTGGCCCTTCTTCAAGTAGCAACCTCAA	4239
Q	y		1487	GlyTrpValAspIleMetTyrlAspGlyLeuAspAlaValGlyValAspGlnGlnProile	1506
D	b		4240	GGCTGGATGACATCATGTATGACAGCTGTAGATTCGCCGAAGCCTGATGAGCAGCTPAAG	4299
Q	y		1507	MetAsnHisAenProTrpMetLeuLeuTyrlPheIleSerPheLeuLeuIleValAlaPhe	1526
D	b		4300	TATGAGACAAATATCTACATGTACATATTTGTCATCTTCATCTTCGGCTCTCTTC	4359
Q	y		1527	PheValLeuAenMetPheValGlyValValGluAenPheHisLysCysArgGlnHis	1546
D	b		4360	TTACCCCTGAACCTGTTTCATTGGTGTTCATCATTTGATAACTTCAATCAACAAAAGAAAG	4419
Q	y		1547	GlnGluGluGluAlaArgArgArgGluGlu-----LysArgLeuArgArgLeuGlu	1564
D	b		4420	TTCCGAGGTCCAGGACATCTTCATGACCGAAGAACAGAAGAAGTACTACAAATGCCATGAA	4479
Q	y		1565	LysLysArgArgLysAlaGlnCysLysProTyrlTyrlSerAspTyrlSerArgPheArgLeu	1584
D	b		4480	AAGCTGGGCTCAAGAAGACCCACAGAACCCCATTTCCCGCCCCCTTGAACAAAATCCAAGGA	4539
Q	y		1585	LeuValHisLeuCysTyrlSerHisTyrlLeuAspLeuPheIleThrGlyValIleGly	1604
D	b		4540	ATCGTCTTGTATTTGTCACTCACCAAGCCCTTGACATTTGATCATGATGCTCATCTCGC	4599
Q	y		1605	LeuAenValValThrMetAlaMetGluHisTyrlGlnGlnProGlnIleLeuAspGluAla	1624
D	b		4600	CTTAACATGTGACAAATGATGGTGGACAGACACTCAAGACGACAGATGGGAAACATC	4659

Qy	1625	LeuLysIleCysAsnTyrllePheThrValIlePheValLeuGluSerValPheIysLeu	1644
Db	4660	CTCTACTGGGATTAACCTGGGTGGTTGGTATCTCTTCCCTGCTGAGTGTGCTCAAAATG	4719
Qy	1645	ValAlaPheGlyPheArgArg---PhePheGlnAspArgTrrAsnGlnLeuAspLeuAla	1663
Db	4720	-----TTTGGGTGAGGCACACTACTACTTACCATTGGCTGGGAACATCTTCGACTTCGGT	4773
Qy	1664	IleValLeuLeuSerIleMetGlyIleThrLeuGluGluIleGluValAsnAlaSerLeu	1683
Db	4774	GTAGTCATCTCTCCATTGTGGGAATGTTCTCTGGCAGATATA-----ATTGAGAAATAC	4827
Qy	1684	ProIleAsnProThrIleIleArgIleMetArgValLeuArgIleAlaArgValLeuLys	1703
Db	4828	TTTGTITCCCAACCCTATTCCGAGTCATCCGATGGCCGCTATTTGGGCGCATCTTGGCGT	4887
Qy	1704	LeuLeuLysMetAlaValGlyMetArgAlaLeuLeuAspThrValMetGlnAlaLeuPro	1723
Db	4888	CTGATAAAGCGCCAAAGGATTCTGTACCTCTCTTTGGCCTTAATGATGTCTTGGCCT	4947
Qy	1724	GlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPhePheIlePheAlaLeuGly	1743
Db	4948	GCCCTGTTCACATCGCCCTTCTGCTCTTCCCTGTCATGTTCATCTTCCTCCATTTTGGG	5007
Qy	1744	ValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGluGlyLeuGlyArg	1763
Db	5008	ATGTCCAAATTTGCATATGTGAAGCAGAG-----CCTGGTATCGATGAC	5052
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Db	5053	ATGTTCAACTTTGAGACATTTGGCAACAGCATGATCGCTGTTTCAAAATCACACACTCA	5112
Qy	1784	AspAsnTrpAsnGlyIleMetLysAspThrLeuArg-----AspCys-----Asp	1798
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Qy	1799	GlnGlu-----SerThrCysTyrrAsnThrValIleSerProIle	1811
Db	5173	AAGGAACACCAGGAGTGCTTTAAGGGAGATTGTGGGAACCCCTCAGTGGGCATCTTC	5232
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Db	5233	TTCTTTGTAGCTACATCATCATCTCTTCTTCTTAATTTGCTGTGAACATGATCATCTTGCAT	5292
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Qy	1849	LeuGluAlaGluLeuGluLeuMetLysThrLeuSerProGlnProHisSerProLeu	1868
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Qy	1869	GlySerProPheLeuTrpProGlyValGluGlyProAspSerProAspSerProLysPro	1888
Db	5371	-----ATCTGGGGAAGATTGCGAC---CCGATGCCACCCAGTTCATTGAGTAC	5415
Qy	1889	GlyAlaLeuHisProAlaHisAlaArgSerAlaSerHisPheSerLeuGluHisPro	1908
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Qy	1909	ThrMetGlnProHisProThr-----GluLeuProGlyProAspLeuThrValArg	1926
Db	5455	CTCCGAGTGCCCAAGCCAAATACCATTTGAGCTCATCGCTATGGATTCGCAATGGTG---	5511
Qy	1927	LysSerGlyValSerArgThrHisSerLeuProAsnAspSerTyrMetCysArgHisGly	1946
Db	5512	---AGCGGG---GATCGCATCCACTGCTTG-----GACATCTCT-TTTTGGCTTCACCA	5558
Qy	1947	SerThrAlaGluGlyProLeuGlyHisArgGlyTrrPglyLeuProLysAlaGlnSerGly	1966
Db	5559	GCG-----GCTCTGGGAGATACGGGGAGTTGGACATCTCTCGCGCAGCAGATGGA	5609

IMAGE:6413458 5', mRNA sequence.

ACCESSION

BU058818

VERSION

BU058818.1 GI:22499107

KEYWORDS

EST.

SOURCE

Mus musculus (house mouse)

ORGANISM

Mus musculus

REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS

NIH-MGC http://mgc.nci.nih.gov/.

TITLE

National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL

Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Dr. Jim Lin, University of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

This clone was contributed by the Brain Molecular Anatomy Project

(BMAP)

Seg primer: pYX-5.

Location/Qualifiers

1..771

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/clone="IMAGE:6413458"

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/dev_stage="embryo 13.5,14.5,16.5,17.5dpc"

/lab_host="DH10B (T1 phage resistant)"

/clone_lib="NIH BMAP FRO"

/notes="Organ: Brain; Vector: pYX-Asc; Site 1: EcoR I;

Site 2: Not I; The library was constructed according

Bonaldo, Lennon and Soares, Genome Research, 6:791-806,

1996. Denatured RNA was size fractionated on a 1% agarose

gel. First strand cDNA synthesis was primed with oligo-dT

primer containing a Not I site. Double strand cDNA was

size selected according to mRNA size fraction, ligated

with EcoR I adaptor, digested with NotI and then cloned

directionally into pYX-Asc vector. The library tag

sequence located between the Not I site and the polyA tail

is AGCCAGACAG. This library was created for the University

Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the

Developing Mouse Nervous System', supported by National

Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,

program coordinator."

ORIGIN

Alignment Scores:

Pred. No.: 2,87e-74 Length: 771

Score: 1215.50 Matches: 242

Percent Similarity: 98.38% Conservative: 1

Best Local Similarity: 97.98% Mismatches: 4

Query Match: 10.21% Indels: 2

DB: 5 Gaps: 0

US-09-611-257A-37 (1-2266) x BU058818 (1-771)

Qy

1569 LysalaGlnCysLysProTyrTyrSerAspTyrSerArgPheArgLeuValHis 1598

Db

31 GAAGCCAGTGCACCAACCTACTACTCTGACTCTCGGCTTCGGCTCTCGTCCACCAC 90

Qy

1589 LeuCysThrSerHisTyrLeuAspLeuPheIleThrGlyValIleGlyLeuAsnVal 1608

Db

91 CTGTGTACCAACCACTACCTGGACCTCTTCATCATCTGTGTGCATCGGGCTGAATGTGGTC 150

Qy

1609 ThrMetAlaMetGluHisTyrGlnGlnProGlnIleLeuAspGluAlaLeuIleCys 1628

Db

151 ACGATGCCATGGAAACATTACACAGCCCCAGATCTCTGGACAGGCTCTGAAGATCTGC 210

Qy 1629 AsnTyrIlePheThrValIlePheValLeuGluSerValPheLysLeuValAlaPheGly 1648
 Db 211 AACTACATCTTTACCGTCATCTTTGTCTTGAGTCAGTATTCAAACCTTGTGGCCTTCGGC 270
 Qy 1649 PheArgArgPhePheGlnAspArgTTPAsnGlnLeuAspLeuAlaIleValLeuLeuSer 1668
 Db 271 TTCCGCCGGTCTTCCAGGACAGGTGGACAGCTGGACCTGGCTGCTATTGTGCTTCTGTCC 330
 Qy 1669 IleMetGlyIleThrLeuGluGluIleValAsnAlaSerLeuProIleAsnProThr 1688
 Db 331 ATCATGGGCATCACGCTGGAGAGATTGAGTCAATGCTTCACTGCCCATCAACCCACC 390
 Qy 1689 IleIleArgIleMetArgValLeuArgIleAlaArgValLeuLysLeuLysMetAla 1708
 Db 391 ATCATCCGTATCATGAGGGTGTCCCGCATTTGCTCGAGTTCTGAAGCTGTGGAAGATGGCT 450
 Qy 1709 ValGlyMetArgAlaLeuLeuAspThrValMetGlnAlaLeuProGlnValGlyAsnLeu 1728
 Db 451 GTGGGCATGGGGCAGCTGTGGACAGCGTATGACAGGCCCTGCCAGGTGGGGAACCTG 510
 Qy 1729 GlyLeuLeuPheMetLeuLeuPheIlePheAlaAlaLeuGlyValGluLeuPheGly 1748
 Db 511 GGACTTCTCTTCATGCTATTATTTTTCATCTTTGCAGCTCTGGCGCTGGAGCTCTTTGA 570
 Qy 1749 AspLeuGlnCysAspGluThrHisProCysGluGlyLeuGlyArgHisAlaThrPheArg 1768
 Db 571 GACCTGGAGTGTGATGAGACACACCCCTGTGAGGGCTTGGCGCGGCATGCCACCTTTAGG 630
 Qy 1769 AsnPheGlyMetAlaPheLeuThrLeuPheArgValSerThrGlyAspAsnThrPheGly 1788
 Db 631 AACTTTGGTATGGCTTTCTGACCCCTTTCCAGATCTCCACTGGTGACACTGGATGGT 690
 Qy 1789 IleMetLysAspThrLeuArgAspCysAspGlnGluSerThrCysTyrAsnThrValIle 1808
 Db 691 ATTATGAAGCAGACCCCTCCGGACTGTGNACAGAGTC-ACCTGCTACAC-ACCGTCTATC 748
 Qy 1809 SerProIleTyrPheValSer 1815
 Db 749 TCACCCATCTACTCTCGTGTCC 769

RESULT 11

BI05383 LOCUS 990 bp mRNA linear EST 16-OCT-2001
 DEFINITION 603167426F1 NCI_CGAP_Lu33 Mus musculus cDNA clone IMAGE:525383 5',
 mRNA sequence.

ACCESSION BI05383
 VERSION BI05383.1 GI:16167886
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 990)

AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Gilbert Smith, Ph.D.
 CDNA Library Preparation: M. Bento Soares, Ph.D., M. Patima
 Bonaldo, Ph.D.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone Distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
 Plate: LUAM1645 row: d column: 08
 High quality sequence stop: 911.
 Location/Qualifiers
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 /organism="Mus musculus"
 /mol_type="mRNA"

FEATURES

source
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 /organism="Mus musculus"
 /mol_type="mRNA"

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/strain="CZECH II"
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/clone="IMAGE:5255383"
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/lab_host="DH10B (phage-resistant)"
/clone_lib="NCI CGAP Lu33"
/notes="Organ: lung; Vector: pT73D-Pac (Pharmacia) with a
modified polylinker; Site 1: NotI; Site 2: EcoRI; 1st
strand cDNA was prepared from mRNA obtained from pooled
lung tumors with a Not I - oligo(dT) primer [5'].
TGTATCAATCTGAAGTGGAGCGGCGCTCTGTTTCTTTTCTTTT 3').
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not
I and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo."
```

ORIGIN

Alignment Scores:

Pred. No.:	4,32e-74	Length:	990
Score:	1215.50	Matches:	261
Percent Similarity:	83.03%	Conservative:	13
Best Local Similarity:	79.09%	Mismatches:	45
Query Match:	10.21%	Indels:	12
DB:	4	Gaps:	3

US-09-611-257A-37 (1-2266) x BI905383 (1-990)

QY 1805 AsnThrValIleSerProIle-TyrPheValSerPheValLeuThrAlaGlnPheValIle 1824

Db 1 AACACCGTCATCTCACCATCTGCTACTTCTGTCCTGCTGCTGACGGCCCGCTTGCT 60

QY 1824 uValAsnValIleAlaValLeuMetLysHsLeuGluGluSerAsnLysGluAlaLys 1844

Db 61 GGTCAAGTGTCTATAGCGTCTGATGACCATCTGGAGAGAGCAACAAGAGGCCAA 120

QY 1844 sGluGluAlaGluLeuGluAlaGluLeuGluMetLysThrLeuSerProGlnPr 1864

Db 121 GGAGGAGCGGAGTTGGAGGCGGAGCTGGAGTAGAGATGAAGACACTCAGCGCCGAGCC 180

QY 1864 OhSerProLeuGlySerProPheLeuTrpGlyValGluGlyProAspSerProAs 1884

Db 181 CCATCTCCCGTGGGAGCCCTTCTCTGTCGCTGGGTGGAGGTGTAATGACCTTGA 240

QY 1884 pSerProLysProGlyAlaLeuHsProAlaAlaHsAlaArgSerAlaSerHis---Ph 1903

Db 241 CAGCCCTAAGCTGGGGTCTCACACACACCGCCACATTGGAGCAGCCTCTTCAGGCTT 300

QY 1903 eSerLeuGluHisProThrMetGlnProHisProThrGluLeuPro-----GlyPr 1920

Db 301 CTCCCTTGAGCACCCACGATGGTACCTCACACTGAGGAGGGCCAGTCCCTTAGGACC 360

QY 1920 OhSplLeuThrValArgLysSerGlyValSerArgThrHisSerLeuProAsnAspSe 1940

Db 361 AGACTGTGCTGATGTGAGGAAGTGTGGTTCAGCCGGACACACTCTCTGCCCATGACAG 420

QY 1940 rTyMetCysArgHisGlySerThrAlaGluGlyProLeuGlyHisArgGlyTrpGlyLe 1960

Db 421 CTACATGTGCCCATGGGACACTGCGGAGAGATCCCTAGGACACAGGGGCTGGGGCT 480

QY 1960 uProLysAlaGlnSerGlySerValLeuSerValHisSerGlnProAlaAspThrSerTy 1980

Db 481 CCCCCAAGGCCAGTCAGGCTCCATCTGCTGTTTCACTCCCAACAGCAGACACAGCTG 540

QY 1980 rIleLeuGlnLeuProLysAspAlaProHisLeuLeuGlnProHisSerAlaProThrTr 2000

Db 541 CATCTTACAGCTTCCCAAGATGACACTATCTCTCCAGCTCATGGGGCTCCACCTG 600

QY 2000 pGlyThrIleProLysLeuProProGlyArgSerProLeuAlaGlnArgProLeuAr 2020

Db 601 GGGCGGCATCTCAACTACCCACCTGGCGCTCCCTCTGGCTCAGAGCCCTCTCAG 660

QY 2020 gArgGlnAlaAlaIleArgThrAspSerLeuAspValGlnGlyLeuGlySerArgGluAs 2040

Db 661 GCGCCAGGCAGCAATAAGGACTGACTCCCTGGAGCTGCGAGGCTTGGTAGCCGGAAGA 720

QY -2040 pLeuLeuAlaGluValSerGlyProSerProProLeuAlaArgAlaTrpSerPheTrpG 2060

Db 721 CTTGTGTGACAGGTGAGTGGGCTCTCTGCTCTGACCCGCTCTCA-TCTTCTGGGG 779

QY 2060 yGln---SerSerThrGlnAlaGlnHsSer-ArgSerHisSerLysLysLeuSerIys- 2078

Db 780 GCGGTCGAGCATCTGTCGAGCAGGCGCTCCGGGCGAGCCAGAGCAAAAGTCTCCAAG 839

QY 2079 HisMetThrProPro-AlaProCysProGlyPro-GluProAsnTrpGlyLysGlyProP 2098

Db 840 CACATCCGCTGCCAGGCGCTTGGCCAGGCGCTGGAAACCCAGGCTGGGCCAGGACCTC 899

QY 2098 roGlu-ThrArgSerSerLeuGluLeuAspThrGluLeuSerTrpIleSerGlyAspLeu 2117

Db 900 AAGAGAACAGAAACAGTAAACTTGGACCGGAGCTGAAGTGGGATCATGGGGAATC 959

QY 2118 LeuProProGlyGlyGln 2123

Db 960 TTGGCAGAAGTCGGAAGA 977

RESULT 12

CF742232

LOCUS

DEFINITION

UI-M-HB0-clk-j-06-0-UI.r1 NIH_BMAP_HB0 Mus musculus cDNA clone

IMAGE:30619901 5', mRNA sequence.

CF742232

VERSION

CF742232.1 GI:37638571

KEYWORDS

EST.

SOURCE

Mus musculus (house mouse)

ORGANISM

Mus musculus

REFERENCE

1. (bases 1 to 784)

AUTHORS

NIH-MGC <http://mgs.nci.nih.gov/>.

TITLE

National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL

Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.

Email: cgabbs@mail.nih.gov

Tissue Procurement: Dr. James Lin University of Iowa

CDNA Library preparation: Dr. M. Bento Soares, University of Iowa

CNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Distribution information can be found at

<http://genome.uiowa.edu/distribution/mousefl.html>

This clone was contributed by the Brain Molecular Anatomy Project

(BMAP)

Seq primer: pYX-5

Location/Qualifiers

1. .784

/organism="Mus musculus"

/mol_type="mRNA"

/strain="C57BL/6"

/db_xref="taxon:10090"

/clone="IMAGE:30619901"

/tissue_type="whole eye"

/dev_stage="embryo 12.5,13.5,14.5 dpc"

/lab_host="DH10B (T1 phage resistant)"

/clone_lib="NIH_BMAP_HB0"

/notes="Organ: Eye; Vector: pYX-Asc; Site 1: EcoR I; Site 2: Not I; The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is TTATGTAGT. This library was created for the University of Iowa Brain Anatomy Project (BMAP). Gene Discovery in the

ORIGIN		Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH)."		UI-M-EMO-caz-e-20-0-UI.r1 NIH_BMAP_EWO Mus musculus cDNA clone IMAGS:6419323 5', mRNA sequence.	
Alignment Scores:		Pred. No.: 4.78e-74 Length: 784		BU709095	
Score:		1212.50 Matches: 243		EST.	
Percent Similarity:		95.40% Conservative: 6		Mus musculus (house mouse)	
Best Local Similarity:		93.10% Mismatches: 10		Mus musculus	
Query Match:		10.19% Indels: 2		Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
DB:		7 Gaps: 1		1 (bases 1 to 810)	
US-09-611-257A-37 (1-2266) x CF742232 (1-784)				NIH-MGC http://mgc.nci.nih.gov/	
Qy		937 SerSerTrpAlaLeuValPheIleAlaLeuMetThrPheGlyAsnTrpValLeuPhe		National Institutes of Health, Mammalian Gene Collection (MGC)	
Db		2 TCATCTTGGGCTGCTTTACTTTCATCGCCCTCATGACTTTTGGCAACTACGTCCTTT		Unpublished (1999)	
Qy		957 AsnLeuValAlaIleLeuValGluGlyPheGlnAlaGluGluIleSerLysArgGlu		Contact: Robert Strausberg, Ph.D.	
Db		62 AACCTGCTTGTGGCCATTCTGTGGAGGGTTTCAGGACAGAGAAATCGCAACCGGAA		Email: cgabs-remail.nih.gov	
Qy		977 AspAlaSerGlyGlnLeuSerCysIleGlnLeuProValAspSerGln-GlyGlyAspAl		Tissue Procurement: Dr. James Lin, University of Iowa	
Db		122 GATACGAGTGGACAGTTAAGCTGTATTTCAGTGCCTGTCACTCCAGGGGAGGATGC		cDNA Library preparation: Dr. M. Bento Soares, University of Iowa	
Qy		996 aAsnLysSerGluSerGluProAspPheSerProSerLeuAspGlyAspArg		cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa	
Db		182 CACCAAGCTGAGTCAGAGCCTGATTCTTTTCCGCCAGTGTGATGCTGATGGGACAG		DNA Sequencing by: Dr. M. Bento Soares, University of Iowa	
Qy		1016 gLysLysCysLeuAlaValSerLeuGlyGluHisProGluLeuArgLysSerLeu		Clone Distribution: MGC clone distribution information can be	
Db		242 GAAGAAGCGCTTGGCCCTGTGGCTTGGGAGAACACTCGGAACACTACGAAAGACCTTT		found through the I.M.A.G.E. Consortium/LINL at:	
Qy		1036 uProProLeuIleHisThrAlaAlaThrProMetSerLeuProLysSerThrSerTh		http://image.llnl.gov	
Db		302 GCACCTCTCATCTACACAGCTGTACACGATGTCTACTGCCCAAGAGCTCCAGCAC		This clone was contributed by the Brain Molecular Anatomy Project	
Qy		1056 rGlyLeuGlyGluAlaLeuGlyProAlaSerArgArgThrSerSerSerGlySerAla		(BMAP)	
Db		362 AGGTGTGGGGAGCACTGGGCTCTGGCTCTCGCCGACCAAGTAGCAGTGGTCCGCTGA		Seq primer: PYX-5.	
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Db		422 GCCTGGAACTGCCCATCATGAGATGAATCACGCCCAAGTCCCGAAGCTCCCGCACAG		1. 810	
Qy		1115 rProTrpSerAlaAlaSerTrpThrSerArgArgSerSerArgAsnSerLeuGlyAr		/organism="Mus musculus"	
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Qy		1195 u 1195		Site: Not 1; the library was constructed according to	
Db		782 A 782		Ronald, Lennon and Soares, Genome Research, 6:791-806,	
RESULT 13				1996. Denatured mRNA was size fractionated on a 1% agarose	
BU709095				gel. First strand cDNA synthesis was primed with an	
LOCUS				oligo-dT primer containing a Not I site. Double stranded	
				cDNA was size selected according to mRNA size fraction,	
				ligated with EcoR I adaptor, digested with Not I, and then	
				sequenced directionally into PYX-Asc vector. The library tag	
				sequence located between the Not I site and the polyA	
				tail, is GTGGTGGAA. This library was created for the	
				University of Iowa Mouse Brain Molecular Anatomy Project	
				(BMAP): 'Gene Discovery in the Developing Mouse Nervous	
				System', supported by National Institutes of Mental Health	
				(NIMH), Hemin Chin, Ph.D., program coordinator."	
		ORIGIN	Alignment Scores:	Pred. No.: 2.79e-72 Length: 810	
		Qy	Score:	1187.50 Matches: 244	
		Db	Percent Similarity:	90.77% Conservative: 2	
		Qy	Best Local Similarity:	90.04% Mismatches: 6	
		Db	Query Match:	9.98% Indels: 22	
		Qy	DB:	5 Gaps: 1	
		US-09-611-257A-37 (1-2266) x BU709095 (1-810)			
		Qy	1358 ValIleAspIleLeu-ValSerMetValSerAspSerGlyThrLysIleLeuGlyMetLe	1377	
		Db	1 GTCATCGACATCTGTGTGTCATGTCCTCTGACAGCGGCACCAAGATTCCTCGCATGCT	60	
		Qy	1377 uArgValLeuArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnG1	1397	
		Db	61 GAGGTGTCTGGGTCTGTGGGACCTTACCTACCTCAGGTTCATCAGCGCGGCCAGGG	120	
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	/note="Organ: pancreas; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected by ligation for average insert size 1.8kb. Library constructed by Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
ORIGIN	
Alignment Scores:	Length: 736
Pred. No.:	3,56e-72
Score:	1185.00
Percent Similarity:	97.15%
Best Local Similarity:	95.93%
Query Match:	9.95%
DB:	4
	US-09-611-257A-37 (1-2266) x B1160856 (1-736)
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DB	2 CTGTGTCACCGGATCATCCCAAGATGTTCCACCACGCTGCTTGTTCATCATCTTC 61
QY	1288 LeuAsnCysIleThrIleAlaMetGluArgProLysIleAspProHisSerAlaGluArg 1307
DB	62 CTTAACTGCATCACCATCGCCATGGAGCGCCCAAAATTGACCCACGAGCTGAACGC 121
QY	1308 IlePheLeuThrLeuSerAsnTyrIlePheThrIleValPheLeuAlaGluMetThrVal 1327
DB	122 ATCTTCTCTGACCTCTCCAAATTACATCTTCACCGAGTCTTCTGCGTGAATACAGATG 181
QY	1328 LysValValAlaLeuGlyTyrCysPheGlyGluGlnAlaTyrLeuArgSerSerTrpAsn 1347
DB	182 AAGGTGGTGGCACTGGGCTGGTCTTCGGGAGCAGGCGTACCTCGCGAGCATGTGGAAC 241
QY	1348 ValLeuAspGlyLeuLeuValLeuIleSerValIleAspIleLeuValSerMetValSer 1367
DB	242 GTGCTGGACGGGCTGTGGTGTCTCATCTCCGTCATCGACATTCGTGGTGTCCATGTCCT 301
QY	1368 AspSerGlyThrIleValLeuGlyMetLeuArgValLeuArgLeuLeuArgThrLeuArg 1387
DB	302 GACAGCGGCACCAAGATCTCTGGGCATGCTGAGGGTGTCTGGGCTGCTCGGACCTGGCC 361
QY	1388 ProLeuArgValIleSerArgAlaGlnGlyLeuLysLeuValValGluThrLeuMetSer 1407
DB	362 CCCTCAGGGTGATCAGCCGGCGCAGGGGCTGAAGCTGGTGGAGACGCTGATGTC 421
QY	1408 SerLeuLysProIleGlyAsnIleValIleCysCysAlaPhePheIleIlePheGly 1427
DB	422 TCACCTGAAACCCCATCGGCAACATTGTAGTCACTCTGCTGTGCCTTCTTCATCATTTCCG 481
QY	1428 IleLeuGlyValGlnLeuPheLysGlyLysPhePheValCysGlnGlyGluAspThrArg 1447
DB	482 ATCTTGGGGTGCAGCTCTTCAAGGAAAGTTTTCGTGTGCGAGCGGAGGATACCAAG 541
QY	1448 AsnIleThrAsnLysSerAspCysAlaGluAlaSerTyrArgTrpValArgHisIleTyr 1467
DB	542 AACATCACCAATAAATCGGACTGTGCGAGCGCAGGTACCGGTGGGTCCGGCACCAAGTAC 601
QY	1468 AsnPheAspAsnLeuGlyGlnAlaLeuMetSerLeuPheVal-LeuAlaSerLysAspG 1487
DB	602 AACTTTGACAACTTGGCCAGGCGCTGATGCTCCCTGTACGCATATGCGCTTCCAAGGATGG 661
Db	
121	GCTGAAGCTGGTGTAGAGACTCTGATGTCATCCCTCAAACCCATGGCAACATTTGGT 180
QY	1417 lIleCysCysAlaPhePheIlePheGlyIleLeuGlyValGlnLeuPheLysGly 1437
Db	181 CATCTGCTGGCTCTTCTATCATATTTTGAAATCTTGGGGTGCAGCTCTTCAAGGGAA 240
QY	1437 sPhePheValCysGlnGlyGluAspThrArgAsnIleThrAsnLysSerAspCysAlaG 1457
Db	241 GTTCTTGTGTGTGTCAGGGTGAGACACCAAGAACATCACTAAACAATCCGACTGTGCTGA 300
QY	1457 uAlaSerTyrArgTrpValArgHisIleValPheAspAsnLeuGlyGlnAlaLeuMe 1477
Db	301 GGCCAGTTACCGTGGTCCGGCACCAAGTACAACTTTGACAACTCTGGGCGAGCTCTGAT 360
QY	1477 tSerLeuPheValLeuAlaSerLysAspGlyTyrValAspIleMetTyrAspGlyLeuAs 1497
Db	361 GTCCCTGTTTGTCTGCTCCAGGATGGCTGGTGTGACATCATGTATGATGGACTGGA 420
QY	1497 pAlaValGlyValAspGlnProlMetAsnHisAsnProTyrMetLeuLeuTyrPh 1517
Db	421 TGCTGTGGAGTGGACAGCAGCCCATCATGAACCAACACCTTGGATGCTGCTCTACTT 480
QY	1517 eIleSerPheLeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValValVa 1537
Db	481 CATCTCTCTCTCTCATCTGCTGCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
QY	1537 lGluAsnPheHisLysCysArgGlnHisGlnGluGluGluAlaArgArgGluGlu 1557
Db	541 GGAGACTTCCATAAGTGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 600
QY	1557 uLysArgLeuArgArgLeuGluLysLysArgArg 1568
Db	601 GAAGCGACTAAAGAGGCTGGGAGAAAGAGAGAGAAATCTAATGTTGACGATGAATTGC 660
QY	1569 -----LysAlaGlnCysLysPheProTyrTyrSerAspTyr 1579
Db	661 TTCGGCAGCTCAGCCAGCGCTGCGTCAGAGGCCAGTGCANACCTTACTACTCTGACTA 720
QY	1579 sSerArgPheArgLeuLeuValHisHisLeuCysThrSerHisTyrLeuAspLeuPheI 1599
Db	721 CTCGGCTTCGGCTCC-CGTCACACCTGTGTACAGC-CACTACTGNA-CTCTTCAT 777
QY	1599 eThrGlyValIleGlyLeuAsnValValThr 1609
Db	778 CACTGGTGTATCGGCTGAATGTGTACG 808
RESULT 14	
LOCUS	B1160856
DEFINITION	602864778P1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:5019018 5', mRNA sequence.
ACCESSION	B1160856
VERSION	B1160856.1 GI:14620857
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini, Hominidae; Homo.
REFERENCE	1 (bases 1 to 736)
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/ .
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished (1999)
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgabbs-r@mail.nih.gov Tissue Procurement: ATCC cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: L1CM1833 row: k column: 19 High quality sequence stop: 710.

Qy 1487 yTrpValAspIleMetTyrAspGly-LeuAspAlaValGlyValAspGlnProIleM 1507
Db 662 TAGGGTGACATCATGATGCGTGGATGCTGTGGGGCGTGGACGAGCCCATCA 721
Qy 1507 etAsnHisAspPro 1511
Db 722 TGAACCAACACCT 735

RESULT 15
BI736618
LOCUS 603361089f1 NIH_MGC_94 Mus musculus CDNA clone IMAGE:5367862 5',
DEFINITION mRNA sequence.

ACCESSION BI736618
VERSION BI736618.1 GI:15713631
KEYWORDS EST.

SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 939)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov

Tissue Procurement: The Cepko Laboratory
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LHAM1936 row: b column: 23
High quality sequence stop: 853.

FEATURES

Location/Qualifiers

1..939
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:5367862"
/tissue_type="retina"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_94"
/note="Organ: eye; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 3.3 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:
Pred. No.: 7.31e-72 Length: 939
Score: 1183.00 Matches: 247
Percent Similarity: 84.69% Conservative: 13
Best Local Similarity: 80.46% Mismatches: 41
Query Match: 9.94% Indels: 9
DB: 4 Gaps: 3

US-09-611-257A-37 (1-2266) x BI736618 (1-939)

Qy 1929 GlyValSerArgThrHisSerLeuProAsnAspSerTyrMetCysArgHisGlySerThr 1948
Db 3 GGTGTACGCGGACACACTCTCTGCCCAATGACAGCTACATGTCCCGCAATGGGAGCACT 62
Qy 1949 AlaGluGlyProLeuGlyHisArgGlyTTrpGlyLeuProLysAlaGlnSerGlySerVal 1968
Db 63 GCCAGAGATCCCTTAGGACACAGAGGGCTGGGGGTCTCCCAAGCCAGTCCAGGCTCCATC 122
Qy 1969 LeuSerValHisSerGlnProAlaAspThrSerTyrTrpIleLeuGlnLeuProLysAspAla 1988
Db 123 TTGTCTGTCTACTCCCAACACGACAGACACCACTGCTGCTTACAGCTTCCCAAGATGCA 182

Qy 1989 ProHisLeuLeuGlnProHisSerAlaProThrTrpGlyThrIleProLysLeuProPro 2008
Db 183 CACTATCTGCTCCAGCCTCATGGGGCTCCCACTGGGGCGCCATCCCTAAACTACCCCA 242
Qy 2009 ProGlyArgSerProLeuAlaGlnArgProLeuArgArgGlnAlaAlaIleArgThrAsp 2028
Db 243 CTTGGCCCTCTCCCTCTGGGCTCAGAGGCTCTCAGGCGCCAGGCGCAGATNAGACTGAC 302
Qy 2029 SerLeuAspValGlnGlyLeuGlySerArgGluAspLeuAlaGluValSerGlyPro 2048
Db 303 TCCTTGACGCTGCAGGCGCTGGGTAGCCGGAAGACCTGTTGTCCAGAGGTGAGTGGGCC 362
Qy 2049 SerProProLeuAlaArgAlaTyrSerPheTrpGlyGlnSerSerThrGlnAlaGlnGln 2068
Db 363 TCCTGCGCTCTGACCCGCTCTCATCTCTGGGGCGGGTCGAGCATCTCCAGGTGACGAC 422
Qy 2069 HisSerArgSerHisSerLysIleSerLysHisMetThrProProAlaProCysProGly 2088
Db 423 CGTCCGGCAGCCAGACCAAGTCTCCAGACACATCCGCTCGCAGGCCCTTGGCCAGGC 482
Qy 2089 ProGluProAsnTrpGlyLysGlyProProGluThrArgSerSerLeuGluLeuAspThr 2108
Db 483 CTGGAACCCAGCTGGGCAAGGACCTCAAGAGACACCAAGAGCAGCTTAGAGCTGGACACG 542
Qy 2109 GluLeuSerTrpIleSerGlyAspLeuLeuProProGlyGlnGlnGluProProSer 2128
Db 543 GAGCTGAGCTGGATTTTCAGGAGACCTCTCTG---CCCAAGCAGTTCAGGAAGAACCCCTGTCC 599
Qy 2129 ProArgAspLeuLysLysCysTyrSerValGluAlaGlnSerCysGlnArgArgProThr 2148
Db 600 CCACGGGACTTGAATAAATGCTACAGTGTAGAGGCCAGAGCTCCCGGCGGAGGCTGGG 659
Qy 2149 SerTrpLeuAspGluGlnArgArgHisSerIleAla-ValSerCysLeuAspSerGlySe 2168
Db 660 TCCTGGCTAGACGAACAGAGAGAGACACTCCATCGCTTGTTCAGTGTCTGGACAGCGGCTC 719
Qy 2168 rGlnProHisLeuGlyThrAspProSerAsnLeu-GlyGlyGlnProLeuGlyGlyProG 2188
Db 720 CCAGCCCCGCTATGTCCAAGCCCCCTCAAGCCTCGGGGGGCCAACCTCTGGGGGCCCTTGG 779
Qy 2188 LysSerArgProLysLysLysLeuSerProProSerIleThrIleAspProProGluSerG 2208
Db 780 GGAGCCGCGCTTAGAAAAAACTCAG-CCACCCAGTATCTCTATAGACCCCCCGGAGAGCA- 837
Qy 2208 InGlyProArgThrProProSerProGlyIleCysLeuArgArgAlaPro-SerSer 2227
Db 838 --GGACCTCGGGCCCCCATGCAGTCT-GGCGTCTGCC-AGGAGGAGG---CCGGCGCAAG 890
Qy 2228 AspSerLysAspPro 2232
Db 891 GACTCGAAGGATCCT 905

Search completed: April 16, 2005, 13:08:47
Job time : 14407 secs

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